Parkinson's Disease Alleles Inquiry

Significance -log pval	SNP	allele	Your Genotype Ref/FM	Genes	study
72.4	rs356182[i]	C	g/ gA predicted type and rate of physical decline in patients with Parkinson's disease	SNCA	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. Infinome. *Chinese:* Subjects carrying GG/AG genotype - (tremors but slows progression) had an increased risk compared with the AA carriers (OR=1.162, 95% CI: 1.143-2.274, P=0.006). Among all the genotypes of rs356182, GG genotype showed the strongest association... SNPedia Articles. MJFox weighting.
64.22	rs356219[ii]		G/ GA	SNCA	Comprehensive research synopsis and systematic meta-analyses in Parkinson's disease genetics: The PDGene database. "This is how we can start thinking about precision

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					medicine in action," said the study's senior author... LINK. Defects in SNCA have been implicated in the pathogenesis of Parkinson disease. SNPedia.
47.7	rs356219[iii]	C	normal	MAPT	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease.
46.7	rs356219[iv]	G	G/ GA Defects in SNCA have been implicated in the pathogenesis of Parkinson disease.	SNCA	Imputation of sequence variants for identification of genetic risks for Parkinson's disease: a meta-analysis of genome-wide association studies.
43	rs34311866[v]	G	normal	TMEM175, GAK, DGKQ	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. ...which is 20 orders of magnitude more significant than any other SNP in the region. Because TMEM175 is a lysosomal gene that has been shown to influence α-synuclein phosphorylation and

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					autophagy...
34.1	rs356220[vi]		T/ TC	SNCA	Meta-analysis of Parkinson's disease: identification of a novel locus, RIT2. Near rs 356219.
29	rs35749011[vii]	A	normal	GBA, SYT11	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. MJFox decreases.
28	rs2942168[viii]	G	normal	MAPT	Imputation of sequence variants for identification of genetic risks for Parkinson's disease: a meta-analysis of genome-wide association studies.
27.7	rs34637584[ix]	A	normal	LRRK2	Web-based genome-wide association study identifies two novel loci and a substantial genetic component for Parkinson's disease.
26.7	rs1442190[x]		normal Censored	LRRK2	Genome-wide mapping of IBD segments in an Ashkenazi PD cohort identifies associated haplotypes. Mutations in this gene have been associated with Parkinson disease-8

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20.7	rs12637471[xi]	G	G/GA	MCCC1	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease.
20.52	rs34778348[xii]		normal	LRRK2	Comprehensive research synopsis and systematic meta-analyses in Parkinson's disease genetics: The PDGene database. concluded that the odds ratio for [[Parkinson's disease]] was 2.1
20.3	rs416[xiii]	G	A/GG	GBA	Web-based genome-wide association study identifies two novel loci and a substantial genetic component for Parkinson's disease. Mutations in this gene cause Gaucher disease, a lysosomal storage disease characterized by an accumulation of glucocerebrosides
20	rs1474055[xiv]	T	normal	STK39	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. 2 new loci SNP. suggesting that this kinase may serve as an

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					intermediate in the response to cellular stress.
19.05	rs6430538[xv]	C	c/Tc	ACMSD, TMEM163	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. Meta new locus TIR2
18.7	rs356220[xvi]	T	T/ TC	SNCA	Web-based genome-wide association study identifies two novel loci and a substantial genetic component for Parkinson's disease. SNCA_ rs356220 was associated with both Sporadic-PD (OR=1.37, P=110 -9) and Familial-PD
17.05	rs11724635[xvii]	A	C/ CA	BST1	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. INTERPRETATION: These data provide an insight into the genetics of Parkinson's disease and the molecular cause of the disease and could provide future targets

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					for therapies.
16.52	rs199515[xviii]		G/CC Was G/GC On 1 2 23 was normal Mutated overnight! ! 12/23/22 Morphing polymorphism	WNT3	Meta-analysis of Parkinson's disease: identification of a novel locus, RIT2. All results included the principal component that accounts for **Ashkenazi** ancestry, which controls for the increased incidence of GBA mutations in the Ashkenazi population. Moreover, when individuals within the Ashkenazi cluster were excluded from the Discovery Sample and the Replication Sample, the association to rs12726330 and to E326K remained at genome-wide significance... MJFox censors.
16.15	rs11931074[xix]		normal	SNCA	Genome-wide association study identifies common variants at four loci as genetic risk factors for Parkinson's disease.
16	rs11724635[xx]	A	C/CA	BST1	Imputation of sequence variants for identification of genetic risks for Parkinson's disease: a meta-analysis of genome-wide association studies. BST1 expression is enhanced in bone marrow stromal cell lines derived from

Significance -log pval	SNP	allele	Your Genotype Ref/FM	Genes	study
					patients with rheumatoid arthritis. MJFox decreases.
15.7	rs393152[xxi]	A	normal	MAPT, C17orf69, KIAA1267, LOC644246	Genome-wide association study reveals genetic risk underlying Parkinson's. disease. Our findings identify the tau-associated MAPT locus as a site of genetic overlap between AD and PD, and extending prior work, we show that the MAPT region increases risk of Alzheimer's neurodegeneration. associated with several neurodegenerative disorders such as Alzheimer's disease, Pick's disease, MJFox censors
15.7	rs2736990[xxii]	G	G/ GA	SNCA	Genome-wide association study reveals genetic risk underlying Parkinson's disease. Defects in SNCA have been implicated in the pathogenesis of Parkinson disease. Slightly increased risk of developing Parkinson's Disease.

Significance -log pval	SNP	allele	Your Genotype Ref/FM	Genes	study
15.7	rs823118[xxiii]	T	C/TC	NUCKS1, RAB7L1	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. two putative nuclear localization signals, and a basic DNA-binding domain.
15.05	rs356220[xxiv]	T	T/ TC	SNCA	Dissection of the genetics of Parkinson's disease identifies an additional association 5' of SNCA and multiple associated haplotypes at 17q21. MAPT gene mutations have been associated with several neurodegenerative disorders such as Alzheimer's disease, Pick's disease, frontotemporal dementia, cortico-basal degeneration and progressive supranuclear palsy.
14.22	rs1491942[xxv]		normal	LRRK2	Comprehensive research synopsis and systematic meta-analyses in Parkinson's disease genetics: The PDGene database.
14	rs199533[xxvi]	G	normal	NSF	Genome-wide association study

Significance -log pval	SNP	allele	Your Genotype Ref/FM	Genes	study
					reveals genetic risk underlying Parkinson's disease. Location: 17:46751565
13.7	rs32588205[xxvii]		GAP	HLA-DRB5	Imputation of sequence variants for identification of genetic risks for Parkinson's disease: a meta-analysis of genome-wide association studies. It plays a central role in the immune system by presenting peptides derived from extracellular proteins. US and European cohorts identified chr6: rs32588205 A/G SNP located in the intronic region of HLA-DRB5 locus with augmented risk for PD under an additive model.
13.52	rs12185268[xxviii]	A	normal	MAPT	Web-based genome-wide association study identifies two novel loci and a substantial genetic component for Parkinson's disease.
13.3	rs76904798[xxix]	T	normal	LRRK2	Large-scale meta-

Significance -log pval	SNP	allele	Your Genotype Ref/FM	Genes	study
					analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. Mutations in this gene have been associated with Parkinson disease-8.
13.22	rs1491942[xxx]		normal	LRRK2	Imputation of sequence variants for identification of genetic risks for Parkinson's disease: a meta-analysis of genome-wide association studies. Mexican Mestizo subjects, found a significant risk association for the variant rs1491942 in LRRK2.
13.15	rs1555399[xxxi]		T/AA	TMEM229B	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease.
12.52	rs12817488[xxxii]	A	normal	CCDC62, HIP1R	Imputation of sequence variants for identification of genetic risks for Parkinson's disease: a meta-analysis of genome-wide association studies. increased risk of PD in Asian and Caucasian populations.

Significance -log pval	SNP	allele	Your Genotype Ref/FM	Genes	study
					/huntingtin interacting protein 1 related (HIP1R) as a risk factor for PD. We conducted a case-control study to evaluate the possible association between rs12817488 and PD in Chinese people
12.4	rs117896735 chr10:119776815	A	g/gA	INPP5F	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease.
12	rs9275326[xxxiii]	C	normal	HLA-DQB	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease.
12	rs199347[xxxiv]	T	normal	GPNMB	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease.
11.7	rs947211[xxxv]		A/GA	SLC45A3, PARK16, PM20D1, NUCKS1, RAB7L1, SLC4	Genome-wide association study identifies common variants at four loci as genetic risk factors for Parkinson's disease. There was a higher expression of G allele in PD patients versus the controls (GWAS) have identified several

Significance -log pval	SNP	allele	Your Genotype Ref/FM	Genes	study
					single-nucleotide polymorphisms (SNPs) at the *PARK16* locus 5that can modulate the risk of Parkinson's disease (PD)
11.7	rs14235[xxxvi]	A	G/GA	BCKDK, STX1B	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease.
11.52	rs11248060[xxxvii]		normal	GAK, DGKQ	Comprehensive research synopsis and systematic meta-analyses in Parkinson's disease genetics: The PDGene database. SNPedia Articles:
11.4	rs34372695[xxxviii]	T	normal	SYT11	Imputation of sequence variants for identification of genetic risks for Parkinson's disease: a meta-analysis of genome-wide association studies. SNPedia Articles:
11.4	rs6599388[xxxix]	T	normal	GAK	Imputation of sequence variants for identification of genetic risks for Parkinson's disease: a meta-analysis of genome-wide association studies. neither rs6599388 nor rs142821586

Significance -log pval	SNP	allele	Your Genotype Ref/FM	Genes	study
					was associated with PD.
11.22	rs11060180[xl]	A	A/GG	CCDC62	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease.
11.15	rs8070723[xli]		normal	MAPT	Dissection of the genetics of Parkinson's disease identifies an additional association 5' of SNCA and multiple associated haplotypes at 17q21. SNPedia Articles.
11.1	rs11711441[xlii]	G	g/gA	MCCC1, LAMP3	**Imputation of sequence variants for identification of genetic risks for Parkinson's disease: a meta-analysis of genome-wide association studies.** MCCC1/LAMP3 reduces risk of sporadic Parkinson's disease in Han Chinese
11.1	rs12456492[xliii]	G	g/gA	RIT2	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for

Significance -log pval	SNP	allele	Your Genotype Ref/FM	Genes	study
11	rs329648[xliv]	T	T/TC	MIR4697	Parkinson's disease. SNPedia Articles. Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease.
11	rs2414739[xlv]	A	g/AA	VPS13C	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease.
10.52	rs356220[xlvi]	T	T/TC	SNCA	Common genetic variation in the HLA region is associated with late-onset sporadic Parkinson's disease. Defects in SNCA have been implicated in the pathogenesis of Parkinson disease SNPedia Articles.
10.52	rs2395163[xlvii]		T/CC 1/2/23 normalized "reached highest scores" Morphing Polymorphism!	LOC642072	Meta-analysis of Parkinson's disease: identification of a novel locus, RIT2. Thus, the PD-associated SNPs in HLA might represent two disease-associated elements, which in our study are best tagged by rs3129882 and by

Significance -log pval	SNP	allele	Your Genotype Ref/FM	Genes	study
					rs9268515 and/or rs2395163. SNPedia Articles. MJFox Decreases.
10.52	rs356220[xlviii]	T	T/TC	SNCA	Identification of a novel Parkinson's disease locus via stratified genome-wide association study. SNPedia Articles.
10.52	rs6812193[xlix]	C	normal	SCARB2, FAM47E	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. SNPedia Articles.
10.52	rs8118008[l]	A	a/Ga	DDRGK1	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease.
10.3	rs6532194[li]		normal	SNCA	Comprehensive research synopsis and systematic meta-analyses in Parkinson's disease genetics: The PDGene database.
10.22	rs11158026[lii]	C	C/TT Mutations in this gene are associated with malignant hyperphenylalaninemia and dopa-responsive dystonia.	GCH1	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. allele carriers show a slight increase in risk

Significance -log pval	SNP	allele	Your Genotype Ref/FM	Genes	study
					for Parkinson's disease,
9.7	rs3129882[liii]	G	normal G/AA Morphing polymorphism. It plays a central role in the immune system	HLA-DRA	Common genetic variation in the HLA region is associated with late-onset sporadic Parkinson's disease. SNPedia Articles.
9.7	rs12456492[liv]		normal	RIT2	Meta-analysis of Parkinson's disease: identification of a novel locus, RIT2. SNPedia Articles.
9.52	rs10513789[lv]	T	T/GT	MCCC1, LAMP3	Web-based genome-wide association study identifies two novel loci and a substantial genetic component for Parkinson's disease. SNPedia Articles.
9.4	rs2102808[lvi]	G	normal Increases Risk	STK39	Imputation of sequence variants for identification of genetic risks for Parkinson's disease: a meta-analysis of genome-wide association studies. common in complete genomics
9.4	rs2338971[lvii]	C	t/CC Reduces Risk	HUSEYO	Identification of a novel Parkinson's disease locus via stratified genome-wide association study. GWAS Article. Censored.

Significance -log pval	SNP	allele	Your Genotype Ref/FM	Genes	study
9.3	rs3129882[lviii]	G	G/AA Reduces risk of Parkinson's disease.	HLA	Identification of a novel Parkinson's disease locus via stratified genome-wide association study. SNPedia Articles. The brains of individuals with Parkinson's disease show upregulation of DR antigens and the presence of DR-positive reactive microglia, and nonsteroidal anti-inflammatory drugs reduce Parkinson's disease risk. Censored MJFox
9.3	rs10797576[lix]	T	C/TC Increases Risk	SIPA1L2	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease.
9.3	rs2338971[lx]	C	*t/CC* Increases Risk	HUSEYO	Identification of a novel Parkinson's disease locus via stratified genome-wide association study. Censored.
9.1	rs6812193[lxi]	C	*normal decreases risk*	SCARB2	Web-based genome-wide association study identifies two novel loci and a substantial genetic component for Parkinson's disease. SNPedia Articles.

Significance -log pval	SNP	allele	Your Genotype Ref/FM	Genes	study
9	rs356220[lxii]	T	T/TC increased risk	SNCA	Identification of a novel Parkinson's disease locus via stratified genome-wide association study. SNPedia Articles.
8.52	rs11248051[lxiii]	T	normal increases risk	GAK	Common genetic variation in the HLA region is associated with late-onset sporadic Parkinson's disease. SNPedia Articles.
8.52	rs11248060[lxiv]		normal increases risk	DGKQ	Meta-analysis of Parkinson's disease: identification of a novel locus, RIT2. SNPedia Articles.
8.52	rs4538475[lxv]		normal increases risk - and has been implicated in the pathogenesis of several neurodegenerative disorders.	BST1	Genome-wide association study identifies common variants at four loci as genetic risk factors for Parkinson's disease. SNPedia. GWAS
8.15	rs6710823[lxvi]		g/gA and has been implicated in the pathogenesis of several neurodegenerative disorders.	ACMSD	Imputation of sequence variants for identification of genetic risks for Parkinson's disease: a meta-analysis of genome-wide association studies.
8.1	rs17577094[lxvii]		normal associated with several neurodegenerative	MAPT	Genome-wide mapping of IBD segments in an Ashkenazi PD

Significance -log pval	SNP	allele	Your Genotype Ref/FM	Genes	study
			disorders such as Alzheimer's disease		cohort identifies associated haplotypes.Censored by MJFox
7.7	rs1630500[lxviii]		Normal Gaucher disease, a lysosomal storage disease characterized by an accumulation of glucocerebrosides.	GBA	Genome-wide mapping of IBD segments in an Ashkenazi PD cohort identifies associated haplotypes.
7.52	rs356220[lxix]	T	T/TC SNPedia Articles.	SNCA	Genome-wide association study confirms BST1 and suggests a locus on 12q24 as the risk loci for Parkinson's disease in the European population. SNPedia Articles.
7.52	rs1994090[lxx]		G/TT associated with Parkinson disease-8	LRRK2	Genome-wide association study identifies common variants at four loci as genetic risk factors for Parkinson's disease. SNPedia Articles. SNPedia Articles. MJFox censors.
7.52	rs3129882[lxxi]	G	Normal 1/4/23 G/AA associated with late-onset sporadic Parkinson's disease morphing	HLA	Identification of a novel Parkinson's disease locus via stratified genome-wide association study.MJFox Censors.

Significance -log pval	SNP	allele	Your Genotype Ref/FM	Genes	study
			polymorphism!		
7.4	rs6599389[lxxii]	A	normal MJFox beneficial.	GAK	Web-based genome-wide association study identifies two novel loci and a substantial genetic component for Parkinson's disease. MJFox weights this mutation favorable.
7.3	rs12726330[lxxiii]		normal	GBA	Meta-analysis of Parkinson's disease: identification of a novel locus, RIT2.MJFox beneficial.
7.22	rs11868035[lxxiv]	G	Normal MJFox beneficial	SREBF1, RAI1	Web-based genome-wide association study identifies two novel loci and a substantial genetic component for Parkinson's disease. SNPedia Articles.
7.22	rs11012[lxxv]	T	normal	MAPT, PLEKHM1, IMP5	Genome-wide association study confirms SNPs in SNCA and the MAPT region as common risk factors for Parkinson disease. SNPedia Articles. MJFox censors.
7.15	rs823128[lxxvi]	A	g/AA a basic DNA-binding domain.	PARK16, NUCKS1	Genome-wide association study reveals genetic risk underlying

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7.15	rs17115100[lxxvii]	G	normal	SFXN2, C10orf32, CNNM2, CYP17A1	Parkinson's disease. SNPedia Articles. MJFox beneficial. Genome-wide association study reveals genetic risk underlying Parkinson's disease. SNPedia Articles. MJFox censors.
7.15	rs2736990[lxxviii]		G/GA Defects in SNCA have been implicated in the pathogenesis of Parkinson disease.	SNCA	Genome-wide association study confirms SNPs in SNCA and the MAPT region as common risk factors for Parkinson disease. SNPedia Articles. MJFox says Beneficial. NIH Articles.
7.15	rs591323[lxxix]	G	g/GA	FGF20	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. SNPedia Articles. MJFox decreases. NIH articles.
7	rs823156[lxxx]	A	G/AA a substantial genetic component for Parkinson's disease.	SLC41A1	Web-based genome-wide association study identifies two novel loci and a substantial genetic component for Parkinson's disease. SNPedia Articles. MJFox says beneficial

Significance -log pval	SNP	allele	Your Genotype Ref/FM	Genes	study
					for Caucasians.
7	rs6532197[lxxxi]	G	normal autosomal-dominant bleeding disorder (factor V Quebec) were found to have a deficiency of platelet multimerin.	MMRN1	Genome-wide association study reveals genetic risk underlying Parkinson's disease. MJFox increases. GWAS
6.7	rs4964469[lxxxii]	A	normal increases risk	Intergenic	Genome-wide association study confirms BST1 and suggests a locus on 12q24 as the risk loci for Parkinson's disease in the European population. MJFox censors. GWAS
6.7	rs4130047[lxxxiii]	C	normal	RIT2, SYT4	Web-based genome-wide association study identifies two novel loci and a substantial genetic component for Parkinson's disease. SNPedia Articles. MJFox increases. GWAS.
6.7	rs6430538[lxxxiv]		c/Tc a benign catabolite and thus prevent the accumulation of quinolinate from ACMS.	Intergenic	Meta-analysis of Parkinson's disease: identification of a novel locus, RIT2.MJFox decreases.
6.7	rs7118648[lxxxv]	C	normal Parkinson disease loci in the mid-western Amish.	CCDC82	Parkinson disease loci in the mid-western Amish. MJFox censored.

Significance -log pval	SNP	allele	Your Genotype Ref/FM	Genes	study
6.7	rs3935740[lxxxvi]	A	normal Parkinson disease loci in the mid-western Amish.	TMC3	Parkinson disease loci in the mid-western Amish.SNPedia. MJFox censored.
6.52	rs183211[lxxxvii]	A	normal Mutations in this gene are associated with autosomal recessive osteopetrosis type 6 (OPTB6).	NSF	Genome-wide association study identifies candidate genes for Parkinson's disease in an Ashkenazi Jewish population. SNPedia. MJFox censors.
6.52	rs4698412[lxxxviii]		normal BST1 expression is enhanced in bone marrow stromal cell lines derived from patients with rheumatoid arthritis.	BST1	Meta-analysis of Parkinson's disease: identification of a novel locus, RIT2. MJFox beneficial.
6.4	rs11865038[lxxxix]		normal	POL3S	Meta-analysis of Parkinson's disease: identification of a novel locus, RIT2.MJFox decreases. SNPedia.
6.4	rs6812193[xc]	C	normal	STBD1	Genome-wide association study reveals genetic risk underlying Parkinson's disease. SNPedia Articles. MJFox decreases while SNPedia increases.
6.4	rs3793947[xci]	G	g/gA to form a multimeric scaffold for the	DLG2	Large-scale meta-analysis of genome-wide association

Significance -log pval	SNP	allele	Your Genotype Ref/FM	Genes	study
			clustering of receptors, ion channels, and associated signaling proteins.		data identifies six new risk loci for Parkinson's disease. MJFox decreases.
6.3	rs1536076[xcii]		t/Gt	SH3GL2	Meta-analysis of Parkinson's disease: identification of a novel locus, RIT2. MJFox increases.
6.3	rs12063142[xciii]		c/Tc Meta-analysis of Parkinson's disease: identification of a novel locus, RIT2.	TAS1R2	Genome-wide association study confirms SNPs in SNCA and the MAPT region as common risk factors for Parkinson disease. MJFox censors.
6.22	rs2823357[xciv]	A	normal Parkinson's Disease Genetic Loci in Rapid Eye Movement Sleep Behavior Disorder	USP25	Web-based genome-wide association study identifies two novel loci and a substantial genetic component for Parkinson's disease. MJFox censors.
6.22	rs17497526[xcv]	C	normal	COL13A1	Parkinson disease loci in the mid-western Amish. MJFox censors.
6.22	rs62120679[xcvi]	T	normal which triggers cytokine expression in the innate and adaptive immunity pathways.	SPPL2B	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. MJFox increases.

Significance -log pval	SNP	allele	Your Genotype Ref/FM	Genes	study
6.15	rs415430[xcvii]	T	normal a key role in some cases of human breast, rectal, lung, and gastric cancer through activation of the WNT-beta-catenin-TCF signaling pathway.	WNT3	Genome-wide association study identifies candidate genes for Parkinson's disease in an Ashkenazi Jewish population. SNPedia Article. MJFox censors. GWAS.
6.1	rs199498[xcviii]	T	Normal Decreases Risk with several neurodegenerative disorders such as Alzheimer's disease,	MAPT	Identification of a novel Parkinson's disease locus via stratified genome-wide association study.
6.05	rs2275336[xcix]		normal	CNKSR3	Meta-analysis of Parkinson's disease: identification of a novel locus, RIT2 .MJFox censors. GWAS.
6	rs199533[c]	G	normal MAPT gene mutations have been associated with several neurodegenerative disorders such as Alzheimer's disease, Pick's disease, frontotemporal dementia, cortico-basal degeneration and progressive supranuclear palsy.	MAPT	Common genetic variation in the HLA region is associated with late-onset sporadic Parkinson's disease. MJFox censors.
6	rs1296028[ci]		normal	Intergenic	Meta-analysis of Parkinson's disease: identification of a

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					novel locus, RIT2.SNPedia Article. MJFox decreases.
6	rs10877840[cii]		normal	SLC2A13	Meta-analysis of Parkinson's disease: identification of a novel locus, RIT2. MJFox censors. GWAS
6	rs10519131[ciii]		normal	Intergenic	Meta-analysis of Parkinson's disease: identification of a novel locus, RIT2. MJFox decreases. GWAS
6	rs4837628[civ]	T	normal	DBC1	Genome-wide association study confirms SNPs in SNCA and the MAPT region as common risk factors for Parkinson disease. MJFox censors. GWAS
5.7	rs2242330[cv]	A/GA We sought to identify any common genetic variability exerting a large effect in risk for Parkinson's disease		BRDG1	Genome-wide genotyping in Parkinson's disease and neurologically normal controls: first stage analysis and public release of data. SNPedia Article. MJFox censors. GWAS
5.7	rs1480597[cvi]		normal	Intergenic	Genome-wide

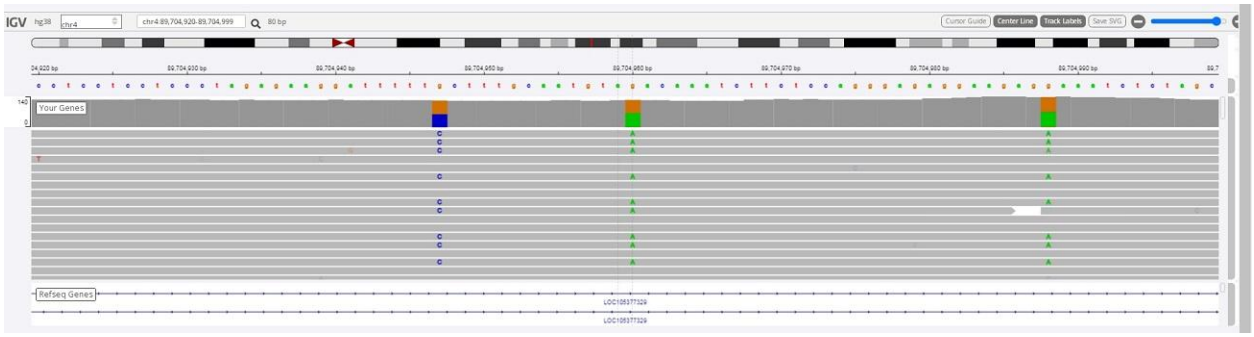
Significance -log pval	SNP	allele	Your Genotype Ref/FM	Genes	study
					genotyping in Parkinson's disease and neurologically normal controls: first stage analysis and public release of data. SNPedia Articles. MJFox censors. GWAS
5.7	rs4698412[cvii]	A	G/GA BST1 expression is enhanced in bone marrow stromal cell lines derived from patients with rheumatoid arthritis.	BST1	Genome-wide association study confirms BST1 and suggests a locus on 12q24 as the risk loci for Parkinson's disease in the European population. SNPedia Articles. MJFox decreases.
5.7	rs11248060[cviii]		normal	DGKQ	Genome-wide association study confirms SNPs in SNCA and the MAPT region as common risk factors for Parkinson disease. SNPedia Articles. MJFox increases.
5.7	rs199498[cix]	T	normal	MAPT	Identification of a novel Parkinson's disease locus via stratified genome-wide association study. MJFox decreases.
5.52	rs7617877[cx]	A	A/GA	Intergenic	Dissection of the genetics of Parkinson's disease

Significance -log pval	SNP	allele	Your Genotype Ref/FM	Genes	study
					identifies an additional association 5' of SNCA and multiple associated haplotypes at 17q21. MJFox censors.
5.52	rs10121009[cxi]	T	t/CC This gene is expressed in the kidney cortical epithelial cells and is upregulated by hyperglycemia.	UNC13B	Genome-wide association study identifies candidate genes for Parkinson's disease in an Ashkenazi Jewish population. SNPedia Article. MJFox censors.
5.52	rs9917256[cxii]		normal	Intergenic	Meta-analysis of Parkinson's disease: identification of a novel locus, RIT2. MJFox increases.
5.52	rs11026412[cxiii]		normal	Intergenic	Meta-analysis of Parkinson's disease: identification of a novel locus, RIT2. MJFox censors.
5.52	rs12431733[cxiv]	T	t/CC This particular family member plays an important role in the onset of endochondral bone formation in humans	BMP4	Genome-wide association study reveals genetic risk underlying Parkinson's disease. SNPedia. MJFox censors.
5.52	rs10464059[cxv]	A	G/GA	Intergenic	Genome-wide association study confirms SNPs in SNCA and the

Significance -log pval	SNP	allele	Your Genotype Ref/FM	Genes	study
					MAPT region as common risk factors for Parkinson disease. MJFox censors. GWAS
5.52	rs823114[cxvi]		G/GA IBD segments in an Ashkenazi PD cohort identifies associated haplotypes.	PARK16	Genome-wide mapping of IBD segments in an Ashkenazi PD cohort identifies associated haplotypes.SNPedia Article. MJFox decreases.
5.3	rs2839398[cxvii]		normal	PRDM15	Meta-analysis of Parkinson's disease: identification of a novel locus, RIT2. MJFox censors.
5.3	rs7077361[cxviii]	T	T/TC This gene regulates the recruitment of mesenchymal cells into epithelial structures, mediates cell-cell interactions, and regulates neurite outgrowth of sensory and motor neurons.	ITGA8	Genome-wide association study reveals genetic risk underlying Parkinson's disease. MJFox decreases.
5.3	rs1223271[cxix]	G	normal	C20orf82	Genome-wide association study reveals genetic risk underlying Parkinson's disease. MJFox censors.
5.15	rs10501570[cxx]		normal	DLG2	Genome-wide

Significance -log pval	SNP	allele	Your Genotype Ref/FM	Genes	study
					genotyping in Parkinson's disease and neurologically normal controls: first stage analysis and public release of data. MJFox censors. GWAS
5.1	rs7702187[cxxi]	T/TA		SEMA5A	High-resolution whole-genome association study of Parkinson disease. SNPedia Articles. GWAS

[i] rs356182

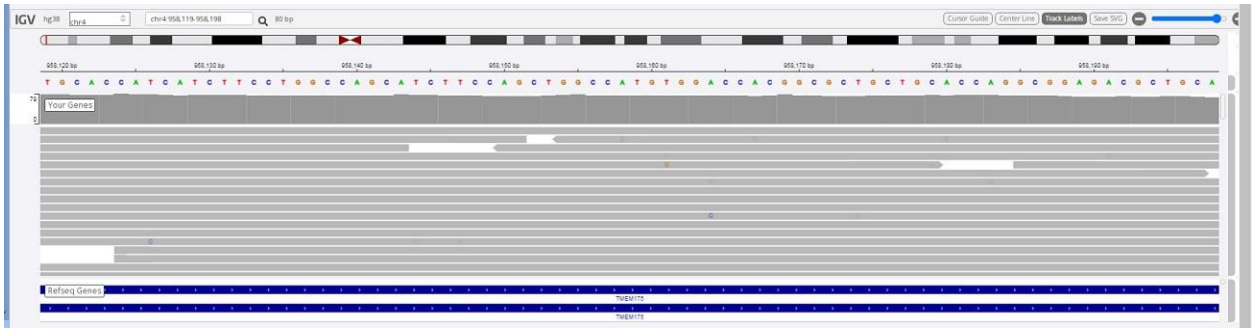


[ii] rs356219

[iii] rs17649553

[iv] rs356219 1 1 23

[v] rs34311866 1 1 23



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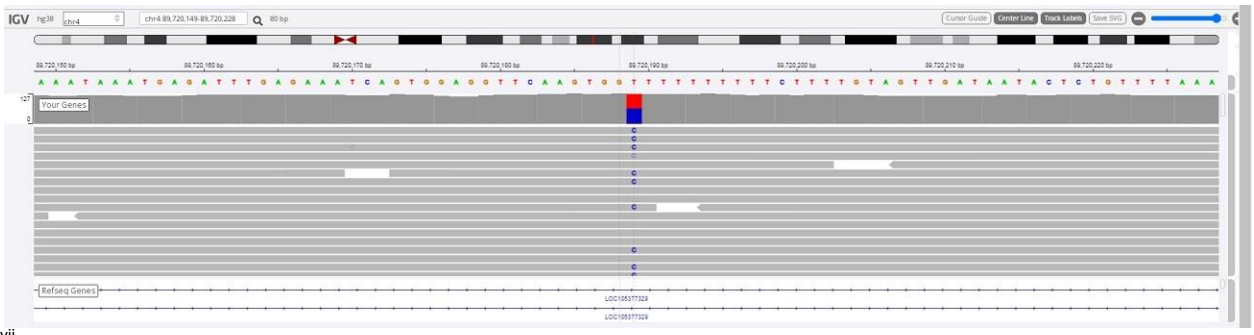

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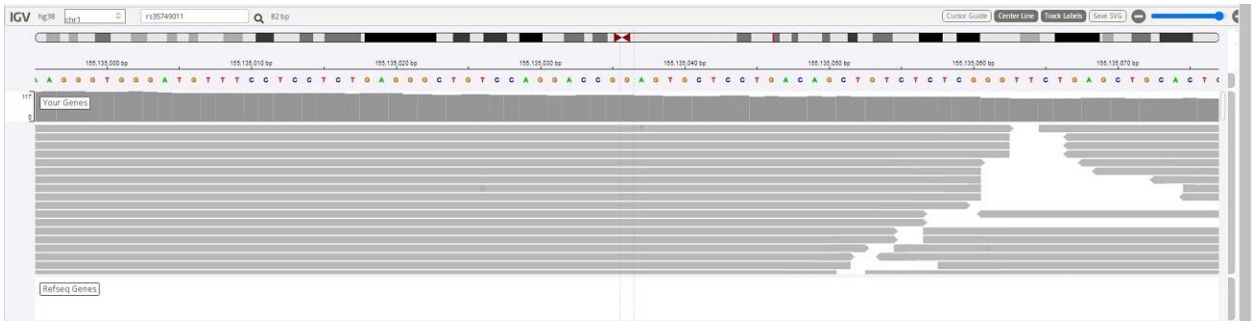

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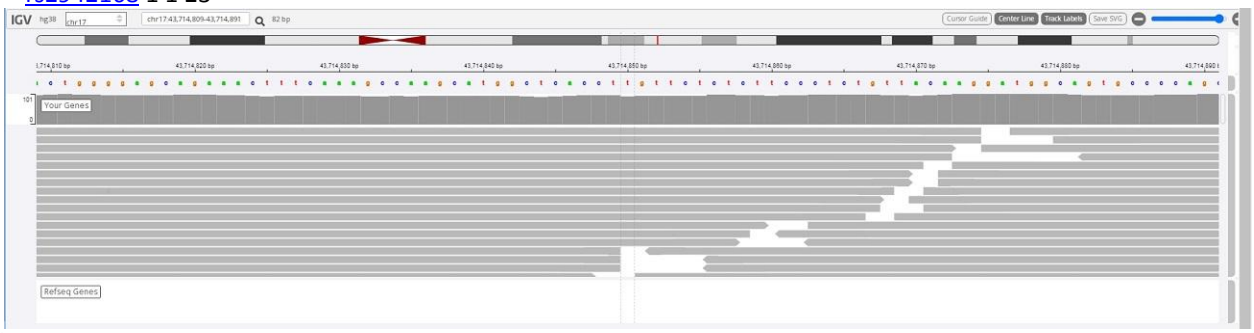

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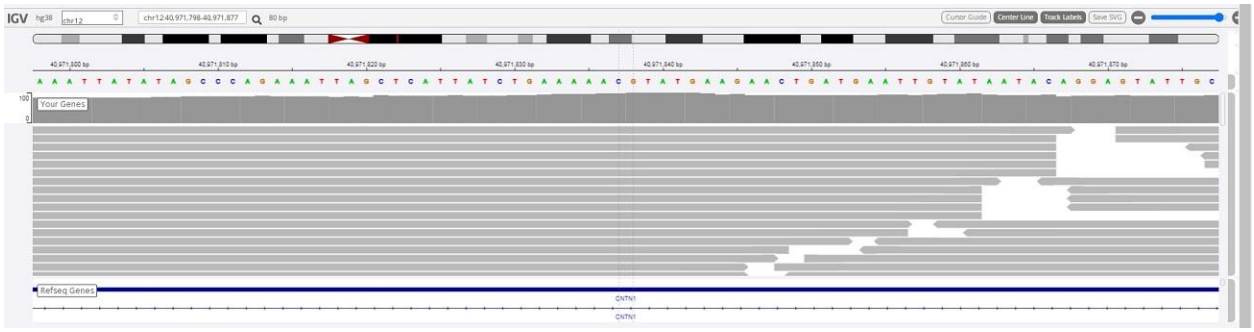
x rs1442190 1 1 23



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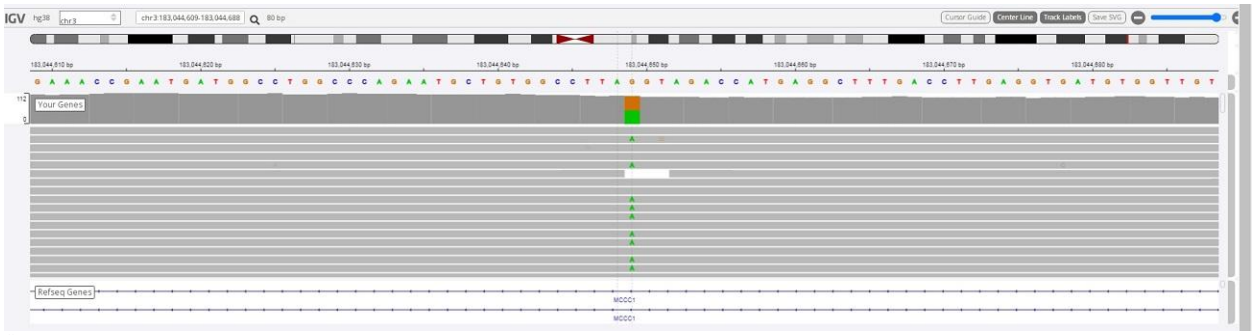

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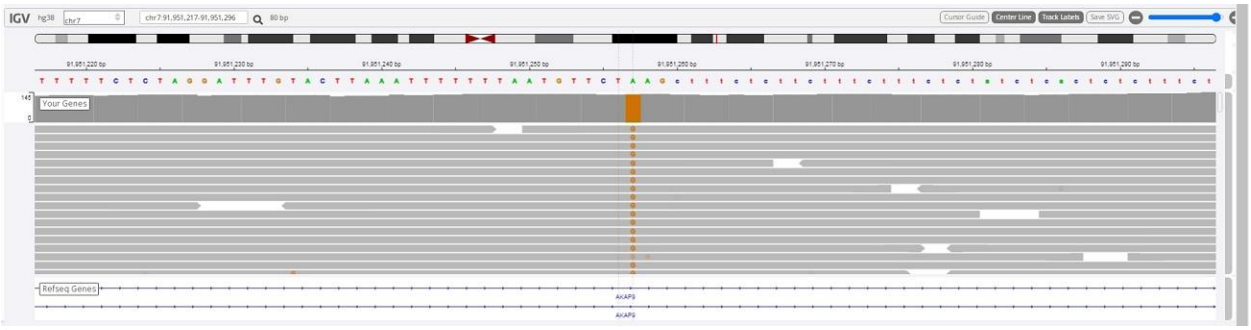

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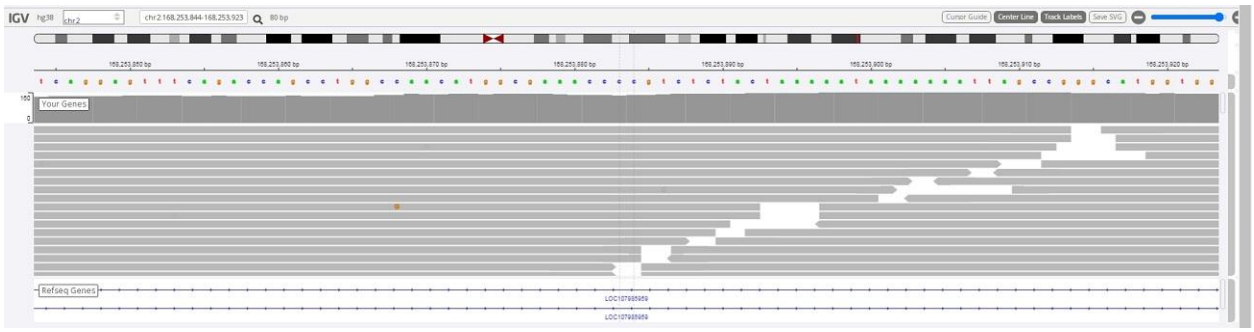

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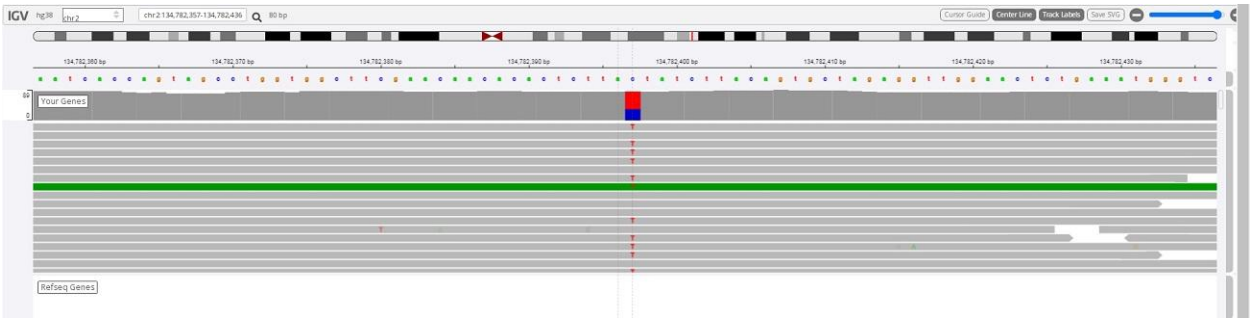

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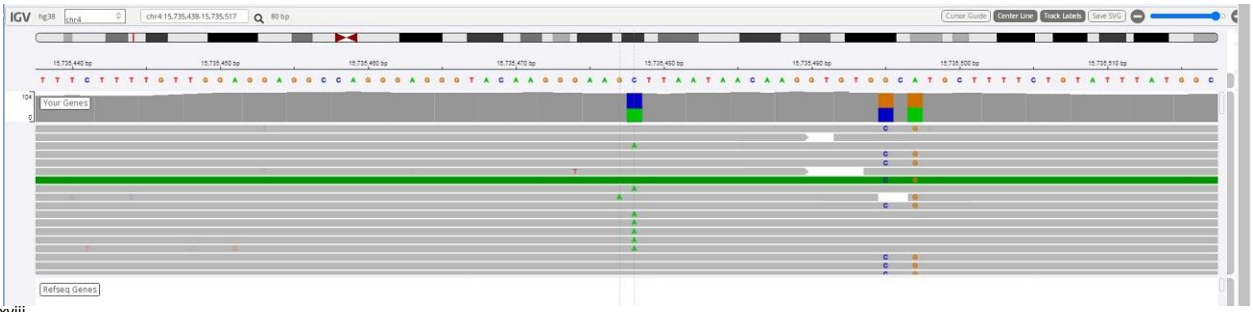
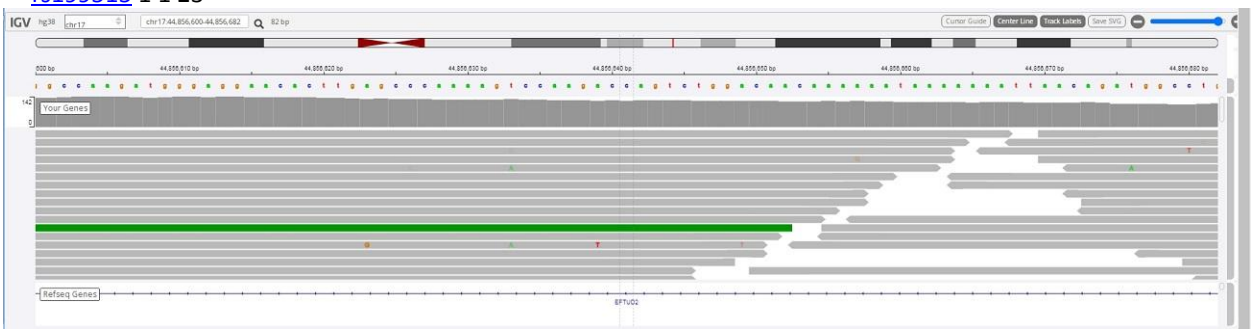
xvii rs11724635 1 1 23



xviii rs199515 1 1 23



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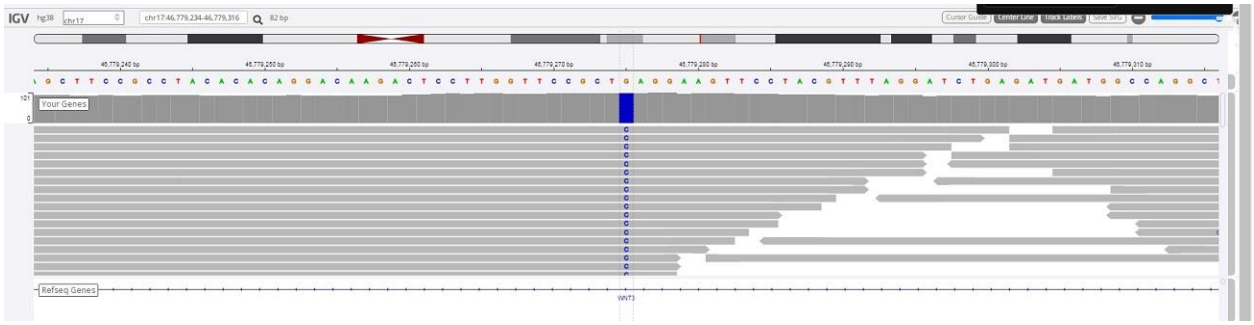

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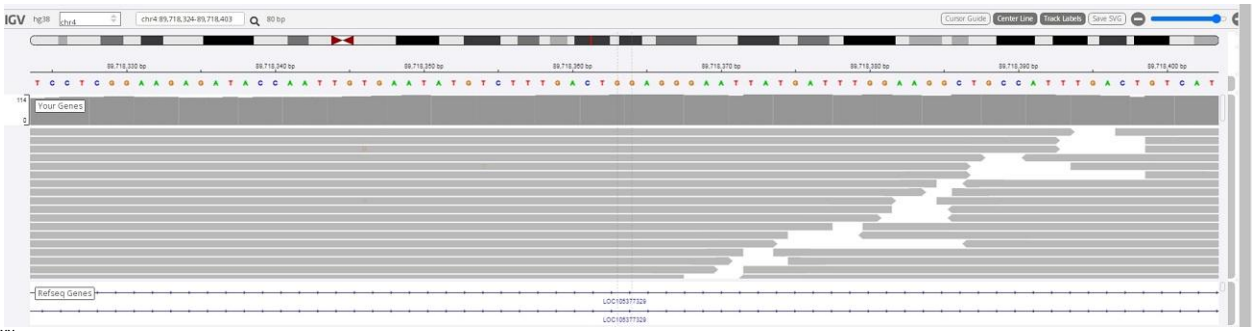

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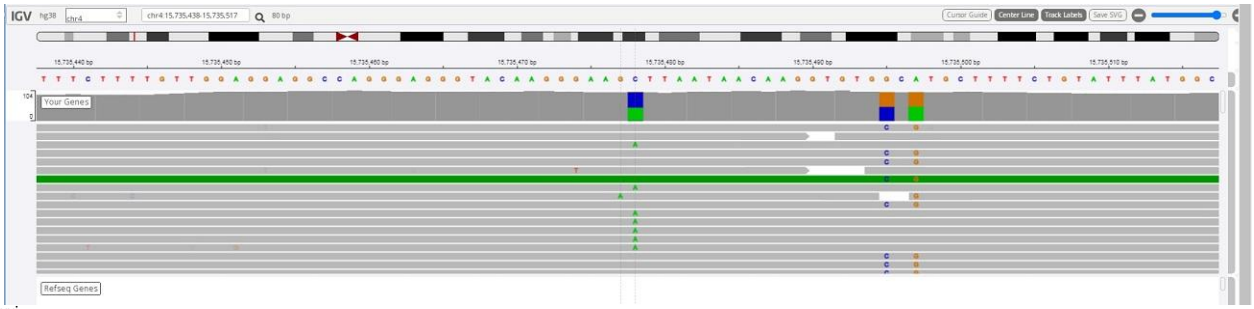

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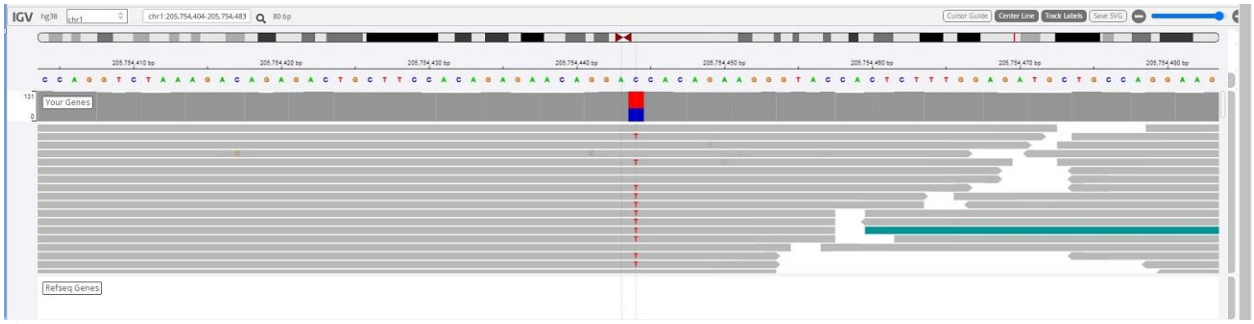
[xxii] rs2736990 1 1 23

[xxiii] rs823118 1 1 23



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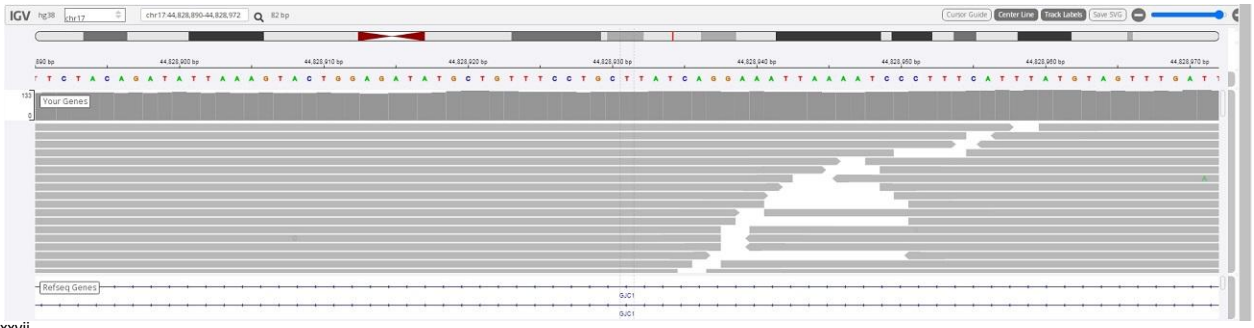
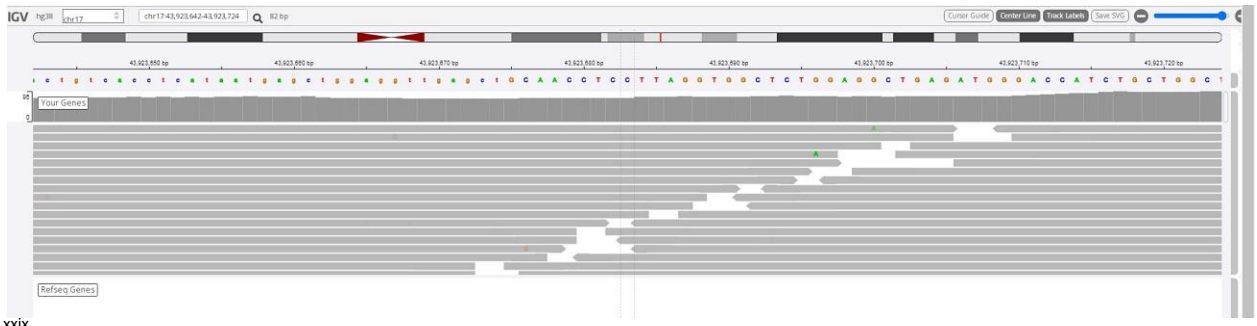


xxvii [rs32588205](#) 1 1 23

xxviii rs12185268 1 2 23



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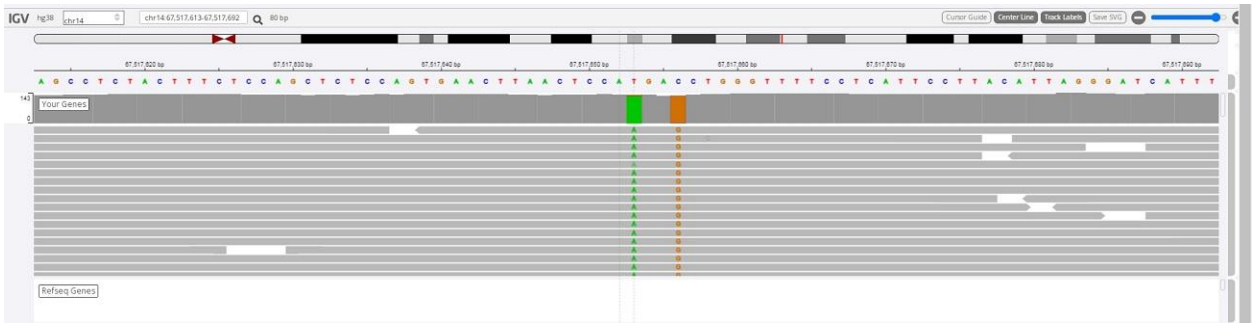

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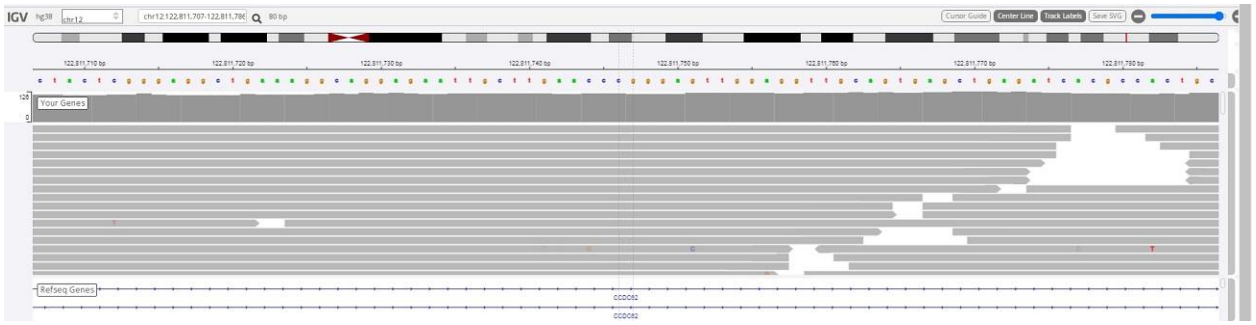

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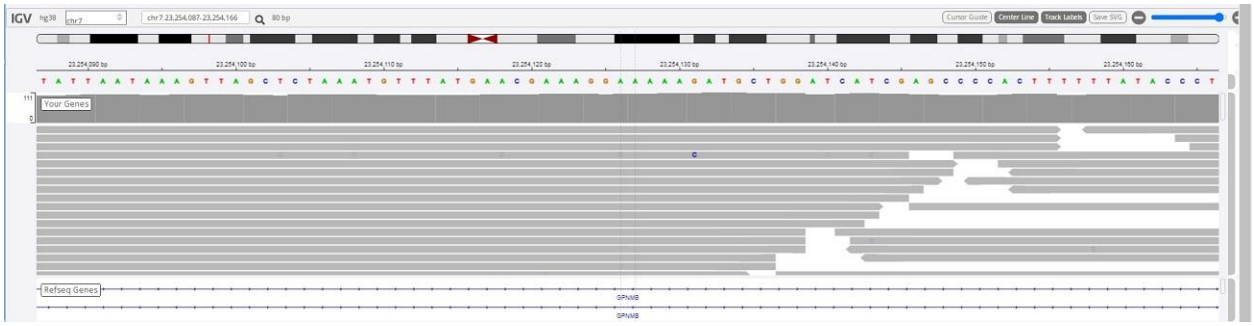

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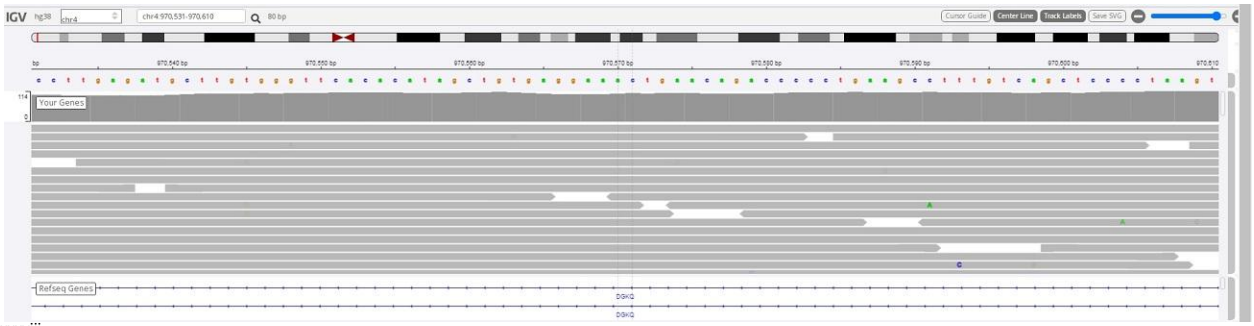

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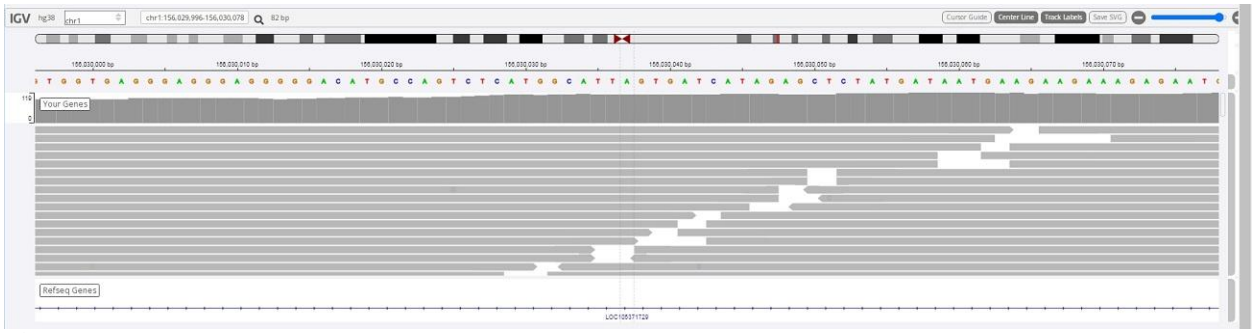

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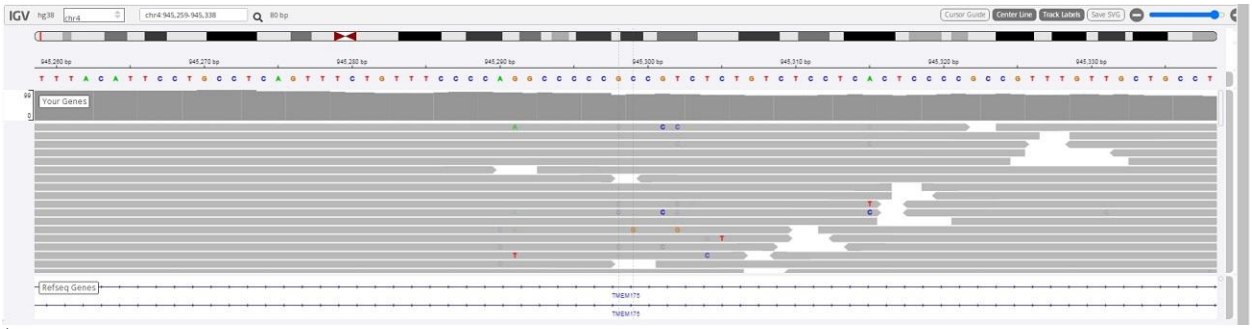

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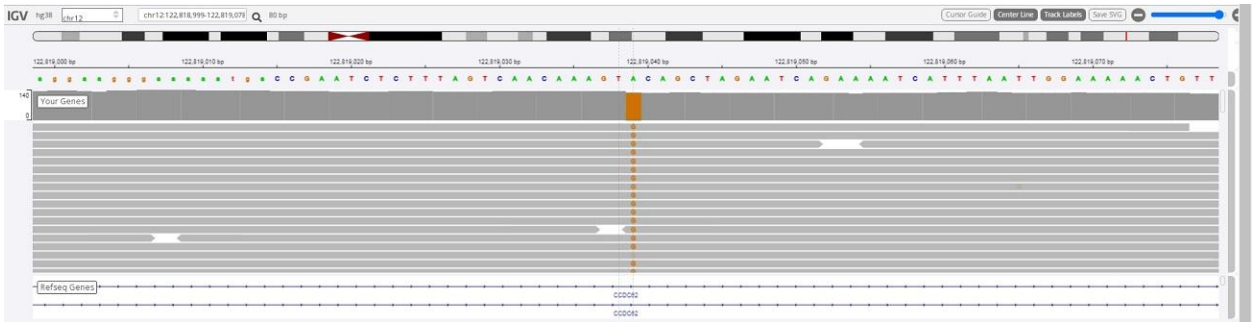

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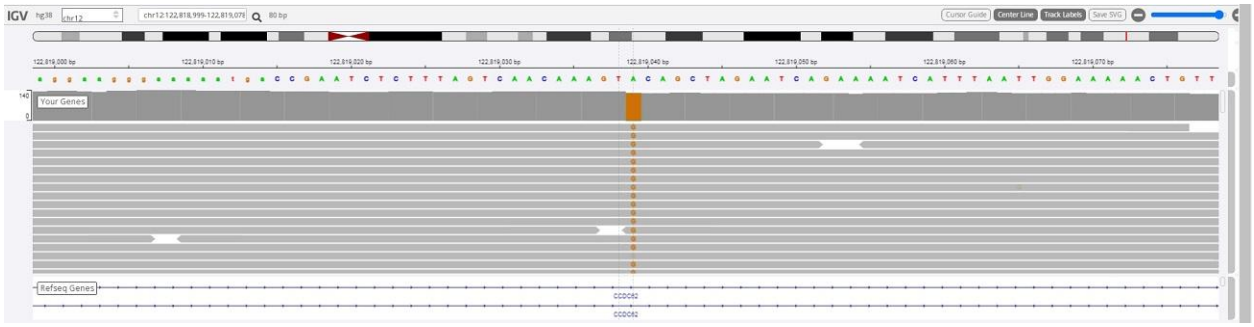

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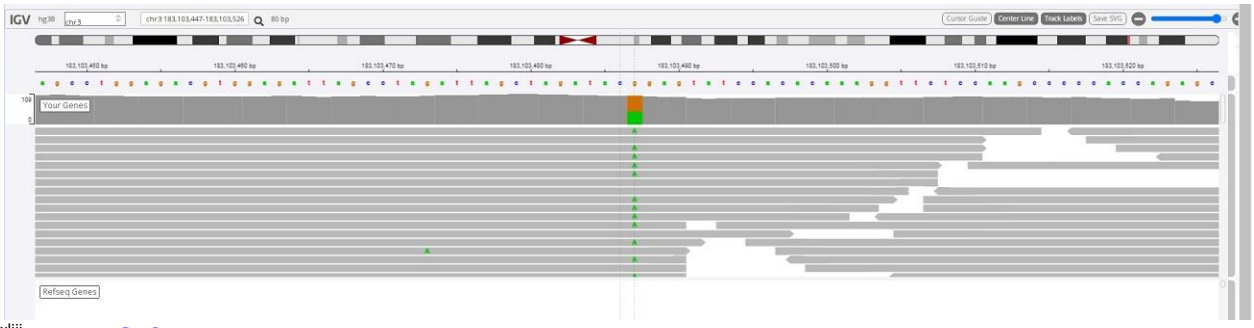

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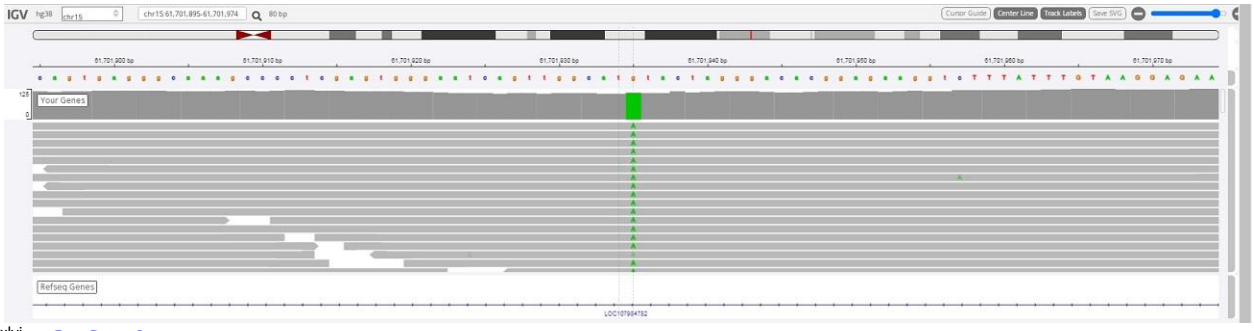

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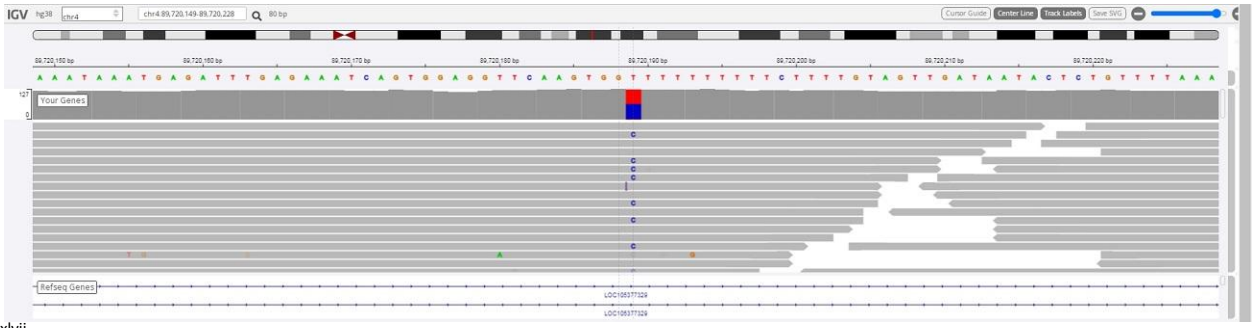

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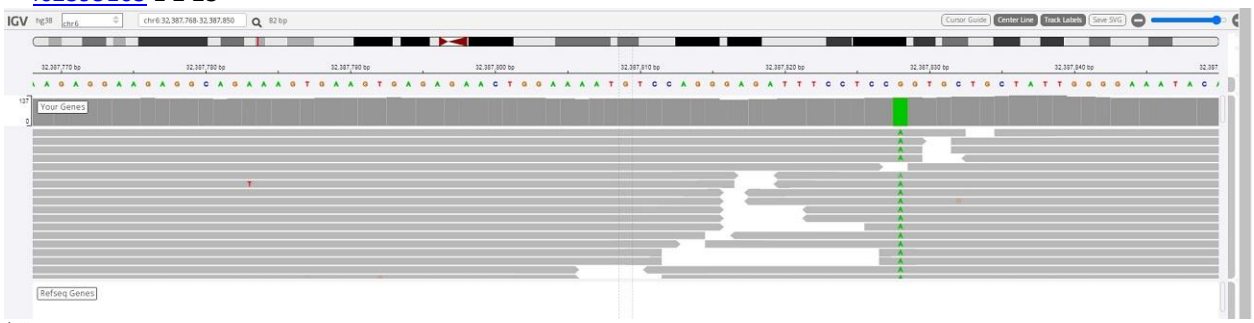

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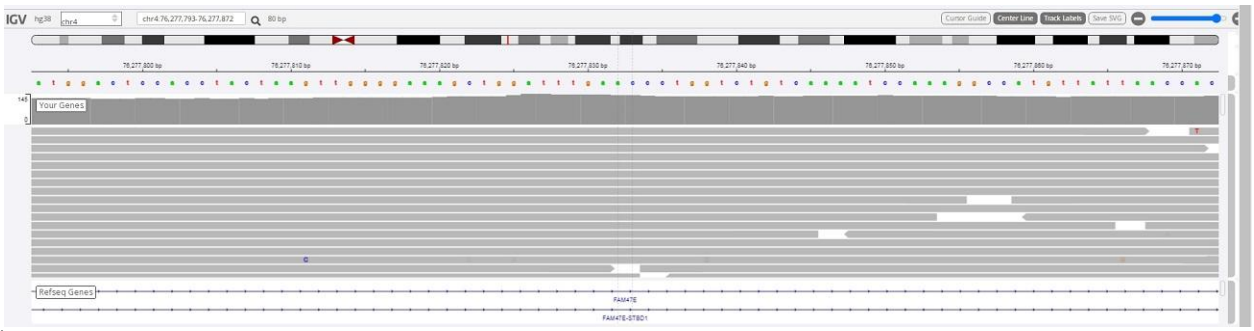

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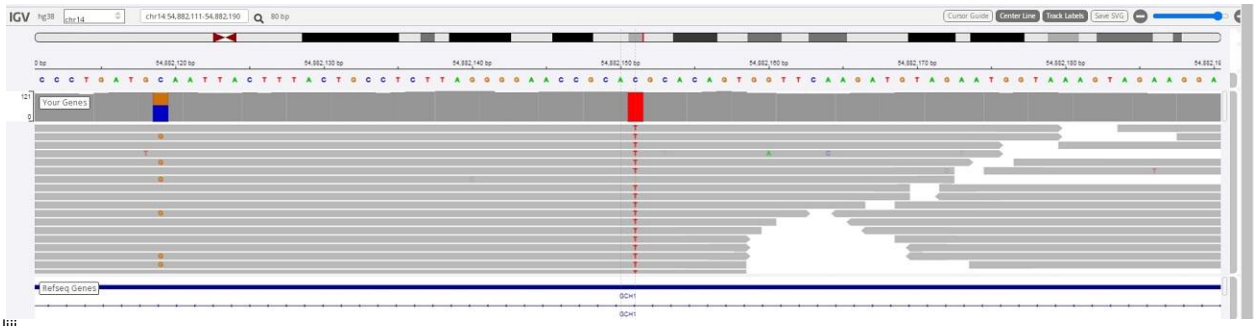

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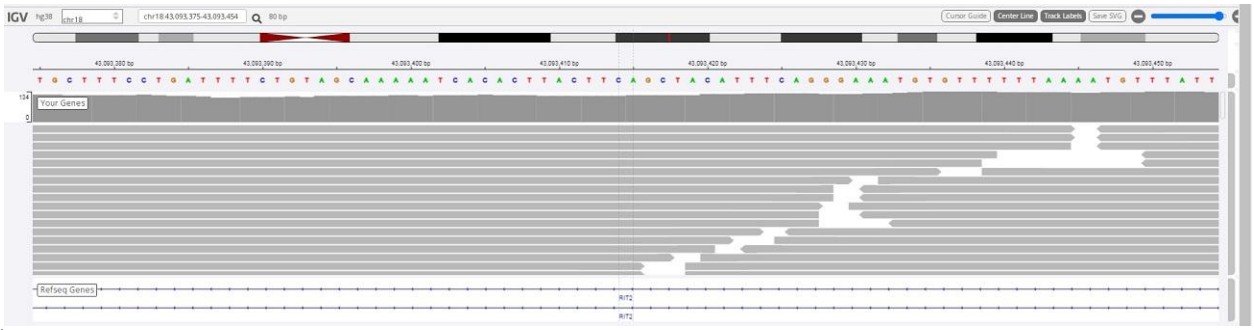

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lvi rs2102808 1 3 23

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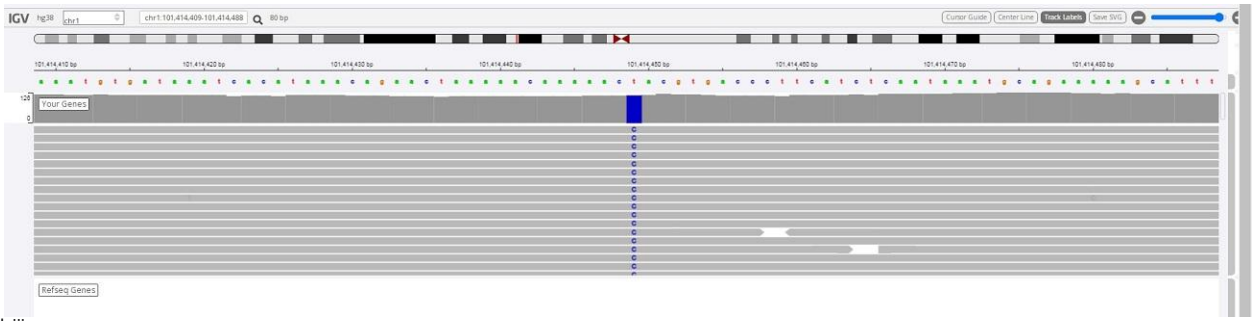

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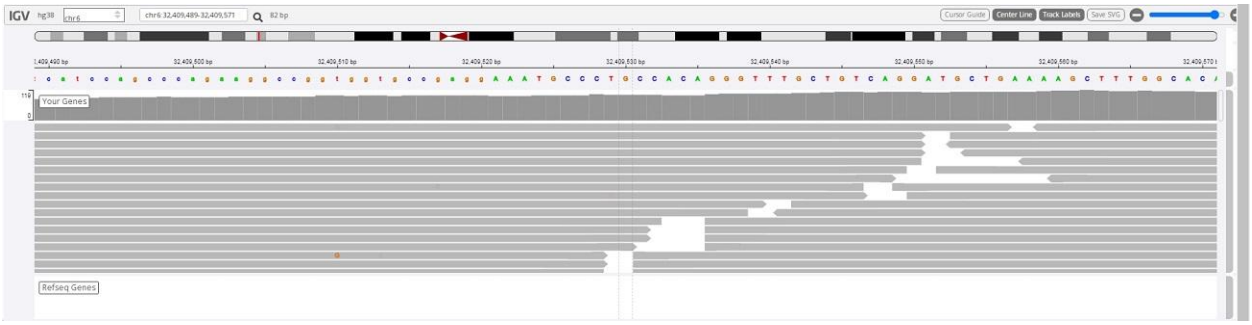

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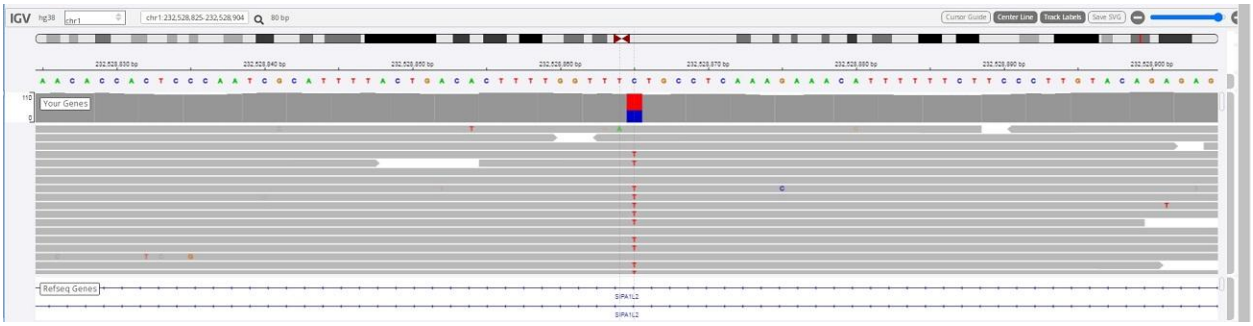

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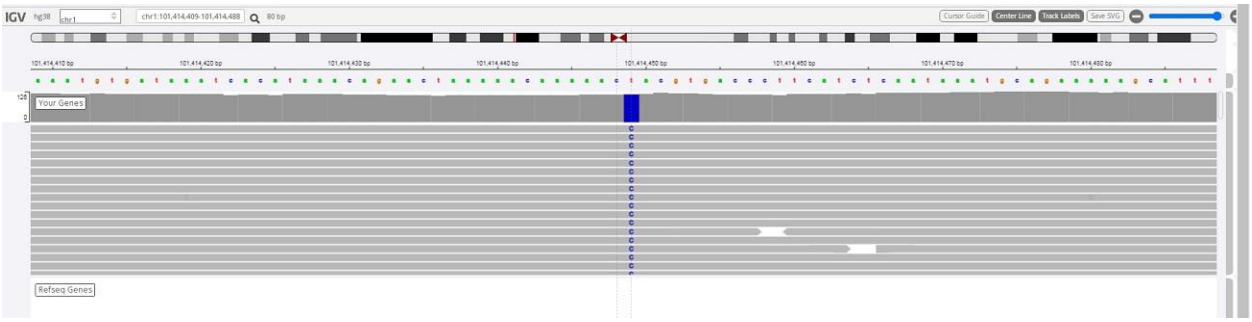

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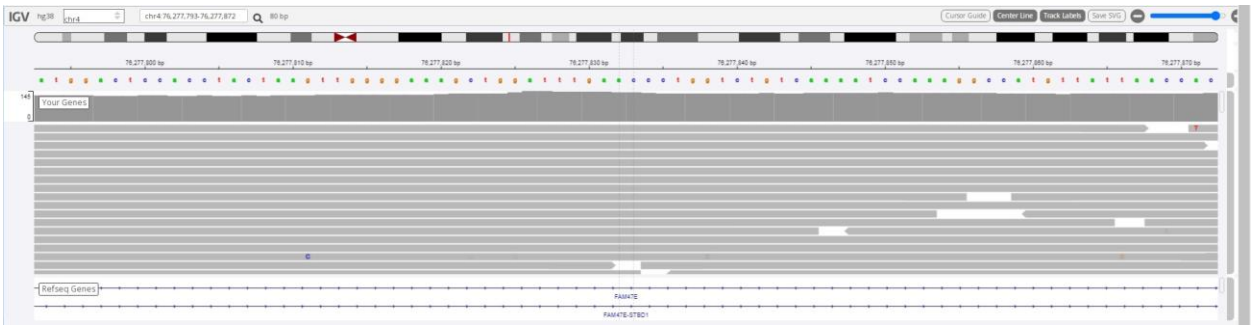

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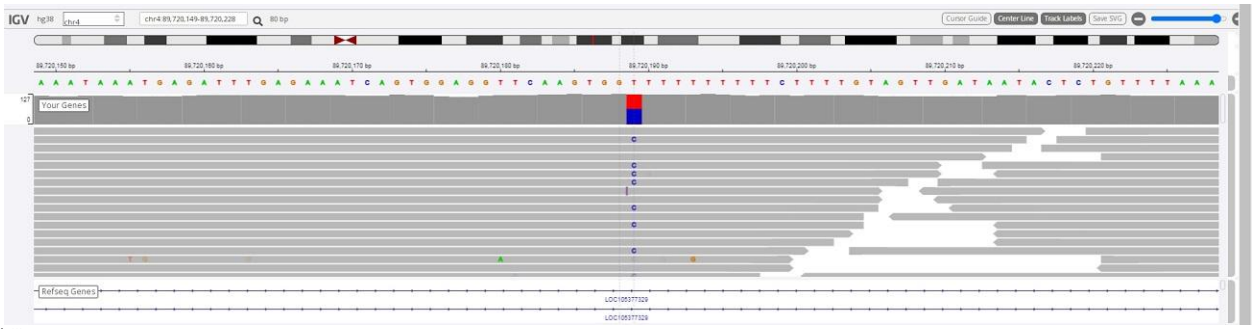

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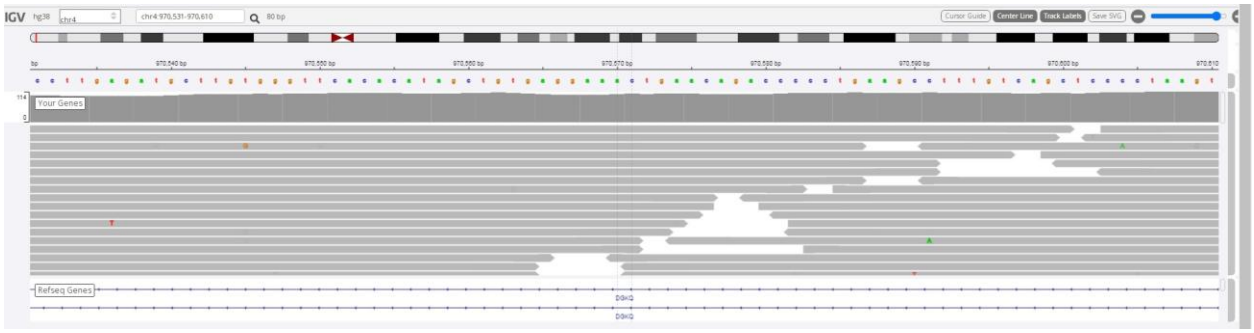

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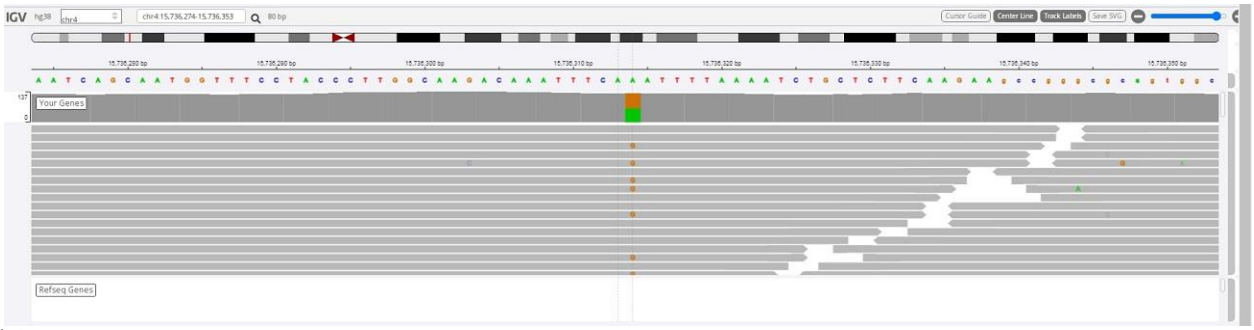

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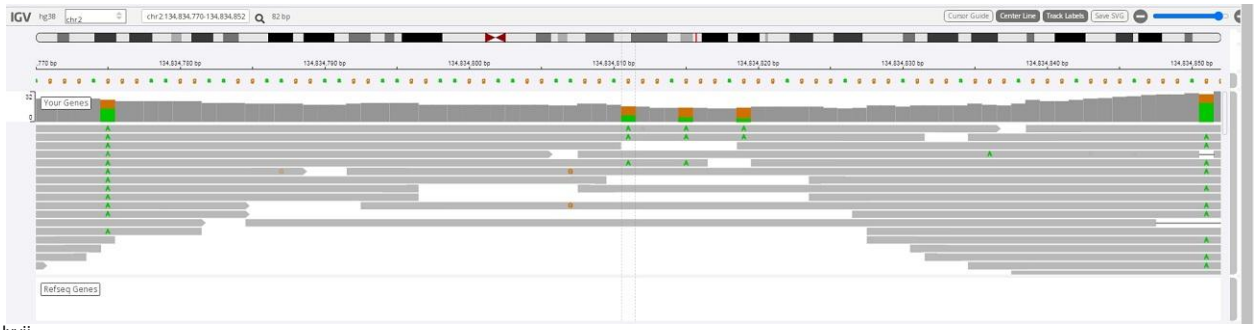

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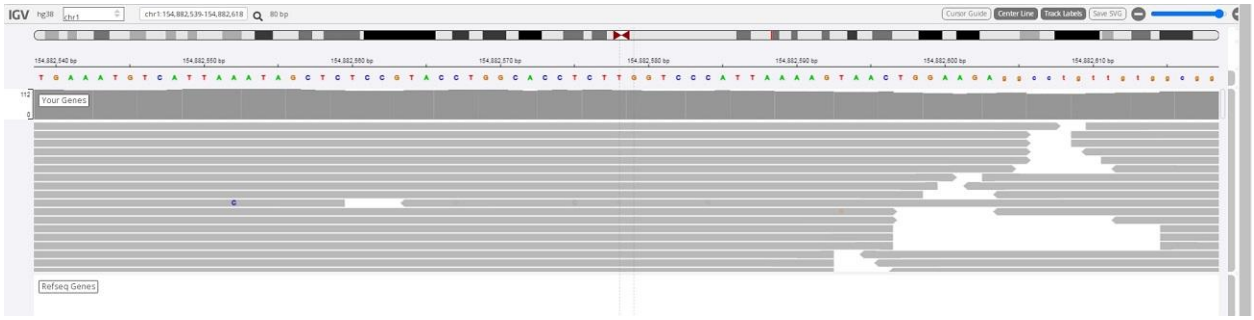

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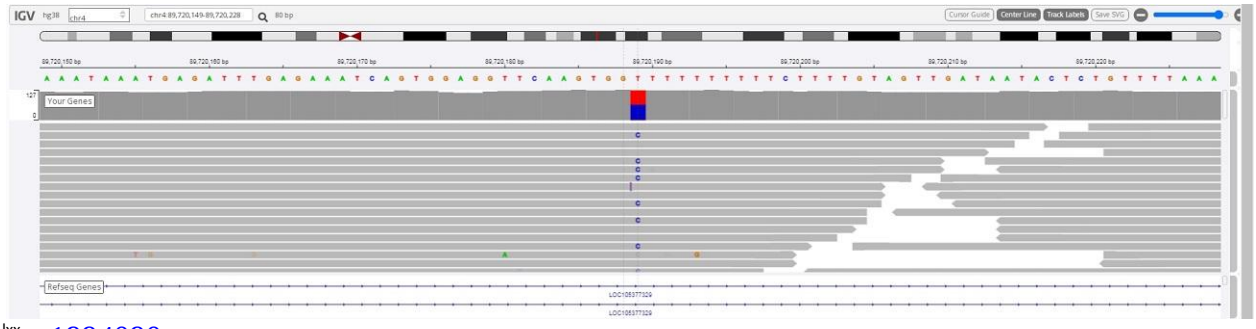

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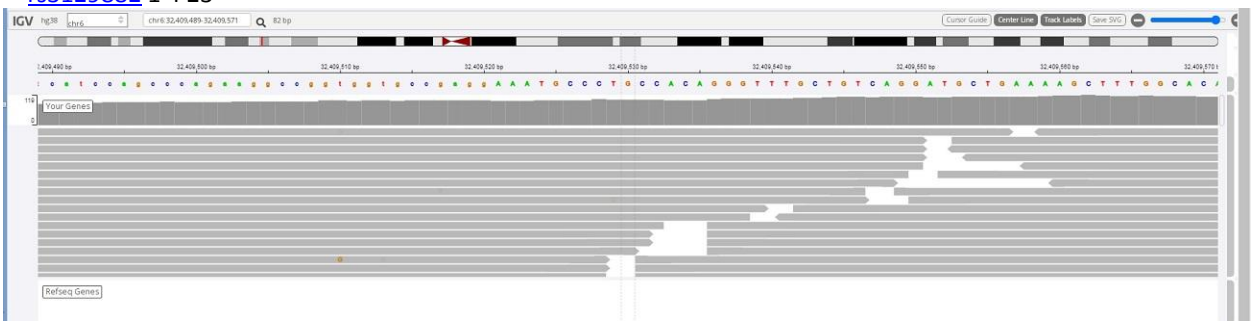
[lxxi] [rs3129882](#) 1 4 23



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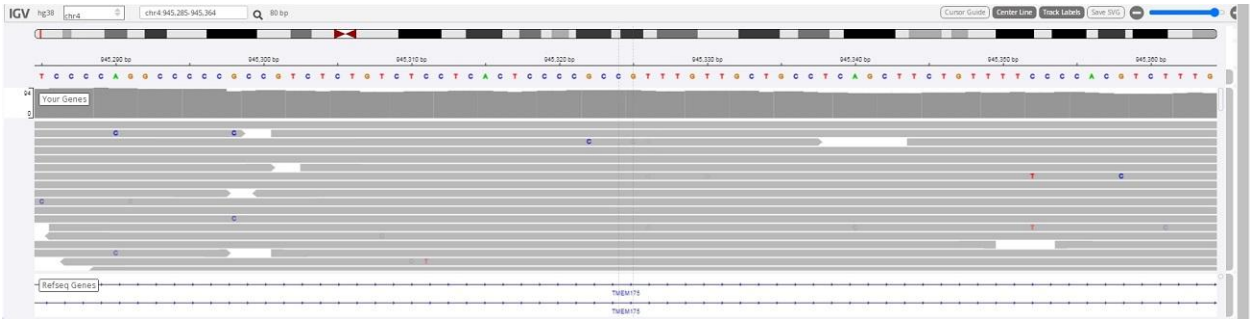

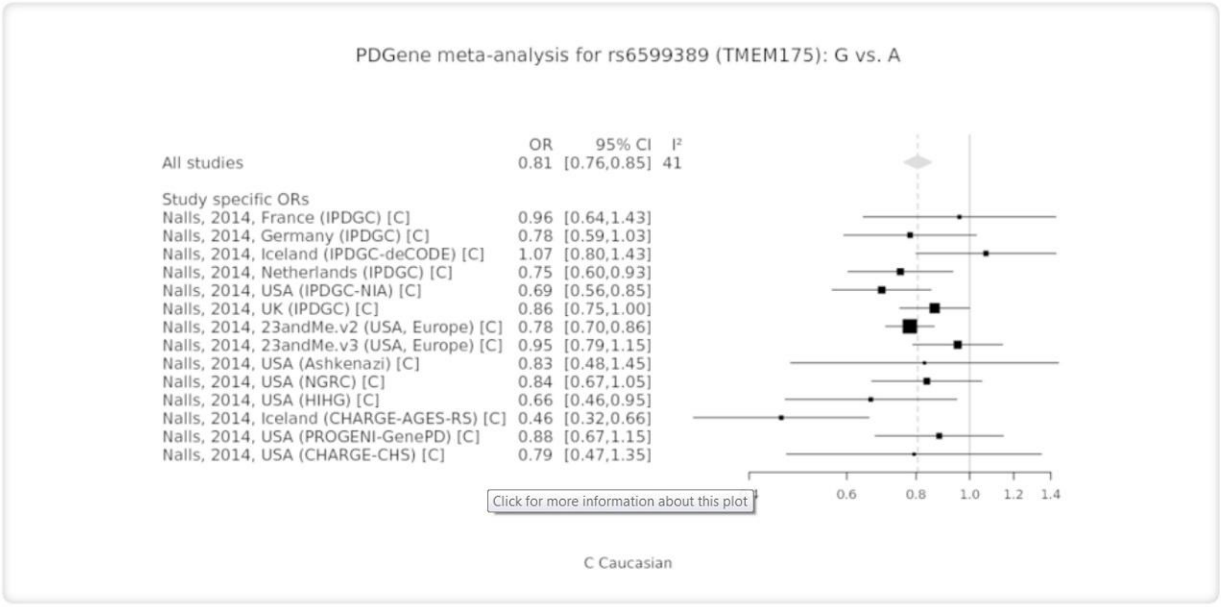

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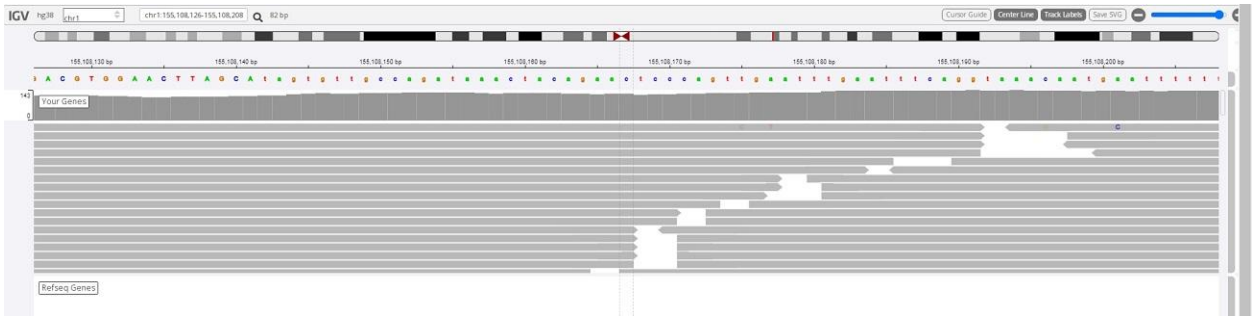

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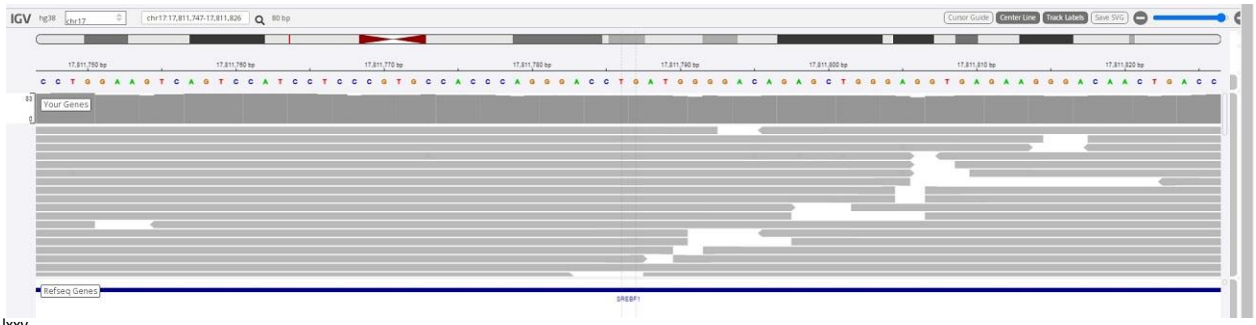

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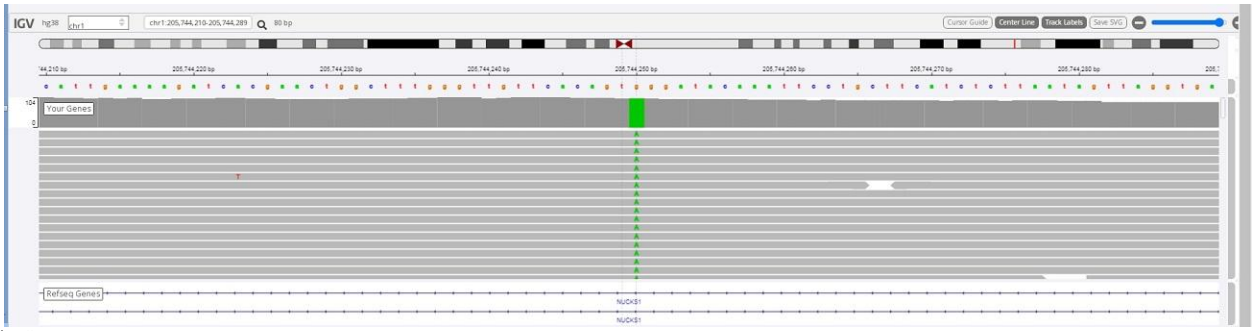

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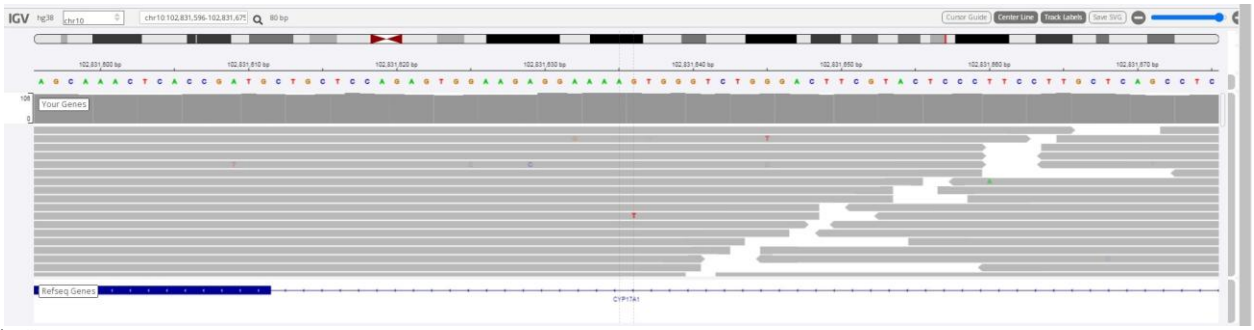

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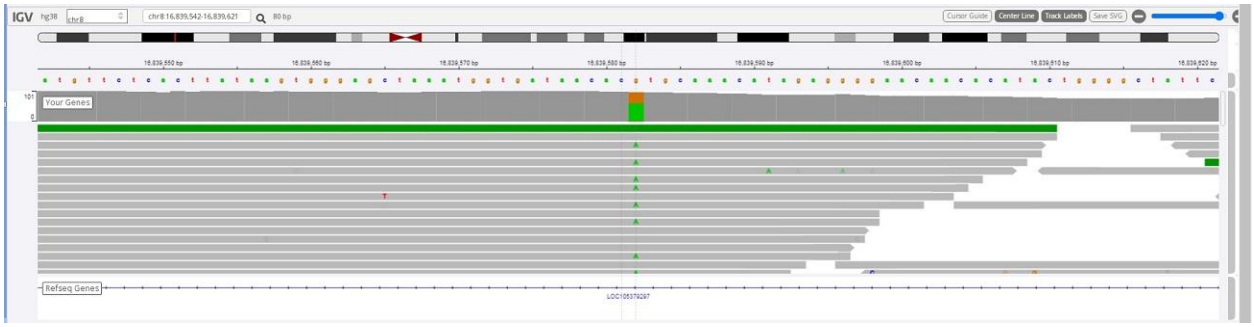

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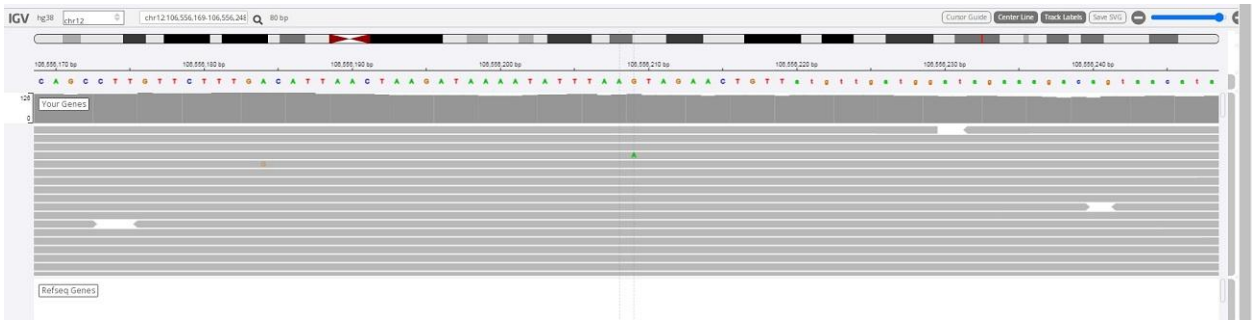

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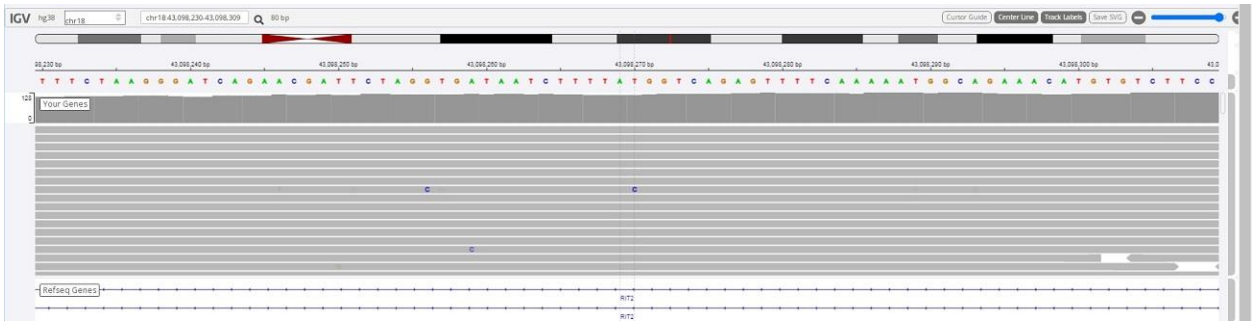

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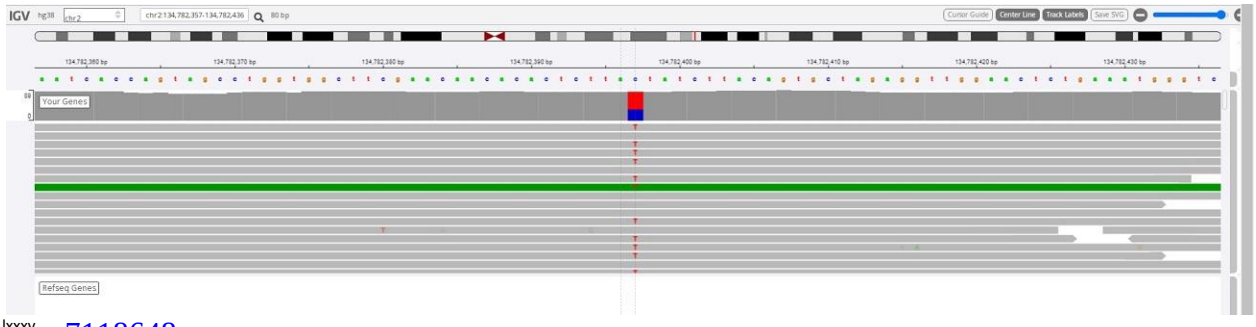

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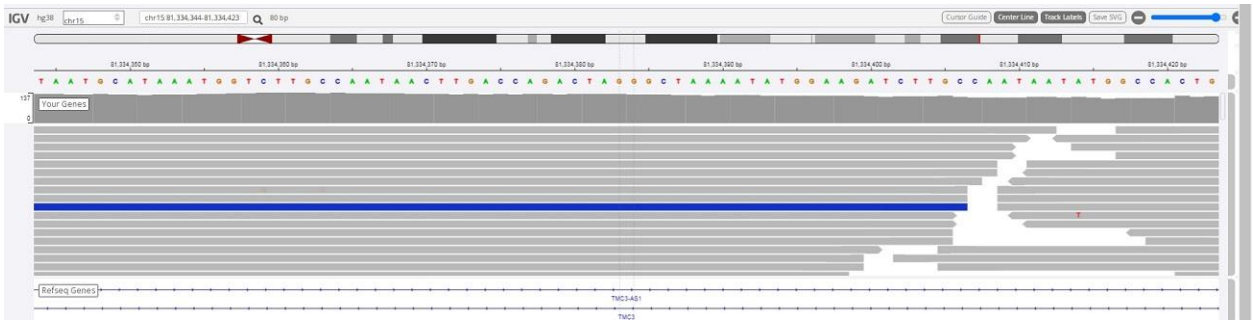

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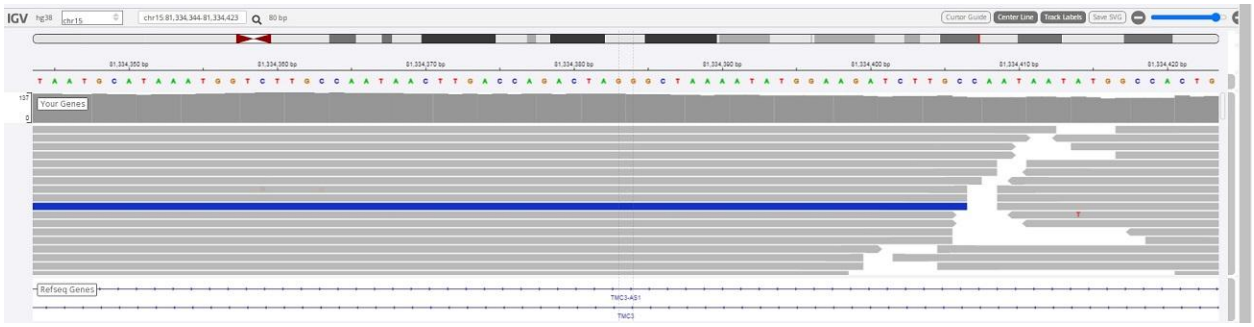

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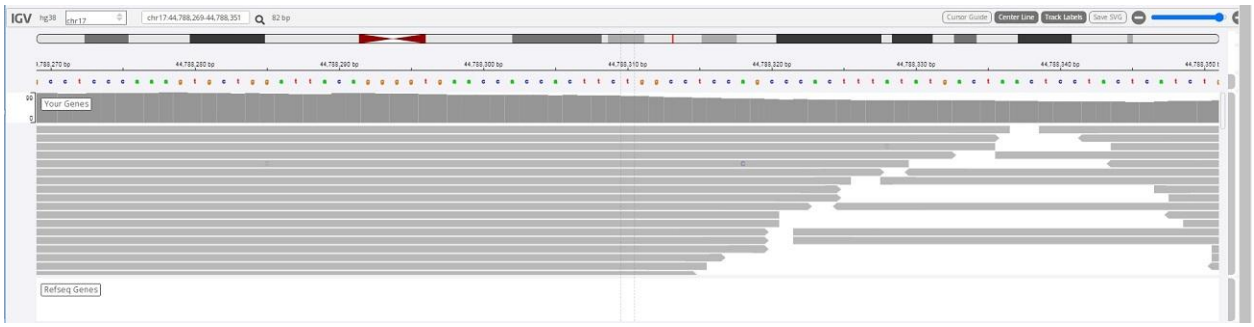

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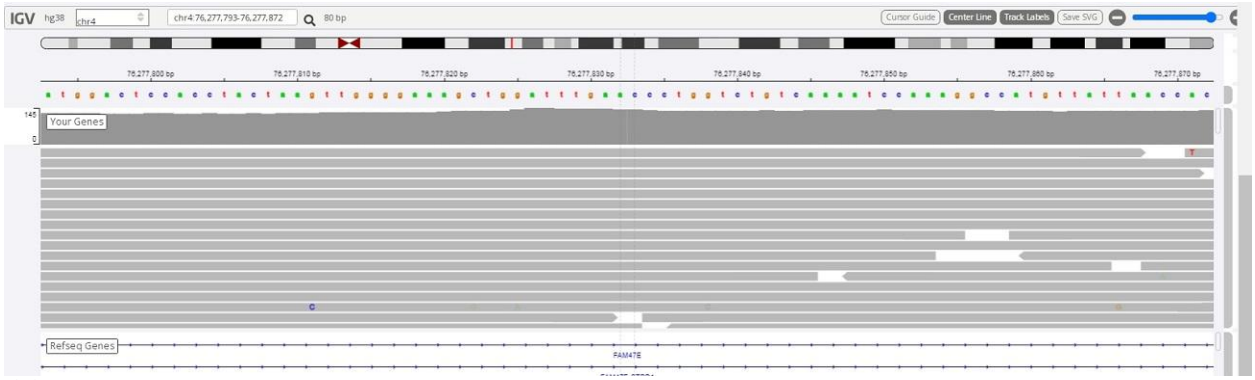

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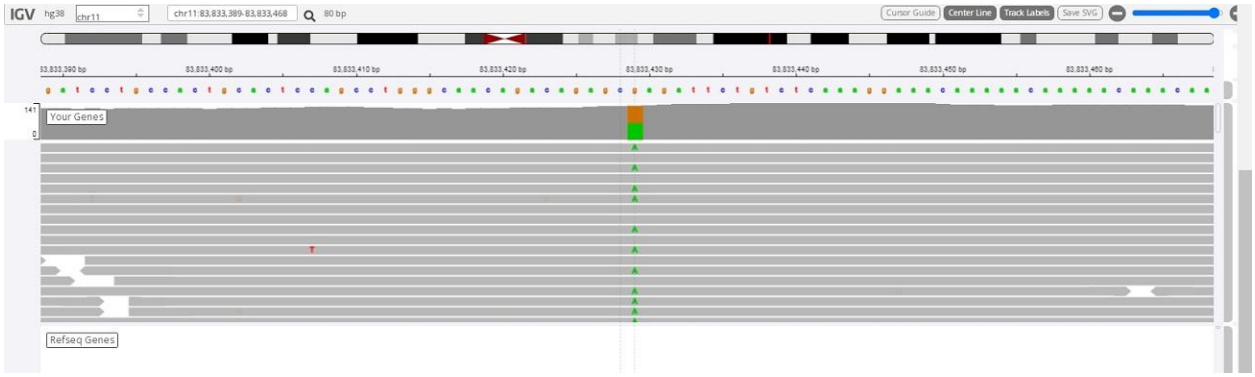

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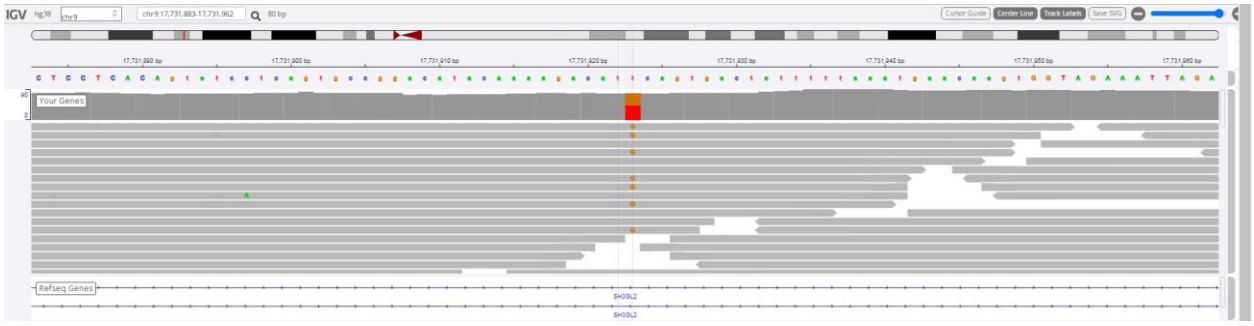

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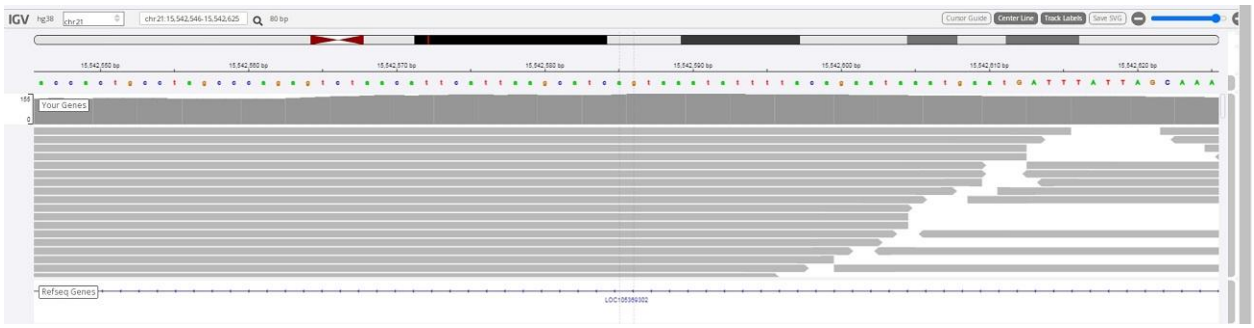

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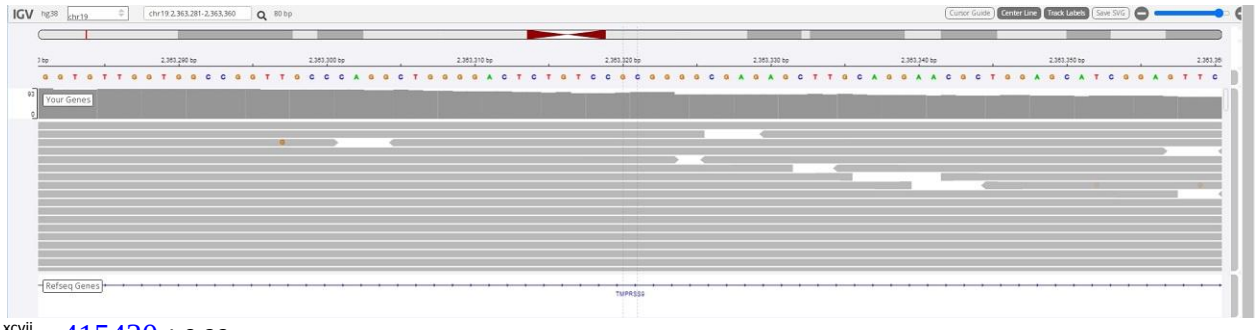

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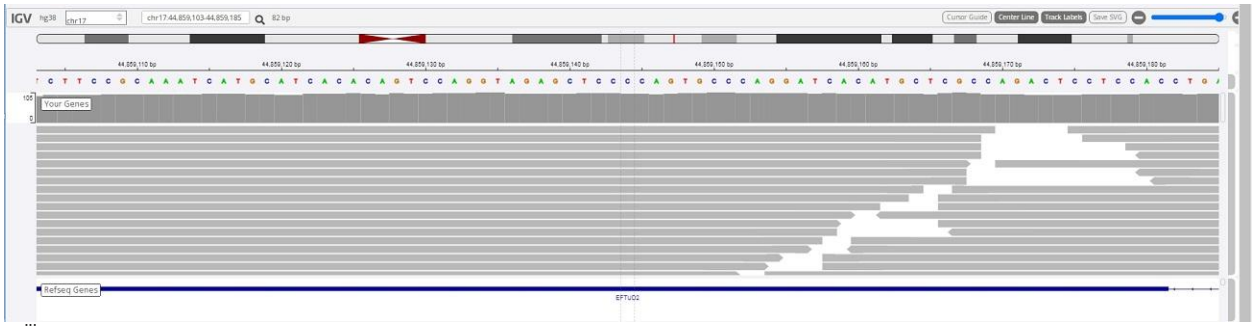

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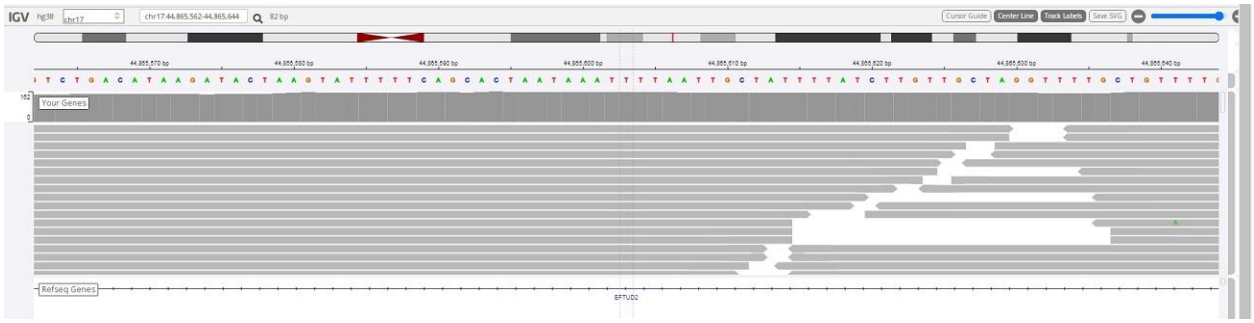

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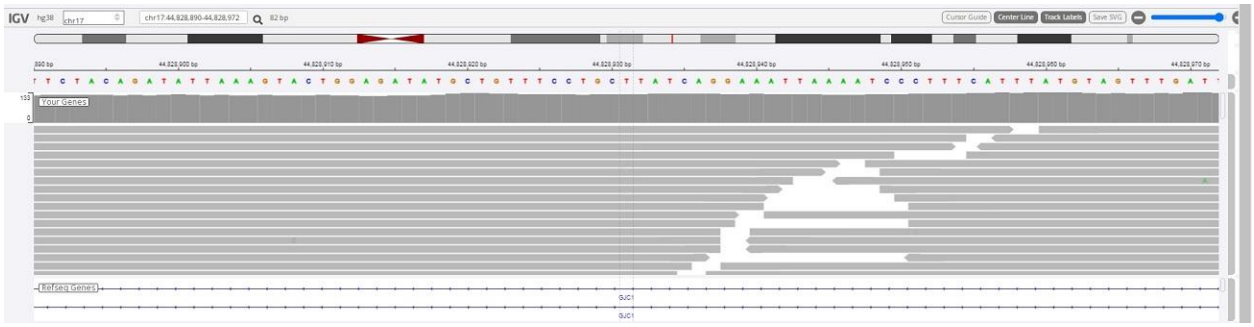

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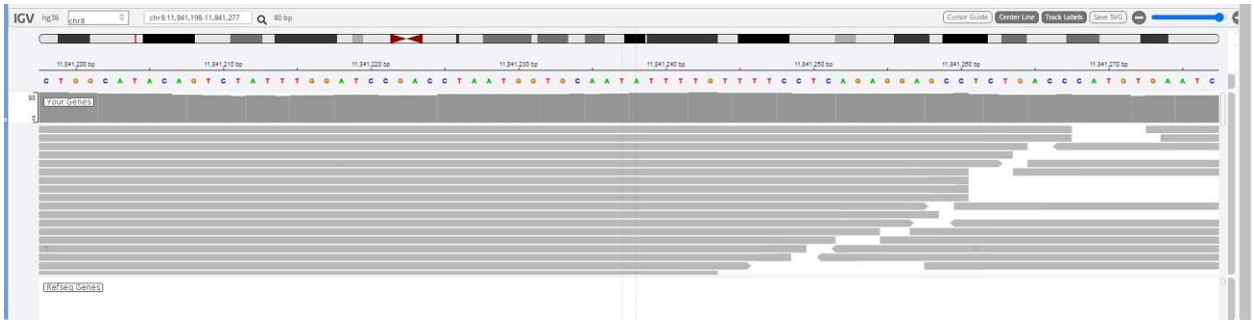

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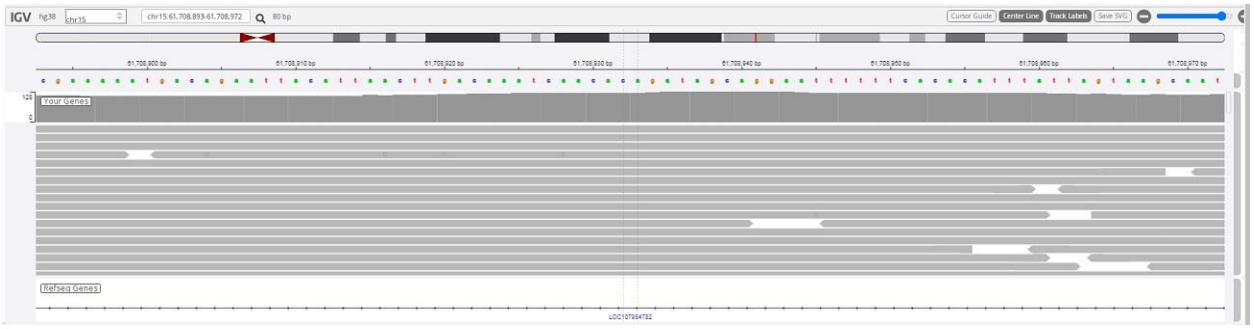

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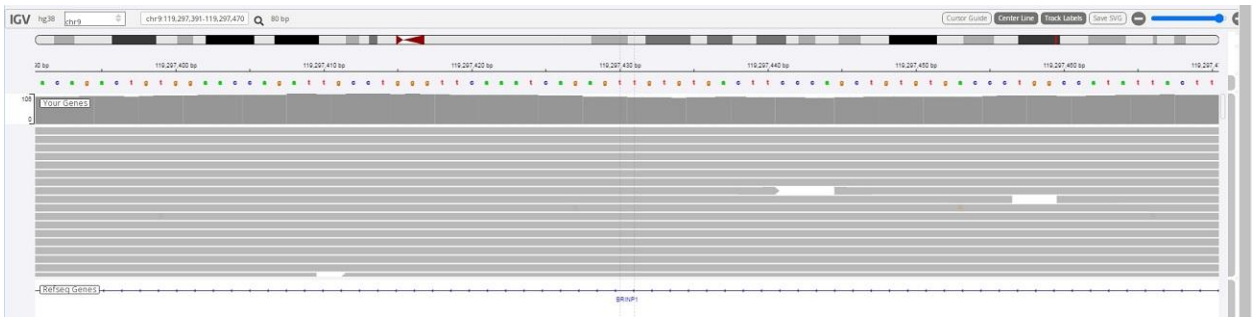

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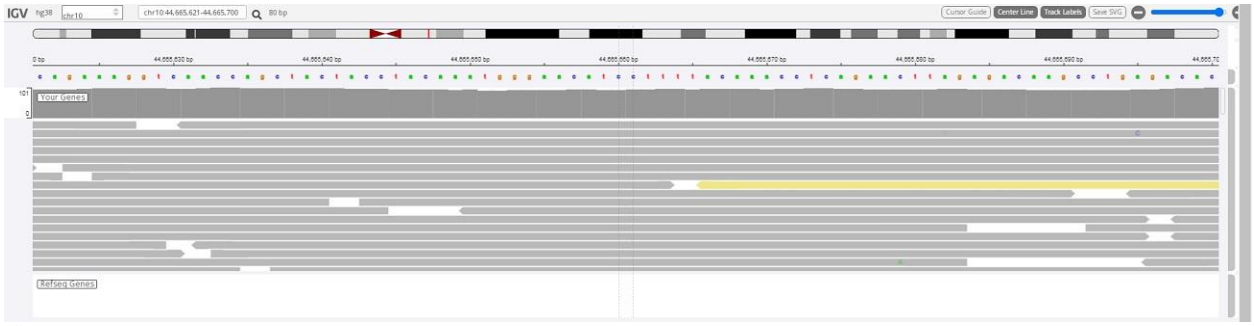

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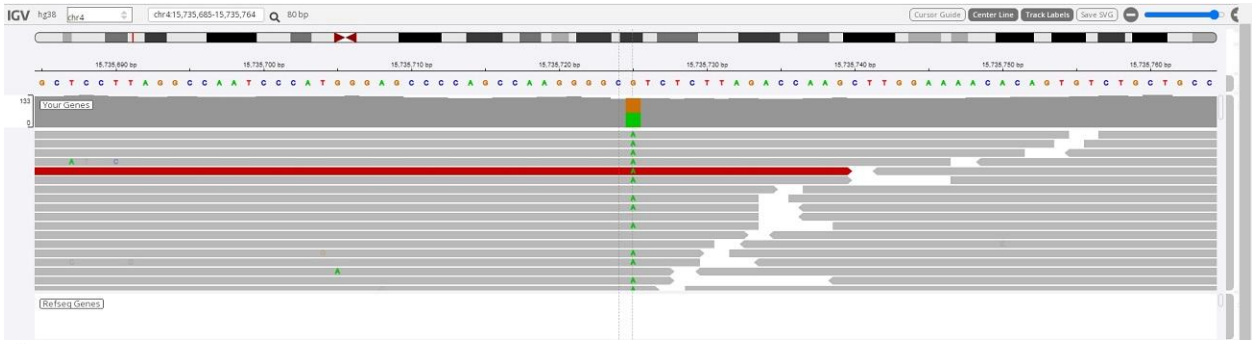

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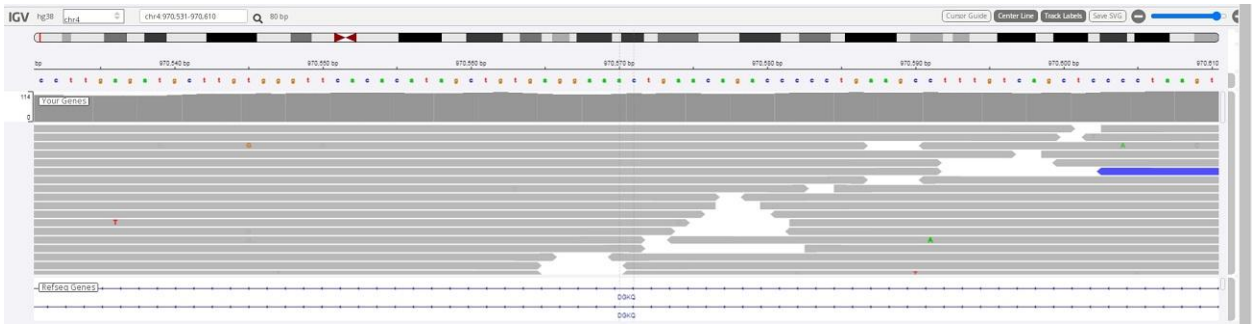

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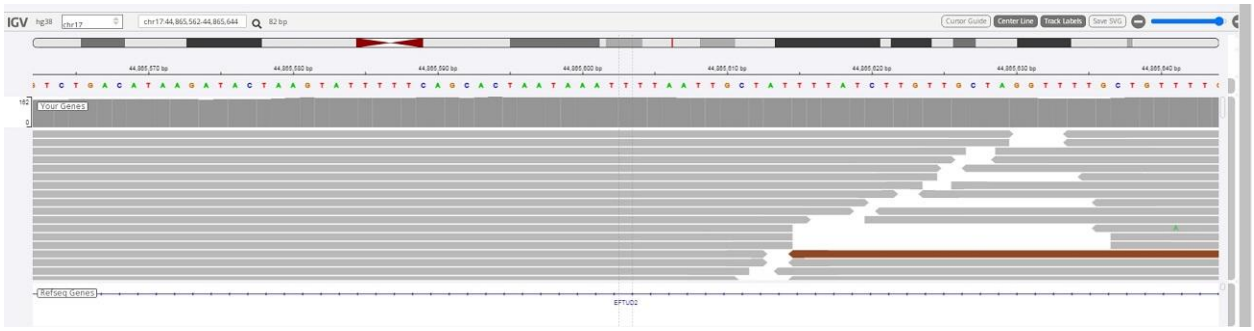

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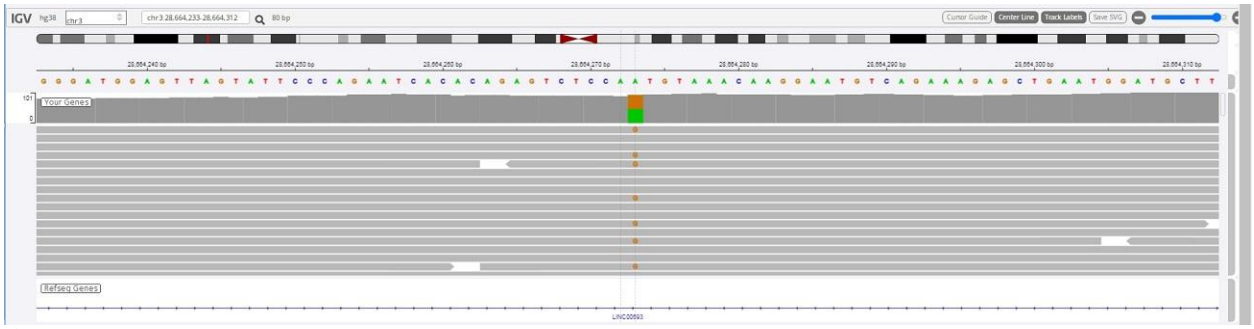

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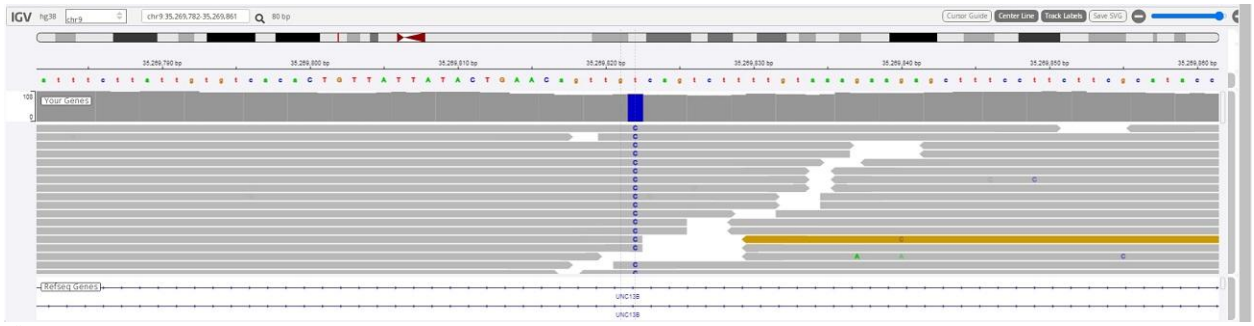

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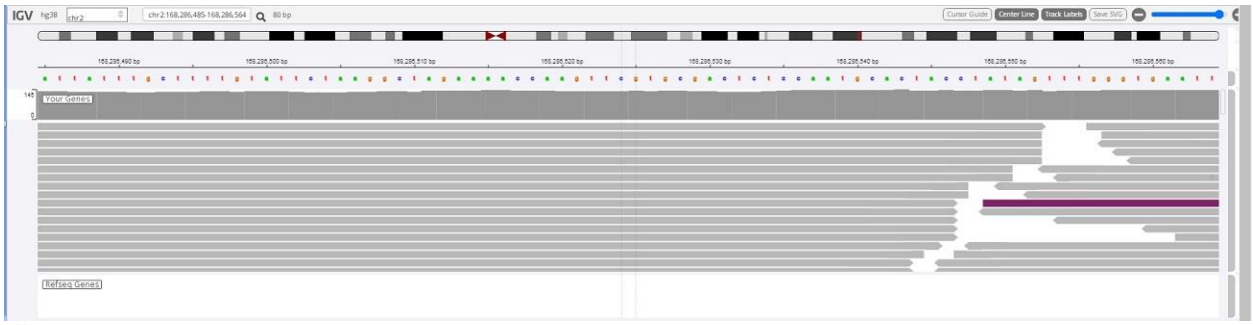

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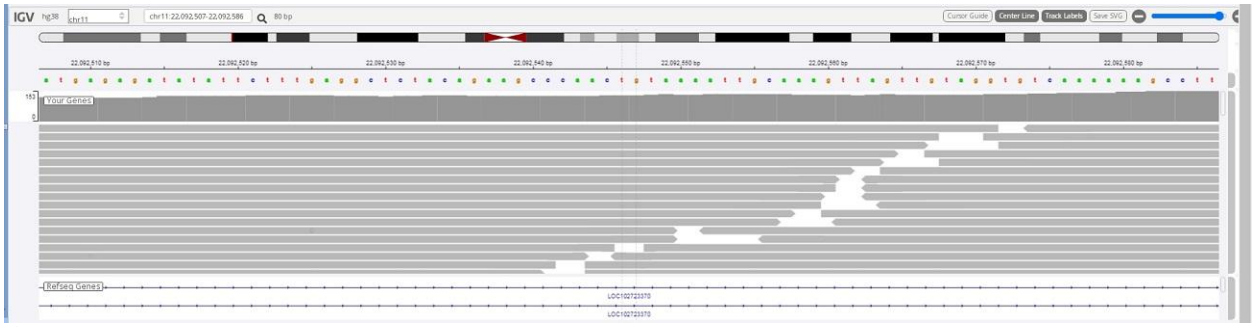

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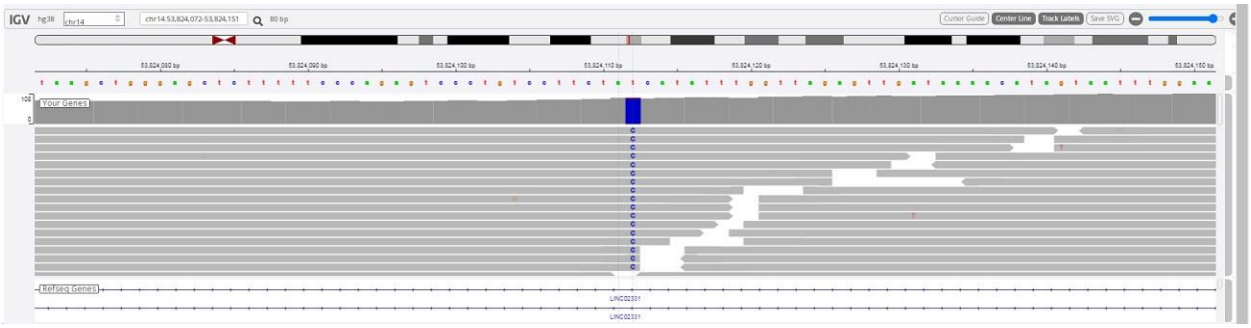

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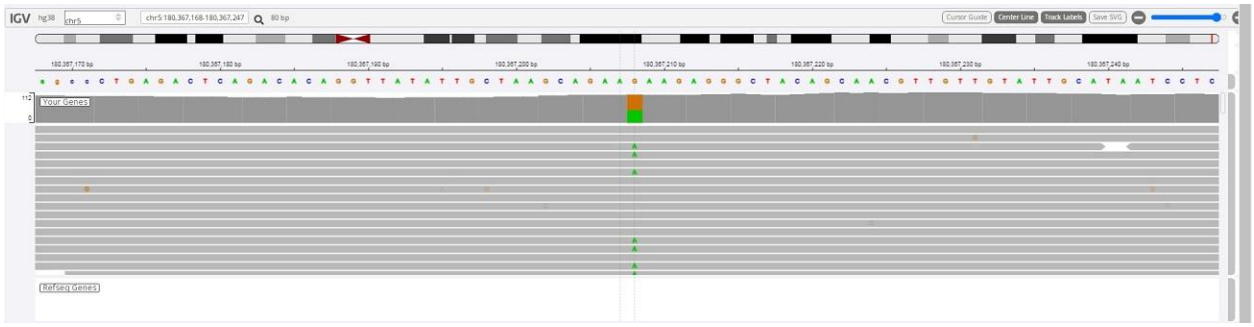

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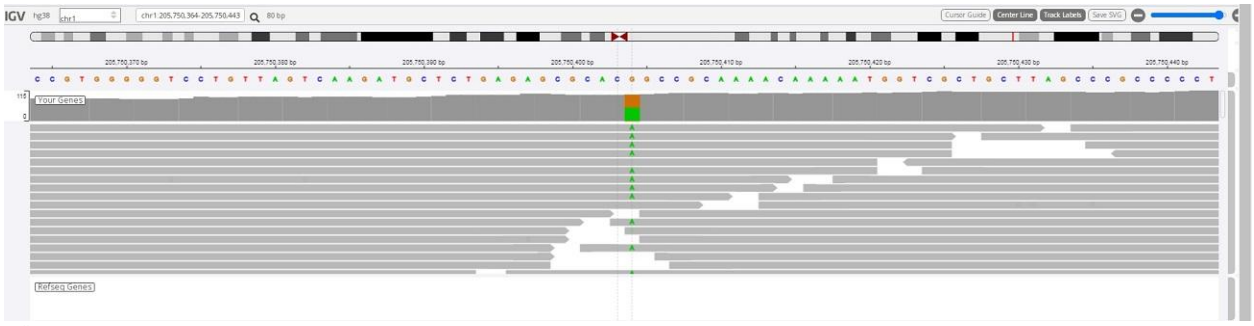

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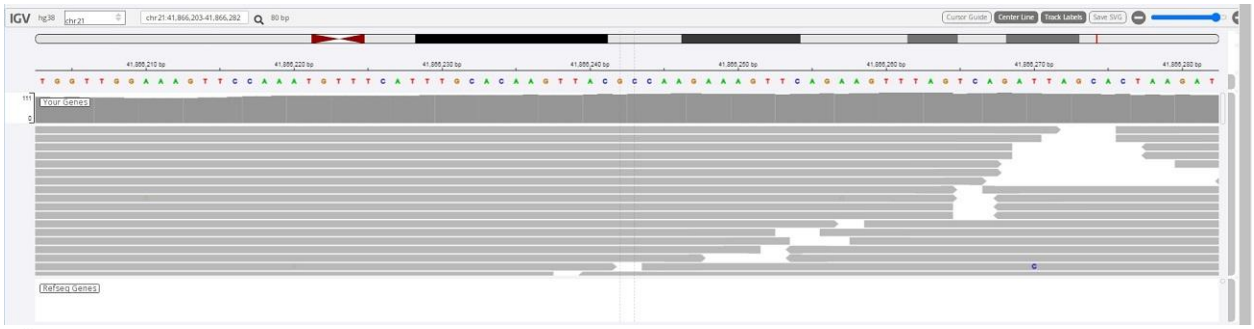

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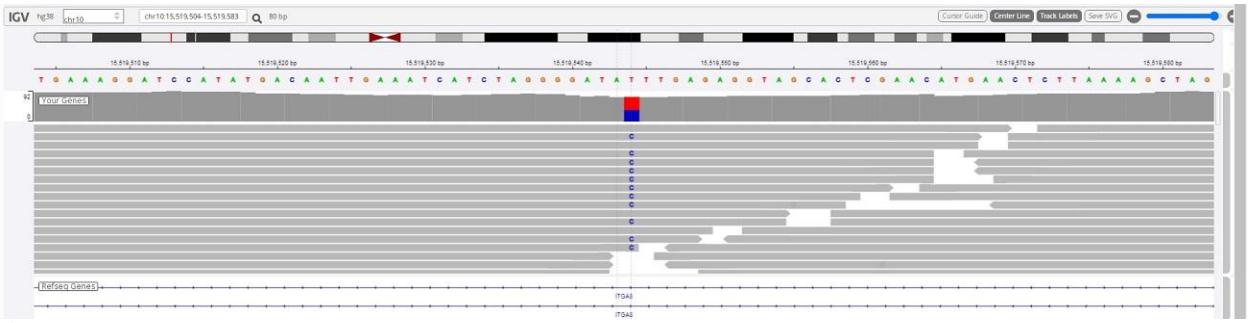

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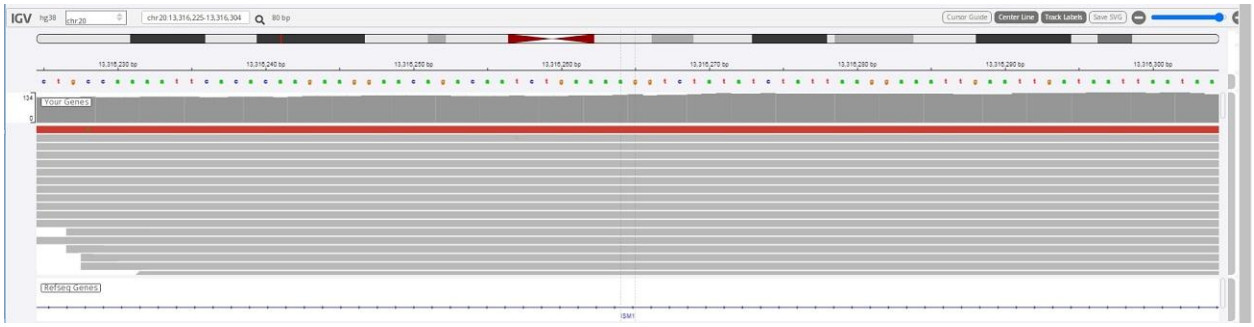

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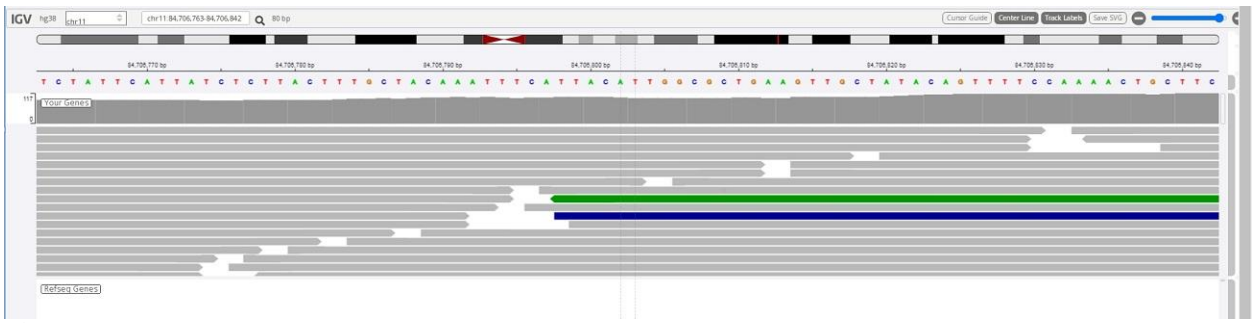

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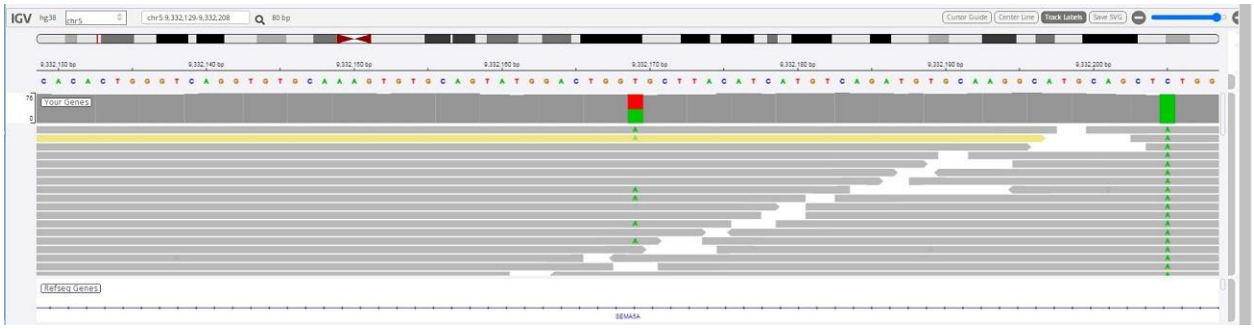
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Your Genes
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