Timestamp	Your name	Your email (if this is your f	Your Institution (if this is y	GIAB Genome	Version of high-confidenc	Optionally, enter the vcf lin	Chromosome number	Start Position on chromos	True Reference base(s)	True Alternate base(s) - 2	Genotype in VCF format	What evidence do you ha	Did you find any other var	If yes, please give some i	Is there any additional inf	rs number of the variant if	Does the GIAB call appea	Is this a repetitive region?	Reference assembly
2/3/2016 16:17:21	John Thompson	thompson.john.f@gmail.c	Claritas Genomics	HG001/NA12878	NISTv2.19		1	3669201	A	G	1/1 (Homozygous variant)	Sanger confirmation, Con	Yes	Yes. rs10910021 is 4 bp away and is also homozygo		rs10797410			
2/3/2016 16:23:29	John Thompson	thompson.john.f@gmail.c	Claritas Genomics	HG001/NA12878	NISTv2.19		3	33138544	A	G	1/1 (Homozygous variant)	Sanger confirmation, Con	Yes	Additional homozygous alternate SNP 5 bp away. rs		rs7614776			
2/3/2016 17:10:35	John Thompson	thompson.john.f@gmail.c	Claritas Genomics	HG001/NA12878	NISTv2.19		6	33644768	A	G	1/1 (Homozygous variant)	Sanger confirmation, Con	Yes	rs4713652 located 5 bp away, also homozygous alte		rs2068236			
2/3/2016 17:15:44	John Thompson	thompson.john.f@gmail.c	Claritas Genomics	HG001/NA12878	NISTv2.19		6	107077507	C	A	0/1 (Heterozygous)	Sanger confirmation, Con	Yes	rs2054365 Homozygous alternate located 5 bp awa		rs72945092			
2/3/2016 17:21:48	John Thompson	thompson.john.f@gmail.c	Claritas Genomics	HG001/NA12878	NISTv2.19		12	80650276	T	TCAAA,TCAAACAAA	1/2 (Compound heterozyg	Confirmation with second	I don't know	Confirmed by Sanger that this is a heterozygous me		rs147846753			
2/3/2016 17:26:06	j	t	c	HG001/NA12878	NISTv2.19		17	71232804	G	T	1/1 (Homozygous variant)	Sanger confirmation, Con	Yes	rs904383 located 3 bp away. homozygous alternate		rs904384			
2/3/2016 17:33:58	John Thompson	thompson.john.f@gmail.c	Claritas Genomics	HG001/NA12878	NISTv2.19		21	47558591	A	C	1/1 (Homozygous variant)	Sanger confirmation, Con	Yes	rs62214031 located 5 bp away, homozygous alterna		rs62214031			
4/29/2016 11:00:45	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta	632574624.AG0PASSmetal=platinum;cgi=.;bwa_freebayes=HD:0,LOOHD:0;bwa_platypus=HD:0,LOOHD:0;bwa_gatk3=HD:0,LOO					0/1 (Heterozygous)	Confirmation with high co	Yes	many variants in this HLA	probably should exclude HLA from high-confidence regions for now				
4/29/2016 11:02:53	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta	421932902.AT0PASSmetal=platinum;cgi=.;bwa_freebayes=HD:0,LOOHD:0;bwa_platypus=.;bwa_gatk3=HD:0,LOOHD:0;cortex=.;i					1/1 (Homozygous variant)	Confirmation with second	Yes	nearby indel	3.1b miscalls as a het				
4/29/2016 11:14:53	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta	2739644.GGA0PASSmetal=platinum;cgi=.;bwa_freebayes=HD:0,LOOHD:0;bwa_platypus=HD:0,LOOHD:0;bwa_gatk3=HD:0,LOOHD:0;cortex=.;isaac2=HD:(						Confirmation with second	Yes	SNP upstream and others	possibly true insertion in 10bp homopolymer, though not in novoalign mappings which had low coverage, many variants in the region, and a likely SV is downstream				
4/29/2016 15:55:02	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta	2 78910526 . A AT 50 PASS platforms=2;platformnames=Illumina,CG;datasets=2;datasetnames=HiSeqPE300x,CGnormal;call						Manual inspection of read	No		This is a 10bp homopolymers and small fraction of Il		It is unclear		
4/29/2016 16:09:32	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta	2172123774.GGTC50PASSplatforms=1;platformnames=Illumina;datasets=1;datasetnames=HiSeqPE300x;callsets=2;callsetnames=HiSeqPE300xfreebayes,						Manual inspection of read	No		PG k-mer incorrectly calls deletion. This is a tandem		Yes, variant and genotype are correct		
4/29/2016 16:27:03	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta	2 205478771 . AT A 50 PASS platforms=1;platformnames=Illumina;datasets=1;datasetnames=HiSeqPE300x;callsets=2;callset						Manual inspection of read	No		10% of Illumina reads have deletion. This is a 10bp		It is unclear	Yes, homopolymer	
4/29/2016 16:42:34	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta	3 16918093 . GT G 50 PASS platforms=2;platformnames=Illumina,CG;datasets=2;datasetnames=HiSeqPE300x,CGnormal;cal						Manual inspection of read	No		~10% of Illumina and CG reads have evidence of de		It is unclear	Yes, homopolymer	
4/29/2016 16:52:56	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta	3 18380321 . A AT 50 PASS platforms=2;platformnames=Illumina,CG;datasets=2;datasetnames=HiSeqPE300x,CGnormal;call						Manual inspection of read	No		1bp insertion in 10bp homopolymer. Illumina and CG		No, Variant is correct but	Yes, homopolymer	
4/29/2016 17:07:12	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta	3 79006193 . G GA 50 PASS platforms=2;platformnames=Illumina,CG;datasets=2;datasetnames=HiSeqPE300x,CGnormal;cal						Manual inspection of read	No		~10% of Illumina and CG reads have evidence of ins		No, position is homozygo	Yes, homopolymer	
4/29/2016 17:21:50	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta	437191158.CCA50PASSplatforms=2;platformnames=Illumina,CG;datasets=2;datasetnames=HiSeqPE300x,CGnormal;callsets=3;callsetnames=HiSeqPE300						Manual inspection of read	No		~10% Illumina and CG have evidence for insertion. I		No, true call is homozygo	Yes, homopolymer	
5/9/2016 13:52:40	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta		20	112015	G	A	0/1 (Heterozygous)	Manual inspection of read	No				Yes, variant and genotype	Low MQ	
5/9/2016 15:02:08	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta		20	2090925	C	T	0/1 (Heterozygous)	Manual inspection of read	No				Yes, variant and genotype	No	
5/9/2016 15:04:41	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta		20	2479984	A	G	0/1 (Heterozygous)	Manual inspection of read	Yes	~10 within 200 bp			Yes, variant and genotype	No	
5/9/2016 15:08:10	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta		20	2480035	TG	CG,CA	1/2 (Compound heterozyg	Manual inspection of read	Yes	adjacent SNPs; near large	low cov in illumina		Yes, variant and genotype	No	
5/9/2016 15:11:15	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta		20	3044286	GGCTCC	TGCTCC,TGCTCG	1/2 (Compound heterozyg	Manual inspection of read	Yes	another compound het pair downstream			Yes, variant and genotype	No	
5/9/2016 15:13:13	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta		20	10447120	G	A	0/1 (Heterozygous)	Manual inspection of read	No				Yes, variant and genotype	No	
5/9/2016 15:16:07	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta		20	11528201	T	C	0/1 (Heterozygous)	Manual inspection of read	Yes	possible long T homopolymer indel downstream 30bp			Yes, variant and genotype	No	
5/9/2016 15:20:17	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta		20	17336156	C	T	0/1 (Heterozygous)	Manual inspection of read	No		Might be a large CNV, but clear in moleculo and a lit		It is unclear	No	
5/9/2016 15:23:55	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta		20	18061537	A	G	0/1 (Heterozygous)	Manual inspection of read	No		May be more complex, but probably not too large, si		Yes, variant and genotype	No	
5/9/2016 15:30:28	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta		20	7284487	C	A	0/0 (Homozygous referen	Evidence from long reads	Yes	SNP downstream looks g	Next to 5 T's. Not in PacBio. In 1/15 moleculo reads		Yes, variant and genotype	No	
5/9/2016 15:33:25	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta		20	22110086	G	A	0/0 (Homozygous referen	Manual inspection of read	No		In ~10% of Illumina and 1/13 moleculo. Not in pacbi		Yes, variant and genotype	No	
5/9/2016 15:38:58	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta		20	16389107	G	A	0/0 (Homozygous referen	Manual inspection of read	No		In <5% of moleculo and illumina. Not in PacBio or C		Yes, variant and genotype	No	
5/9/2016 15:44:01	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta		20	10783438	C	CAT	0/1 (Heterozygous)	Manual inspection of read	Yes	AT del in upstream AT rep	complex, but likely good		Yes, variant and genotype	Yes, tandem repeat	
5/9/2016 15:47:06	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta		20	11837479	GA	G	0/1 (Heterozygous)	Manual inspection of read	No		Looks good in Illumina, CG, and moleculo. Not in P		Yes, variant and genotype	Yes, homopolymer	
5/9/2016 15:55:42	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta	20 16421193 . CACAC C 50 PASS platforms=1;platformnames=Illumina;datasets=1;datasetnames=HiSeqPE300x;callsets=2;callsetnam						Manual inspection of read	Yes	compound het in CA repeat			Correct but this part of co	Yes, tandem repeat	
5/9/2016 16:01:12	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta	20 59933876 . GAC AGG 50 PASS platforms=2;platformnames=Illumina,CG;datasets=2;datasetnames=HiSeqPE300x,CGnormal;call						Manual inspection of read	Yes	downstream phased SNP			Yes, variant and genotype	No	
5/9/2016 16:06:23	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta		20	32310237	TG	T	0/0 (Homozygous referen	Evidence from long reads	No		In Illumina-bwa but not novoalign, moleculo, CG, or		Yes, variant and genotype	No	
5/9/2016 16:13:47	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta		20	58508810	GC	G	0/1 (Heterozygous)	Evidence from long reads	No		Unclear - should probably expand low confidence re		It is unclear	Yes, homopolymer	
5/9/2016 16:16:48	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta		20	30089846	A	AT	0/0 (Homozygous referen	Manual inspection of read	No		In small fraction of illumina and moleculo reads in 1(		It is unclear	Yes, homopolymer	
5/9/2016 16:18:51	Justin Zook		NIST	HG001/NA12878	NISTv3.1beta		20	54146967	GT	G	0/0 (Homozygous referen	Manual inspection of read	No				Yes, variant and genotype	Yes, homopolymer	
5/11/2016 17:14:55	Justin Zook		NIST	HG001/NA12878	NISTv3.2	2 193407934 . T TA 50 PASS platforms=2;platformnames=CG,Illumina;datasets=2;datasetnames=CGnormal,HiSeqPE300x;ca						Manual inspection of read	No		This is likely a SSE in multiple technologies or a true		It is unclear	Yes, homopolymer	
5/11/2016 17:37:54	Justin Zook		NIST	HG001/NA12878	NISTv3.2	318380321.AAT50PASSplatforms=2;platformnames=Illumina,CG;datasets=2;datasetnames=HiSeqPE300x,CGnormal;callsets=2;callsetnames=HiSeqPE300						Evidence from phasing us	No		Illumina, SOLiD, CG and Moleculo have small fractio		No, Variant is correct but	Yes, homopolymer	
5/11/2016 17:45:25	Justin Zook		NIST	HG001/NA12878	NISTv3.2	437191158.CCA50PASSplatforms=2;platformnames=Illumina,CG;datasets=2;datasetnames=HiSeqPE300x,CGnormal;callsets=3;callsetnames=HiSeqPE300						Manual inspection of read	No		Variant is only in a small fraction of Illumina and CG		No, true call is homozygo	Yes, homopolymer	
5/11/2016 17:51:21	Justin Zook		NIST	HG001/NA12878	NISTv3.2	4101197879.TA,G50PASSplatforms=3;platformnames=Illumina,CG,Solid;datasets=3;datasetnames=HiSeqPE300x,CGnormal,SolidSE75bp;callsets=4;callset						Manual inspection of read	No		PG incorrectly calls homozygous variant.		Yes, variant and genotype	No	
5/11/2016 18:06:52	Justin Zook		NIST	HG001/NA12878	NISTv3.2	4119117261.AG50PASSplatforms=2;platformnames=CG,Illumina;datasets=2;datasetnames=CGnormal,HiSeqPE300x;callsets=2;callsetnames=CGnormal,Hi						Manual inspection of read	Yes	Confident of homozygous SNP at previous position.			This appears to be a true	No	
5/13/2016 13:43:28	Justin Zook		NIST	HG001/NA12878	NISTv3.2	4138641605.GGA50PASSplatforms=2;platformnames=Illumina,CG;datasets=2;datasetnames=HiSeqPE300x,CGnormal;callsets=3;callsetnames=HiSeqPE30						Manual inspection of read	Yes	True homozygous SNP	Homozygous variant in PGv7 and no call for v8. No		No, Variant is correct but	Yes, homopolymer	
5/13/2016 13:51:06	Justin Zook		NIST	HG001/NA12878	NISTv3.2	5 27306485 . C CT 50 PASS platforms=2;platformnames=Illumina,CG;datasets=2;datasetnames=HiSeqPE300x,CGnormal;cal						Manual inspection of read	No		Variant only in 10-20% of Illumina and CG reads.		No, true call is homozygo	Yes, homopolymer	
5/13/2016 14:15:27	Justin Zook		NIST	HG001/NA12878	NISTv3.2	583046430.TAT50PASSplatforms=2;platformnames=CG,Illumina;datasets=2;datasetnames=CGnormal,HiSeqPE300x;callsets=2;callsetnames=CGnormal,Hi						Manual inspection of read	No		It's in 10-20% of Ilumina, CG and Molecule reads. E		It is unclear	No	
5/13/2016 14:24:56	Justin Zook		NIST	HG001/NA12878	NISTv3.2	584697030.CTC50PASSplatforms=2;platformnames=Illumina,CG;datasets=2;datasetnames=HiSeqPE300x,CGnormal;callsets=3;callsetnames=HiSeqPE300						Manual inspection of read	No		Variant only in 10-20% of CG and Illumina reads.		No, true call is homozygo	Yes, homopolymer	
5/13/2016 14:37:33	Justin Zook		NIST	HG001/NA12878	NISTv3.2	6109713384.CCT50PASSplatforms=2;platformnames=Illumina,CG;datasets=2;datasetnames=HiSeqPE300x,CGnormal;callsets=3;callsetnames=HiSeqPE30						Manual inspection of read	No		Variant only in 15-30% of Illumina, CG and Moleculo		No, true call is homozygo	Yes, homopolymer	
5/13/2016 14:50:20	Justin Zook		NIST	HG001/NA12878	NISTv3.2	6112769586.AG50PASSplatforms=3;platformnames=Illumina,CG,Solid;datasets=3;datasetnames=HiSeqPE300x,CGnormal,SolidSE75bp;callsets=3;callsetna						Manual inspection of read	No		Variant in 85-95% of CG and Illumina reads.		It is unclear	No	
5/13/2016 15:02:11	Justin Zook		NIST	HG001/NA12878	NISTv3.2	6 114480340 . T G 50 PASS platforms=2;platformnames=Illumina,CG;datasets=2;datasetnames=HiSeqPE300x,CGnormal;call						Manual inspection of read	No		Variant in ~90% of GC, SOLiD and Illumina reads.		It is unclear	No	
5/13/2016 15:47:06	Justin Zook		NIST	HG001/NA12878	NISTv3.2	6 167245524 . T TGATA 50 PASS platforms=1;platformnames=Illumina;datasets=1;datasetnames=HiSeqPE300x;callsets=2;ca						Manual inspection of read	No		This was an error in PG7 that was fixed in PG8.		Yes, variant and genotype	Yes, tandem repeat	
5/13/2016 15:55:33	Justin Zook		NIST	HG001/NA12878	NISTv3.2	6168780695.AC50PASSplatforms=1;platformnames=Illumina;datasets=1;datasetnames=HiSeqPE300x;callsets=2;callsetnames=HiSeqPE300xfreebayes,HiS						Manual inspection of read	No		Long reads show evidence for duplication. Long and		It is unclear	No	
5/13/2016 16:08:09	Justin Zook		NIST	HG001/NA12878	NISTv3.2	827278795.CTATTTATTTATTTATTTATTTATTCTATTTATTTATTTATTTATT,C50PASSplatforms=1;platformnames=Illumina;datasets=1;datasetnames=HiSeqPE						Manual inspection of read	Yes	SNP phased with shorter	Error in PG calls		Yes, variant and genotype	Yes, tandem repeat	
5/13/2016 16:28:11	Justin Zook		NIST	HG001/NA12878	NISTv3.2	2143366875.TC.PASSMTD=isaac2GT1|0						Manual inspection of read	No		Illumina has low mapping quality reads with multiple		Yes, variant and genotype are correct		
5/26/2016 14:24:34	Justin Zook		NIST	HG001/NA12878	NISTv3.2	842384671.AC50PASSplatforms=3;platformnames=Illumina,CG,Solid;datasets=3;datasetnames=HiSeqPE300x,CGnormal,SolidSE75bp;callsets=4;callsetnar						Manual inspection of read	No				Yes, variant and genotype	No	
5/26/2016 14:25:52	Justin Zook		NIST	HG001/NA12878	NISTv3.2	8114484792.TTGAAA50PASSplatforms=1;platformnames=Illumina;datasets=1;datasetnames=HiSeqPE300x;callsets=2;callsetnames=HiSeqPE300xfreebay						Manual inspection of read	No		Error in PG7		Yes, variant and genotype	Yes, tandem repeat	
5/26/2016 14:26:48	Justin Zook		NIST	HG001/NA12878	NISTv3.2	987032826.TTTTTA50PASSplatforms=1;platformnames=Illumina;datasets=1;datasetnames=HiSeqPE300x;callsets=2;callsetnames=HiSeqPE300xfreebayes						Manual inspection of read	No		Error in PG7		Yes, variant and genotype	Yes, tandem repeat	
5/26/2016 14:27:42	Justin Zook		NIST	HG001/NA12878	NISTv3.2	1067516838.TTTTTA50PASSplatforms=1;platformnames=Illumina;datasets=1;datasetnames=HiSeqPE300x;callsets=2;callsetnames=HiSeqPE300xfreebaye						Manual inspection of read	No		Error in PG7		Yes, variant and genotype	Yes, tandem repeat	
5/26/2016 14:30:15	Justin Zook		NIST	HG001/NA12878	NISTv3.2	10127738581.CCTGGC50PASSplatforms=1;platformnames=Illumina;datasets=1;datasetnames=HiSeqPE300x;callsets=2;callsetnames=HiSeqPE300xfreeba						Manual inspection of read	Yes	Overlapping deletion	partial compound het in PG		Yes, variant and genotype	Yes, tandem repeat	
5/26/2016 14:33:01	Justin Zook		NIST	HG001/NA12878	NISTv3.2	11125295399.CTCCAATAACGATCAGAGAGCAGCCACTGTGCCTTGATGGTTTGCCGTGAC50PASSplatforms=1;platformnames=Illumina;datasets=1;datas						Manual inspection of read	No		Partially in high-confidence region		Yes, variant and genotype are correct		
5/26/2016 14:34:34	Justin Zook		NIST	HG001/NA12878	NISTv3.2	1910489509.ATATCTTATCTATATCT,A50PASSplatforms=1;platformnames=Illumina;datasets=1;datasetnames=HiSeqPE300x;callsets=2;callsetnames=HiSec						Manual inspection of read	No		compound het with incorrect length in PG7		Yes, variant and genotype	Yes, tandem repeat	
5/26/2016 20:35:51	Justin Zook		NIST	HG001/NA12878	NISTv3.2	1153697703.TACT50PASSplatforms=2;platformnames=Illumina,CG;datasets=2;datasetnames=HiSeqPE300x,CGnormal;callsets=3;callsetnames=HiSeqPE3						Manual inspection of read	Yes	nearby compound het in TR			Yes, variant and genotype	Yes, tandem repeat	
5/26/2016 20:38:52	Justin Zook		NIST	HG001/NA12878	NISTv3.2	2229289081.GC50PASSplatforms=1;platformnames=Illumina;datasets=1;datasetnames=HiSeqPE300x;callsets=2;callsetnames=HiSeqPE300xfreebayes,HiS						Manual inspection of read	Yes	Many phased nearby varia	Probably true but many nearby variants so possibly		Yes, variant and genotype	No	
5/26/2016 20:42:00	Justin Zook		NIST	HG001/NA12878	NISTv3.2	4118979242.CACTTATGAGCAC50PASSplatforms=2;platformnames=Illumina,CG;datasets=2;datasetnames=HiSeqPE300x,CGnormal;callsets=3;callsetnam						Manual inspection of read	No		missing in 2.19		Yes, variant and genotype	No	
5/26/2016 20:44:35	Justin Zook		NIST	HG001/NA12878	NISTv3.2	672011579.GAGAG50PASSplatforms=4;platformnames=Illumina,CG,Ion,Solid;datasets=4;datasetnames=HiSeqPE300x,CGnormal,IonExome,SolidPE50x50						Manual inspection of read	No		missing in 2.19		Yes, variant and genotype	No	
5/26/2016 20:50:21	Justin Zook		NIST	HG001/NA12878	NISTv3.2	8116818941.GAAGGAAAGAG50PASSplatforms=1;platformnames=Illumina;datasets=1;datasetnames=HiSeqPE300x;callsets=2;callsetnames=HiSeqPE300:						Manual inspection of read	Yes		Multiple nearby deletions. One deletion dearby may		Yes, variant and genotype	Yes, tandem repeat	
5/26/2016 20:52:35	Justin Zook		NIST	HG001/NA12878	NISTv3.2	1113069952.GC50PASSplatforms=3;platformnames=Illumina,CG,Solid;datasets=4;datasetnames=HiSeqPE300x,CGnormal,SolidPE50x50bp,SolidSE75bp;c						Manual inspection of read	Yes	multiple nearby homozygo	missed in 2.19		Yes, variant and genotype	No	
5/26/2016 20:56:08	Justin Zook		NIST	HG001/NA12878	NISTv3.2	12121087853.TGCT50PASSplatforms=1;platformnames=Illumina;datasets=1;datasetnames=HiSeqPE300x;callsets=1;callsetnames=HiSeqPE300xGATK;dat						Manual inspection of read	Yes	phased SNP and del	partially excluded in 2.19		Yes, variant and genotype	No	
5/26/2016 20:58:59	Justin Zook		NIST	HG001/NA12878	NISTv3.2	1680203808.ACATAAAATTATAGCACAATGA50PASSplatforms=2;platformnames=Illumina,CG;datasets=2;datasetnames=HiSeqPE300x,CGnormal;callsets=						Manual inspection of read	No		phased SNP ~60bp away		Yes, variant and genotype	No	
5/26/2016 21:01:05	Justin Zook		NIST	HG001/NA12878	NISTv3.2	2245514995.CATC50PASSplatforms=3;platformnames=Illumina,CG,Solid;datasets=3;datasetnames=HiSeqPE300x,CGnormal,SolidSE75bp;callsets=4;callse						Manual inspection of read	No				Yes, variant and genotype	No	
5/26/2016 21:03:19	Justin Zook		NIST	HG001/NA12878	NISTv3.2	X151572041.CGTCGTGT,C50PASSplatforms=2;platformnames=Illumina,CG;datasets=2;datasetnames=HiSeqPE300x,CGnormal;callsets=3;callsetnames=H						Manual inspection of read	No		error in 2.19		Yes, variant and genotype are correct		
5/26/2016 21:07:23	Justin Zook		NIST	HG001/NA12878	NISTv2.19	139563402.AGA8804PASSDPSum=619;HRun=0;HapNoVar=0;NoPLTot=10;PLCG=386,386,386,65,386,0;PLHSWG=1114,1114,1114,179,1114,0;PLILL250=2						Manual inspection of read	No		SNP correct in 3.2		No, true call is missing fro	No	
5/26/2016 21:13:33	Justin Zook		NIST	HG001/NA12878	NISTv2.19	281081493.ATCTCA6944PASSDPSum=471;HRun=0;HapNoVar=0;NoPLTot=0;PLCG=138,10,0;PLHSWG=659,88,0;PLILL250=589,59,0;PLILLCLIA=311,24,						Manual inspection of read	Yes		error in 2.19 due to variants in adjacent TRs		No, true call is homozygo	Yes, tandem repeat	
5/26/2016 21:23:42	Justin Zook		NIST	HG001/NA12878	NISTv2.19	3127735960.TGAGACAGAGT1787PASSDPSum=259;HRun=2;HapNoVar=0;NoPLTot=0;PLILLCLIA=216,0,2467;PLIllPCRFree=271,0,3117;PLPlatGen=130(						Evidence from long reads	I don't know		next to long T homopolymer. Deletion is not in PacBi		No, true call is homozygo	Yes, homopolymer	
5/26/2016 21:27:00	Justin Zook		NIST	HG001/NA12878	NISTv2.19	482007747.GTAATAAG3431PASSDPSum=552;HRun=0;HapNoVar=0;NoPLTot=0;PL454WG=72,0,303;PLHSWG=189,0,1513;PLILL250=261,0,1071;PLILLC						Manual inspection of read	Yes		error in 2.19. Near true het and hom SNP		No, true call is missing from GIAB calls or both variant and genotype are incorrect		
5/26/2016 21:36:49	Justin Zook		NIST	HG001/NA12878	NISTv2.19	6102743484.TC3201PASSDPSum=407;HRun=2;HapNoVar=0;NoCG;NoPLTot=1;PL454WG=67,0,257;PLCG=0,48,956;PLHSWG=215,0,1048;PLILL250=12(						Evidence from long reads	Yes		Looks likely to be an SV. Is not excluded by high co		It is unclear		
6/17/2016 16:54:22	Justin Zook			HG002/AJ Son	NISTv3.2.2	1 1661704 . A G . . BS=1661704;Regions=CONF, map_siren GT:QQ:BD:BK:BI:BVT:BLT .:.:.:.:.:NOCALL:nocall 0/1:232.77:FP:: ti:SNP:het						Manual inspection of read	I don't know		Difficult to map region but likely true since in pacbio		No, true call is missing fro	No	
6/17/2016 16:56:04	Justin Zook			HG002/AJ Son	NISTv3.2.2	1 1677120 . A C . . BS=1677120;Regions=CONF, lowcmp_Human_Full_Genome_TRDB_hg19_150331,lowcmp_Human_Full_Genome_TRDB_hg19_150 331_all_merged,map_l100_m1_e0,map_l100_m2_e0,map_l100_m2_e1,map_l125_m1_e0,map_l 125_m2_e0,map_l125_m2_e1,map_siren GT:QQ:BD:BK:BI:BVT:BLT .:.:.:.:.:NOCALL :nocall 1/1:76.77:FP::tv:SNP:het						Manual inspection of read	I don't know		Clear evidence in pacbio - likely hom var but possibl		No, true call is missing fro	No	
6/17/2016 16:57:15	Justin Zook			HG002/AJ Son	NISTv3.2.2	1 2050152 . C CTG,CTGTGTGTG . . BS=2050153;Regio ns=CONF,HG002compoundhet GT:BD:BK:BI:QQ:BVT:BLT 1|2:FN:am:i1_5,i6_15::I NDEL:hetalt						Manual inspection of read	Yes	SNP in father nearby not inherited			Yes, variant and genotype	Yes, tandem repeat	
6/17/2016 16:58:23	Justin Zook			HG002/AJ Son	NISTv3.2.2	1 2563532 . A C . . BS=2563532;Regions=CONF GT:QQ:BD:BK:BI:BVT:BLT 0/0						Manual inspection of read	Yes	More FPs in poly-C			Yes, variant and genotype	Yes, homopolymer	
11/9/2016 16:10:10	Justin Zook			HG001/NA12878	NISTv3.3.2	17667459.GGTGGA.PASSMTD=isaac_strelka,bwa_freebayes,bwa_platypus,bwa_gatk;KM=12.14;KFP=0;KFF=0GT1|0						Manual inspection of read	No				No, true call is missing fro	Yes, tandem repeat	
11/9/2016 16:14:19	JZ			HG001/NA12878	NISTv3.3.2	140283025.GA.PASSMTD=isaac_strelka,bwa_freebayes,bwa_gatk;KM=5.00;KFP=0;KFF=0GT0|1						Manual inspection of read	No		low frequency variant in one 10X haplotype and in p		It is unclear	No	
11/9/2016 16:16:26	JZ			HG001/NA12878	NISTv3.3.2	163644380.AATATATC,ATATATCTATATC50PASSplatforms=1;platformnames=Illumina;datasets=1;datasetnames=HiSeqPE300x;callsets=2;callsetnames=HiS						Manual inspection of read	No				Yes, variant and genotype	Yes, tandem repeat	
11/9/2016 16:53:35	JZ			HG001/NA12878	NISTv3.3.2	176807290.TTTTCTTTCTTTTCTTTCTTTCTTTC,T50PASSplatforms=2;platformnames=Illumina,10X;datasets=2;datasetnames=HiSeqPE300x,10XChromium						Manual inspection of read	No		mis-genotype in PG		Yes, variant and genotype	Yes, tandem repeat	
11/9/2016 16:55:47	JZ			HG001/NA12878	NISTv3.3.2	1105751350.TTTAAA50PASSplatforms=2;platformnames=Illumina,10X;datasets=2;datasetnames=HiSeqPE300x,10XChromium;callsets=3;callsetnames=HiS						Manual inspection of read	No		FN in PG		Yes, variant and genotype	Yes, tandem repeat	
11/9/2016 17:00:11	JZ			HG001/NA12878	NISTv3.3.2	1110622663.AATCTATTCTAT50PASSplatforms=2;platformnames=Illumina,10X;datasets=2;datasetnames=HiSeqPE300x,10XChromium;callsets=3;callsetnar						Manual inspection of read	No		Likely true but another del and ins 100 and 200bp do		Yes, variant and genotype	Yes, tandem repeat	
11/9/2016 17:02:40	JZ			HG001/NA12878	NISTv3.3.2	1242554329.TTA50PASSplatforms=2;platformnames=CG,Illumina;datasets=2;datasetnames=CGnormal,HiSeqPE300x;callsets=2;callsetnames=CGnormal,H						Manual inspection of read	No		in one haplotype of 10X and CG, so seems likely to		Yes, variant and genotype	Yes, homopolymer	
11/9/2016 17:04:58	JZ			HG001/NA12878	NISTv3.3.2	26810453rs376388976GGTG50PASSplatforms=2;platformnames=Illumina,10X;datasets=2;datasetnames=HiSeqPE300x,10XChromium;callsets=3;callsetna						Manual inspection of read	No		miscalled 4bp del in PG		Yes, variant and genotype	Yes, tandem repeat	
11/9/2016 17:06:33	JZ			HG001/NA12878	NISTv3.3.2	246904585.GTG50PASSplatforms=3;platformnames=Illumina,CG,10X;datasets=3;datasetnames=HiSeqPE300x,CGnormal,10XChromium;callsets=4;callsetr						Manual inspection of read	No		FN in PG		Yes, variant and genotype	No	
11/9/2016 17:08:18	JZ			HG001/NA12878	NISTv3.3.2	2172123774rs57883612GGTC50PASSplatforms=2;platformnames=Illumina,10X;datasets=2;datasetnames=HiSeqPE300x,10XChromium;callsets=3;callsetna						Manual inspection of read	No		called a del in PG		Yes, variant and genotype	Yes, tandem repeat	
11/9/2016 17:11:21	JZ			HG001/NA12878	NISTv3.3.2	2137019290.CT.PASSMTD=bwa_freebayes;KM=14.40;KFP=0;KFF=0GT0/0						Manual inspection of read	No		appears to be FP in PG due to mapping error. not in		Yes, variant and genotype	No	
11/9/2016 17:14:54	JZ			HG001/NA12878	NISTv3.3.2	2143366875.TC.PASSMTD=isaac_strelka;KM=1.80;KFP=2;KFF=0GT0/0						Manual inspection of read	Yes	multiple phased SNPs in I	Likely a CNV or mapping error based on pacbio high		Yes, variant and genotype	No	
11/9/2016 17:21:43	JZ			HG001/NA12878	NISTv3.3.2	2159243800.TTATCTAT.PASSMTD=isaac_strelka,bwa_freebayes,bwa_platypus,bwa_gatk;KM=12.62;KFP=0;KFF=0GT1|1						Manual inspection of read	No		FN in CG and other callsets are "not callable"		No, true call is missing fro	Yes, tandem repeat	
11/9/2016 17:24:12	JZ			HG001/NA12878	NISTv3.3.2	2193407934.TTA50PASSplatforms=2;platformnames=Illumina,CG;datasets=2;datasetnames=HiSeqPE300x,CGnormal;callsets=2;callsetnames=HiSeqPE30(						Manual inspection of read	No		In low fraction of illumina and CG reads but in all rea		Yes, variant and genotype	Yes, homopolymer	
11/9/2016 17:28:10	JZ			HG001/NA12878	NISTv3.3.2	2207404940.TACACACACACACACACACACTACACACACACACACACACACACAC,T50PASSplatforms=2;platformnames=Illumina,10X;datasets=2;da						Manual inspection of read	No		PG calls compound del instead of del/ins		Yes, variant and genotype	Yes, tandem repeat	
11/9/2016 17:30:31	JZ			HG001/NA12878	NISTv3.3.2	2240521404.CATTCATTAC.PASSMTD=isaac_strelka,bwa_gatk;KM=24.92;KFP=0;KFF=0GT1|1						Manual inspection of read	No		FN from CG and other callsets "not callable"		No, true call is missing fro	Yes, tandem repeat	
11/9/2016 17:33:37	JZ			HG001/NA12878	NISTv3.3.2	2241529084.TG.PASSMTD=bwa_freebayes;KM=3.80;KFP=0;KFF=1GT0/0						Manual inspection of read	Yes	nearby true SNP	Likely a GGT SSE that inherits properly in PG due to		Yes, variant and genotype	Yes, homopolymer	
11/9/2016 20:23:01	JZ			HG001/NA12878	NISTv3.3.2	314706745.TTATTG.PASSMTD=bwa_platypus;KM=11.44;KFP=0;KFF=0GT0/0						Manual inspection of read	Yes		PG double-calls insertion		Yes, variant and genotype	Yes, tandem repeat	
11/9/2016 20:26:09	JZ			HG001/NA12878	NISTv3.3.2	329623640.TTATAG,TATAGATAG50PASSplatforms=1;platformnames=Illumina;datasets=1;datasetnames=HiSeqPE300x;callsets=2;callsetnames=HiSeqPE3						Manual inspection of read	No		Erroneous del/ins compound het in PG when actuall		Yes, variant and genotype	Yes, tandem repeat	
11/10/2016 9:01:23	JZ			HG001/NA12878	NISTv3.3.2	396651621.TG50PASSplatforms=3;platformnames=10X,Illumina,CG;datasets=3;datasetnames=10XChromium,HiSeqPE300x,CGnormal;callsets=3;callsetna						Evidence from long reads	No		Clearly on one haplotype in 10X, but low allele freq i		Yes, variant and genotype	No	
11/10/2016 9:03:10	JZ			HG001/NA12878	NISTv3.3.2	3115421463.TG.PASSMTD=cortex;KM=4.57;KFP=0;KFF=0GT0/0						Manual inspection of read	No		Appears to be FP from cortex in PG		Yes, variant and genotype	No	
11/10/2016 9:11:09	JZ			HG001/NA12878	NISTv3.3.2	3195429269.CG.PASSMTD=cgi,bwa_freebayes,bwa_gatk;KM=14.00;KFP=0;KFF=0GT1|0						Manual inspection of read	No		Another SNP 60bp away on opposite haplotype, and		It is unclear	No	
11/10/2016 9:51:19	JZ			HG001/NA12878	NISTv3.3.2	379104110.GC50PASSplatforms=1;platformnames=10X;datasets=1;datasetnames=10XChromium;callsets=1;callsetnames=10XGATKhaplo;datasetsmissing						Evidence from phasing us	No		Clearly on one HP in 10X, but not in other data, so u		It is unclear	No	
11/18/2016 21:05:01	JZ			HG001/NA12878	NISTv3.3.2	437191158.CCA50PASSplatforms=2;platformnames=Illumina,CG;datasets=2;datasetnames=HiSeqPE300x,CGnormal;callsets=3;callsetnames=HiSeqPE300						Manual inspection of read	No		low fraction in illumina and CG. In one 10X haplotyp		It is unclear	Yes, homopolymer	
11/18/2016 21:06:59	JZ			HG001/NA12878	NISTv3.3.2	4163269323rs35776072TAT50PASSplatforms=3;platformnames=Illumina,CG,Solid;datasets=3;datasetnames=HiSeqPE300x,CGnormal,SolidPE50x50bp;cal						Manual inspection of read	No		Erroneously called 2bp del in PG		Yes, variant and genotype	Yes, homopolymer	
11/18/2016 21:09:46	JZ			HG001/NA12878	NISTv3.3.2	4174513732rs147065183AACACACACA50PASSplatforms=2;platformnames=Illumina,10X;datasets=2;datasetnames=HiSeqPE300x,10XChromium;callsets=						Manual inspection of read	No		PG erroneously calls del of 2 extra bp		Yes, variant and genotype	Yes, tandem repeat	
11/18/2016 21:14:11	JZ			HG001/NA12878	NISTv3.3.2	58295076rs34654973TTG50PASSplatforms=3;platformnames=Illumina,CG,Solid;datasets=4;datasetnames=HiSeqPE300x,CGnormal,SolidPE50x50bp,Solid						Manual inspection of read	Yes	Preceding base deleted o	PG only calls del, not ins, at compound het		Yes, variant and genotype	Yes, homopolymer	
11/18/2016 21:20:01	JZ			HG001/NA12878	NISTv3.3.2	58490808.GTTTGT,G50PASSplatforms=1;platformnames=Illumina;datasets=1;datasetnames=HiSeqPE300x;callsets=2;callsetnames=HiSeqPE300xGATK,H						Manual inspection of read	No		Very long homopolymer - looks likely to be compoun		It is unclear	Yes, homopolymer	
11/18/2016 21:23:01	JZ			HG001/NA12878	NISTv3.3.2	527306485.CCT50PASSplatforms=2;platformnames=Illumina,CG;datasets=2;datasetnames=HiSeqPE300x,CGnormal;callsets=3;callsetnames=HiSeqPE300						Manual inspection of read	No		Clearly in one 10X haplotype, though strange that it'		Yes, variant and genotype	Yes, homopolymer	
11/18/2016 21:27:15	JZ			HG001/NA12878	NISTv3.3.2	5176131597rs55863842CT50PASSplatforms=3;platformnames=Illumina,CG,10X;datasets=3;datasetnames=HiSeqPE300x,CGnormal,10XChromium;callsets						Manual inspection of read	Yes		Looks like PG mis-calls SNP in long TR as a deletio		Yes, variant and genotype	Yes, tandem repeat	
11/18/2016 21:29:33	JZ			HG001/NA12878	NISTv3.3.2	5178293175.CCT.PASSMTD=bwa_gatk;KM=8.38;KFP=0;KFF=0GT0/0						Manual inspection of read	No		Not in 10X, and only in discordantly mapped reads i		Yes, variant and genotype	No	
11/18/2016 21:33:57	JZ			HG001/NA12878	NISTv3.3.2	624582702rs72007936CTC50PASSplatforms=2;platformnames=Illumina,CG;datasets=2;datasetnames=HiSeqPE300x,CGnormal;callsets=3;callsetnames=H						Manual inspection of read	No		In illumina and CG at normal freq and in one 10X ha		Yes, variant and genotype	Yes, homopolymer	
11/18/2016 21:41:53	JZ			HG001/NA12878	NISTv3.3.2	650687160rs3835215GGAGAA50PASSplatforms=1;platformnames=Illumina;datasets=1;datasetnames=HiSeqPE300x;callsets=1;callsetnames=HiSeqPE30(						Manual inspection of read	No		There is another larger insertion ~60bp downstream		Yes, variant and genotype	Yes, tandem repeat	
11/18/2016 21:43:18	JZ			HG001/NA12878	NISTv3.3.2	653028051rs70980809CAATAAAATAAC50PASSplatforms=2;platformnames=Illumina,10X;datasets=2;datasetnames=HiSeqPE300x,10XChromium;callsets=						Manual inspection of read	No		PG calls too long of a del		Yes, variant and genotype	Yes, tandem repeat	
11/18/2016 21:45:28	JZ			HG001/NA12878	NISTv3.3.2	681915349.TTCCAATATAGAACAATGACATGTTCTATATTAATCTAT50PASSplatforms=1;platformnames=Illumina;datasets=1;datasetnames=HiSeqPE300x;c						Evidence from long reads	No		No clear evidence in short reads but seems to be co		Yes, variant and genotype	Yes, tandem repeat	
12/8/2016 14:14:51	JZ			HG001/NA12878	NISTv3.3.2	6109713384.CCT50PASSplatforms=2;platformnames=Illumina,CG;datasets=2;datasetnames=HiSeqPE300x,CGnormal;callsets=3;callsetnames=HiSeqPE30						Manual inspection of read	No		In 10-20% of Ill and CG reads at 10bp homopol. like		It is unclear	Yes, homopolymer	
12/8/2016 14:17:44	JZ			HG001/NA12878	NISTv3.3.2	6167245524rs202168257TTGATA50PASSplatforms=2;platformnames=Illumina,10X;datasets=2;datasetnames=HiSeqPE300x,10XChromium;callsets=3;calls						Manual inspection of read	No		erroneous del in PG		Yes, variant and genotype	Yes, tandem repeat	
12/8/2016 14:21:17	JZ			HG001/NA12878	NISTv3.3.2	6167605939.GA.PASSMTD=bwa_freebayes;KM=4.88;KFP=0;KFF=0GT0/0						Manual inspection of read	No		variant in low MQ reads from Ill and unphased reads		Yes, variant and genotype	No	
12/8/2016 14:26:55	JZ			HG001/NA12878	NISTv3.3.2	827278795.CTATTTATTTATTTATTTATTTATTCTATTTATTTATTTATTTATT,C50PASSplatforms=2;platformnames=Illumina,10X;datasets=2;datasetnames=HiS						Manual inspection of read	Yes	phased snp downstream	Partial call from PG		Yes, variant and genotype	Yes, tandem repeat	
12/8/2016 14:31:52	JZ			HG001/NA12878	NISTv3.3.2	82268267.CG.PASSMTD=bwa_freebayes,bwa_gatk;KM=10.40;KFP=0;KFF=0GT0/0						Manual inspection of read	No		Only in unphased 10X reads, and in low frac of PacB		Yes, variant and genotype	No	
12/8/2016 14:35:02	JZ			HG001/NA12878	NISTv3.3.2	838142735rs7823681TC50PASSplatforms=3;platformnames=Illumina,CG,10X;datasets=3;datasetnames=HiSeqPE300x,CGnormal,10XChromium;callsets=4						Manual inspection of read	No		Erroneously called a del in long TR in PG		Yes, variant and genotype	Yes, tandem repeat	
12/8/2016 14:51:12	JZ			HG001/NA12878	NISTv3.3.2	842384671rs72643247AC50PASSplatforms=4;platformnames=Illumina,CG,10X,Solid;datasets=4;datasetnames=HiSeqPE300x,CGnormal,10XChromium,So						Manual inspection of read	No		Not sure why this is missed by PG		Yes, variant and genotype	No	
12/8/2016 14:53:50	JZ			HG001/NA12878	NISTv3.3.2	850773938.TTTCCT50PASSplatforms=3;platformnames=Illumina,10X,Solid;datasets=3;datasetnames=HiSeqPE300x,10XChromium,SolidSE75bp;callsets=4						Manual inspection of read	No		Erroneously called larger del in PG		Yes, variant and genotype	Yes, tandem repeat	
12/8/2016 14:56:09	JZ			HG001/NA12878	NISTv3.3.2	8114484792rs142439420TTGAAA50PASSplatforms=1;platformnames=Illumina;datasets=1;datasetnames=HiSeqPE300x;callsets=2;callsetnames=HiSeqPE:						Manual inspection of read	No		Erroneous del in PG		Yes, variant and genotype	Yes, tandem repeat	
12/8/2016 14:57:30	JZ			HG001/NA12878	NISTv3.3.2	987032826rs5898857TTTTTA50PASSplatforms=2;platformnames=Illumina,10X;datasets=2;datasetnames=HiSeqPE300x,10XChromium;callsets=3;callsetna						Manual inspection of read	No		Erroneous del in PG		Yes, variant and genotype	Yes, tandem repeat	
12/8/2016 15:04:11	JZ			HG001/NA12878	NISTv3.3.2	9116106911rs59280241TTC50PASSplatforms=3;platformnames=Illumina,CG,10X;datasets=3;datasetnames=HiSeqPE300x,CGnormal,10XChromium;callset						Manual inspection of read	No		Clear ins in 8bp homopolymer missed by PG. In 50%		Yes, variant and genotype	Yes, homopolymer	
12/13/2016 16:50:37	JZ			HG001/NA12878	NISTv3.3.2	1067516838rs142083711TTTTTA50PASSplatforms=1;platformnames=Illumina;datasets=1;datasetnames=HiSeqPE300x;callsets=2;callsetnames=HiSeqPE3						Manual inspection of read	No		Missed by PG - unclear why		Yes, variant and genotype	Yes, tandem repeat	
12/13/2016 16:52:32	JZ			HG001/NA12878	NISTv3.3.2	1091179118.CTC50PASSplatforms=3;platformnames=Illumina,CG,10X;datasets=3;datasetnames=HiSeqPE300x,CGnormal,10XChromium;callsets=4;callset						Manual inspection of read	No		Missed by PG		Yes, variant and genotype	Yes, homopolymer	
12/13/2016 16:53:58	JZ			HG001/NA12878	NISTv3.3.2	1092299647rs146334425AAT50PASSplatforms=3;platformnames=Illumina,CG,10X;datasets=3;datasetnames=HiSeqPE300x,CGnormal,10XChromium;callse						Manual inspection of read	No		Missed by PG		Yes, variant and genotype	Yes, homopolymer	
12/13/2016 17:10:42	JZ			HG001/NA12878	NISTv3.3.2	1098163178.TC.PASSMTD=bwa_freebayes;KM=7.88;KFP=0;KFF=0GT0/0						Manual inspection of read	No		Appears to be a mapping error in PG since not in Pa		Yes, variant and genotype	No	
12/13/2016 17:12:26	JZ			HG001/NA12878	NISTv3.3.2	10106168859.TAATA,T50PASSplatforms=2;platformnames=Illumina,CG;datasets=2;datasetnames=HiSeqPE300x,CGnormal;callsets=3;callsetnames=HiSeq						Manual inspection of read	No		partial compound het in PG		Yes, variant and genotype	Yes, homopolymer	
12/13/2016 17:14:01	JZ			HG001/NA12878	NISTv3.3.2	10131251852rs3036418CCAC50PASSplatforms=2;platformnames=Illumina,10X;datasets=2;datasetnames=HiSeqPE300x,10XChromium;callsets=3;callsetna						Manual inspection of read	No		Missed in PG		Yes, variant and genotype	Yes, tandem repeat	
12/13/2016 17:20:45	JZ			HG001/NA12878	NISTv3.3.2	1145077445.TTAT.PASSMTD=isaac_strelka,bwa_freebayes,bwa_gatk;KM=7.50;KFP=0;KFF=0GT0|1						Manual inspection of read	Yes	phased SNP upstream	Error FN from CG in GIAB 3.3.2. In TRlt51bp		No, true call is missing fro	Yes, tandem repeat	
12/13/2016 17:24:01	JZ			HG001/NA12878	NISTv3.3.2	1170385069.AC.PASSMTD=bwa_freebayes;KM=9.00;KFP=0;KFF=0GT0/0						Manual inspection of read	Yes	SNP upstream	Appears to be a GGT SSE in the PG calls - maybe i		Yes, variant and genotype	No	
12/13/2016 17:27:11	JZ			HG001/NA12878	NISTv3.3.2	1271332502.GA.PASSMTD=bwa_freebayes;KM=11.43;KFP=0;KFF=0GT0/0 1271332508.AGA.PASSMTD=bwa_freebayes;KM=12.43;KFP=0;KFF=0GT0/0 1271332521.CATC.PASSMTD=bwa_freebayes;KM=12.14;KFP=0;KFF=0GT0/0						Manual inspection of read	Yes	PG finds lots of FP varian	These 3 variants are probably mapping errors in PG		Yes, variant and genotype	No	
12/13/2016 17:29:55	JZ			HG001/NA12878	NISTv3.3.2	1279853553.GA.PASSMTD=bwa_freebayes,bwa_gatk;KM=14.71;KFP=0;KFF=0GT0/0						Manual inspection of read	Yes	PG finds 3 variants in this	PG finds 3 variants in this region that have no evide		Yes, variant and genotype	No	
12/13/2016 17:31:37	JZ			HG001/NA12878	NISTv3.3.2	12110707073.AC.PASSMTD=bwa_freebayes;KM=2.33;KFP=1;KFF=1GT0/0						Manual inspection of read	No		No evidence in either 10X haplotype or pacbio, so lik		Yes, variant and genotype	No	
12/13/2016 17:38:44	JZ			HG001/NA12878	NISTv3.3.2	1336952876rs71663534TTTTTCT50PASSplatforms=2;platformnames=Illumina,10X;datasets=2;datasetnames=HiSeqPE300x,10XChromium;callsets=3;calls						Manual inspection of read	No		PG erroneously calls larger del		Yes, variant and genotype	Yes, tandem repeat	
12/13/2016 17:41:14	JZ			HG001/NA12878	NISTv3.3.2	13110455934rs56331139CCT50PASSplatforms=2;platformnames=Illumina,CG;datasets=2;datasetnames=HiSeqPE300x,CGnormal;callsets=3;callsetnames=						Manual inspection of read	Yes	PG correctly calls del on c	PG correctly calls del on other haplotype but misses		Yes, variant and genotype	Yes, homopolymer	
12/13/2016 17:43:02	JZ			HG001/NA12878	NISTv3.3.2	1381387475.GA.PASSMTD=bwa_freebayes;KM=1.40;KFP=1;KFF=0GT0/0						Manual inspection of read	No		PG calls this and SNP 100bp downstream but no ev		Yes, variant and genotype	No	
12/14/2016 13:03:08	JZ			HG001/NA12878	NISTv3.3.2	1425076753.GT.PASSMTD=bwa_freebayes,bwa_gatk;KM=8.00;KFP=0;KFF=0GT0/0						Evidence from long reads	Yes	Multiple likely FP SNPs in	Multiple likely FP SNPs in this region from PG; not in		Yes, variant and genotype	No	
12/14/2016 13:13:33	JZ			HG001/NA12878	NISTv3.3.2	1683952175.CCAGG50PASSplatforms=1;platformnames=Illumina;datasets=1;datasetnames=HiSeqPE300x;callsets=1;callsetnames=HiSeqPE300xfreebaye						Evidence from long reads	Yes	It appears that it may actu	Moleculo reads have a large complex set of deletion		It is unclear	No	
12/14/2016 13:15:58	JZ			HG001/NA12878	NISTv3.3.2	1686927986.AC.PASSMTD=bwa_freebayes;KM=7.00;KFP=0;KFF=1GT0/0						Manual inspection of read	No		Probably a GGT SSE in illumina and PG, but unclea		Yes, variant and genotype	No	
12/14/2016 13:21:00	JZ			HG001/NA12878	NISTv3.3.2	189866565rs6506711CT50PASSplatforms=2;platformnames=Illumina,10X;datasets=2;datasetnames=HiSeqPE300x,10XChromium;callsets=3;callsetnames=						Manual inspection of read	No		PG calls a large del instead of a SNP, likely due to a		Yes, variant and genotype	Possibly a long unit TR	
12/14/2016 13:22:35	JZ			HG001/NA12878	NISTv3.3.2	1835077388.GA.PASSMTD=bwa_freebayes;KM=5.91;KFP=0;KFF=0GT0/0						Manual inspection of read	No		Likely FP in PG since no evidence in 10X, pacbio, or		Yes, variant and genotype	No	
12/14/2016 13:27:03	JZ			HG001/NA12878	NISTv3.3.2	1853460570.TTTTTATTTA.PASSMTD=isaac_strelka,bwa_freebayes,bwa_gatk;KM=9.00;KFP=0;KFF=0GT0|1						Manual inspection of read	No		FN due to CG missing call in small TR and GATK is		No, true call is missing fro	Yes, tandem repeat	
12/14/2016 13:29:40	JZ			HG001/NA12878	NISTv3.3.2	1870098910.AC.PASSMTD=cortex;KM=8.00;KFP=0;KFF=0GT0/0						Manual inspection of read	No		Appears to be a GGT SSE in PG, though unclear wh		Yes, variant and genotype	No	
12/14/2016 13:32:19	JZ			HG001/NA12878	NISTv3.3.2	1923686943rs71165829CCT50PASSplatforms=3;platformnames=Illumina,CG,10X;datasets=3;datasetnames=HiSeqPE300x,CGnormal,10XChromium;callse						Manual inspection of read	No		In one 10X HP and 50% of illumina and CG reads, s		Yes, variant and genotype	Yes, homopolymer	
12/14/2016 13:36:46	JZ			HG001/NA12878	NISTv3.3.2	1927940280.AC50PASSplatforms=1;platformnames=10X;datasets=1;datasetnames=10XChromium;callsets=1;callsetnames=10XGATKhaplo;datasetsmissin						Manual inspection of read	No		Unclear why this was called by 10X, since it does no		No, true call is homozygo	No	
12/19/2016 16:16:40	JZ			HG001/NA12878	NISTv3.3.2	1258728252.TC..BS=58728252;Regions=CONF,HG001allgenomespecificandifficult,HG002HG003HG004SVs,HG002allgenomespecific,HG002allgenomespe						Manual inspection of read	No				Yes, variant and genotype	No	
12/19/2016 16:24:03	JZ			HG001/NA12878	NISTv3.3.2	103139115.AC..BS=3139115;Regions=CONF,HG001allgenomespecific,HG001allgenomespecificandifficult,HG001complexindelNIST3_3_2,HG001snpswithir						Manual inspection of read	Yes	many variants in 300bp re	this and many nearby variants supported by molecul		Yes, variant and genotype	No	
12/19/2016 16:26:16	JZ			HG001/NA12878	NISTv3.3.2	1275879480.GA..BS=75879480;Regions=CONF,HG001allgenomespecificandifficult,HG002allgenomespecificandifficult,HG003allgenomespecificandifficult,H						Manual inspection of read	No		Erroneous homvar from 50x data when actually a he		Yes, variant and genotype	No	
12/19/2016 16:29:08	JZ			HG001/NA12878	NISTv3.3.2	3138604035.AG..BS=138604035;Regions=CONF,gc_l100_gc55to60_slop50,gc_l100_gclt30orgt55_slop50,notinHG001allgenomespecificandifficult,notinHG(						Manual inspection of read	No				Yes, variant and genotype	No	
12/19/2016 16:32:56	JZ			HG001/NA12878	NISTv3.3.2	1293314109.TC..BS=93314109;Regions=CONF,HG001allgenomespecificandifficult,HG002HG003HG004SVs,HG002allgenomespecific,HG002allgenomespe						Manual inspection of read	I don't know	PacBio has nearby SNP, l	PacBio has strong support for either het or homvar.		It is unclear	No	
12/19/2016 16:35:53	JZ			HG001/NA12878	NISTv3.3.2	2222570821.CT..BS=22570821;Regions=CONF,HG005HG006HG007SVs,HG005allgenomespecific,HG005allgenomespecificandifficult,gc_l100_gc60to65_s						Evidence from long reads	No		in large somatic del found by PG, so unclear		It is unclear	No	
12/19/2016 16:37:51	JZ			HG001/NA12878	NISTv3.3.2	623701458.GA..BS=23701458;Regions=CONF,HG001allgenomespecificandifficult,HG002allgenomespecificandifficult,HG003allgenomespecificandifficult,HG						Evidence from long reads	No		HomVar clearly supported by pacbio.		Yes, variant and genotype	No	
12/19/2016 16:39:24	JZ			HG001/NA12878	NISTv3.3.2	8123462549.TA..BS=123462549;Regions=CONF,gc_l100_gc30to55_slop50,notinHG001allgenomespecificandifficult,notinHG002allgenomespecificandifficult						Manual inspection of read	Yes	nearby SNP			Yes, variant and genotype	No	
12/19/2016 16:45:01	JZ			HG001/NA12878	NISTv3.3.2	388168598.CT..BS=88168598;Regions=CONF,HG001allgenomespecificandifficult,HG002allgenomespecificandifficult,HG003allgenomespecificandifficult,HG						Manual inspection of read	No		correctly called a het		Yes, variant and genotype	No	
12/19/2016 16:47:39	JZ			HG001/NA12878	NISTv3.3.2	2222590546.CG..BS=22590546;Regions=CONF,HG005HG006HG007SVs,HG005allgenomespecific,HG005allgenomespecificandifficult,gc_l100_gc30to55_s						Evidence from long reads	No		In large somatic del from PG.		It is unclear	No	
12/19/2016 16:58:00	JZ			HG001/NA12878	NISTv3.3.2	170218521.TA..BS=70218521;Regions=CONF,gc_l100_gc30to55_slop50,notinHG001allgenomespecificandifficult,notinHG002allgenomespecificandifficult,nc						Manual inspection of read	No		Likely a somatic mutation (CAT3 in PG), though pos		It is unclear	No	
12/19/2016 16:59:43	JZ			HG001/NA12878	NISTv3.3.2	1874652028.TC..BS=74652028;Regions=CONF,HG002HG003HG004SVs,HG002allgenomespecific,HG002allgenomespecificandifficult,HG003allgenomespe						Manual inspection of read	No				Yes, variant and genotype	No	
12/19/2016 17:01:27	JZ			HG001/NA12878	NISTv3.3.2	396246593.TC..BS=96246593;Regions=CONF,gc_l100_gc30to55_slop50,notinHG001allgenomespecificandifficult,notinHG002allgenomespecificandifficult,nc						Manual inspection of read	No		Likely a somatic mutation (CAT3 in PG) or a mappin		It is unclear	No	
12/19/2016 17:02:59	JZ			HG001/NA12878	NISTv3.3.2	1369826828.GA..BS=69826828;Regions=CONF,HG001allgenomespecificandifficult,HG002allgenomespecificandifficult,HG003allgenomespecificandifficult,H						Manual inspection of read	No		likely a somatic mut (CAT3 in PG) or a mapping erro		It is unclear	No	
12/19/2016 17:04:39	JZ			HG001/NA12878	NISTv3.3.2	1779300953.AC..BS=79300953;Regions=CONF,HG002HG003HG004SVs,HG002allgenomespecific,HG002allgenomespecificandifficult,HG003allgenomespe						Manual inspection of read	No		Likely a GGT SSE		Yes, variant and genotype	No	
12/19/2016 17:06:14	JZ			HG001/NA12878	NISTv3.3.2	1336982911.TC..BS=36982911;Regions=CONF,gc_l100_gc30to55_slop50,notinHG001allgenomespecificandifficult,notinHG002allgenomespecificandifficult,n						Manual inspection of read	No		likely a somatic mutation (CAT3 in PG) or mapping e		It is unclear	No	
12/19/2016 17:10:53	JZ			HG001/NA12878	NISTv3.3.2	199278028.GA..BS=9278028;Regions=CONF,gc_l100_gc30to55_slop50,notinHG001allgenomespecificandifficult,notinHG002allgenomespecificandifficult,not						Manual inspection of read	Yes	multiple nearby phased S	multiple nearby phased SNPs in 10X and a few pact		It is unclear	No	
12/19/2016 17:13:23	JZ			HG001/NA12878	NISTv3.3.2	630954534.TA..BS=30954534;Regions=CONF,HG001allgenomespecificandifficult,HG002HG003HG004SVs,HG002allgenomespecific,HG002allgenomespec						Manual inspection of read	Yes	nearby questionable varia	Likely a mapping error since self-chain has many sir		Yes, variant and genotype	No	
12/19/2016 17:15:41	JZ			HG001/NA12878	NISTv3.3.2	11116443941.CG..BS=116443941;Regions=CONF,HG001allgenomespecificandifficult,HG002allgenomespecificandifficult,HG003allgenomespecificandifficult,						Manual inspection of read	No		possibly a mapping error, but no evidence in most m		Yes, variant and genotype	No	
12/19/2016 17:17:24	JZ			HG001/NA12878	NISTv3.3.2	1292373095.GA..BS=92373095;Regions=CONF,HG001allgenomespecific,HG001allgenomespecificandifficult,HG001compoundhetsnpNIST3_3_2,HG001cor						Manual inspection of read	Yes	near hom snp	Good het call near hom snp		Yes, variant and genotype	No	
12/19/2016 17:22:03	JZ			HG001/NA12878	NISTv3.3.2	691577264.CTTCT,C..BS=91577265;Regions=CONF,HG001allgenomespecific,HG001allgenomespecificandifficult,HG001compoundhetindelNIST3_3_2,HG(						Manual inspection of read	No		seems to follow 10X haplotypes and 50/50 in illumin		Yes, variant and genotype	Yes, homopolymer	
12/19/2016 17:23:53	JZ			HG001/NA12878	NISTv3.3.2	203880350.CTC..BS=3880351;Regions=CONF,HG001allgenomespecificandifficult,HG002allgenomespecificandifficult,HG003allgenomespecificandifficult,HG						Manual inspection of read	No		very long homopol but seems pretty clear in illumina		Yes, variant and genotype	Yes, homopolymer	
12/19/2016 17:27:05	JZ			HG001/NA12878	NISTv3.3.2	83622261.CTTTTTCTTTT,C..BS=3622262;Regions=CONF,HG001allgenomespecific,HG001allgenomespecificandifficult,HG001compoundhetindelNIST3_3_						Manual inspection of read	No		segregates with 10X haplotypes as expected		Yes, variant and genotype	Yes, homopolymer	
12/20/2016 9:10:59	JZ			HG001/NA12878	NISTv3.3.2	1250693721rs36079362ATA50PASScallable=CS_HiSeqPE300xGATK_callable;callsetnames=HiSeqPE300xGATK,HiSeqPE300xfreebayes;callsets=2;datase						Manual inspection of read	No		clear homvar in illumina, though long homopolymer		Yes, variant and genotype	Yes, homopolymer	
12/20/2016 9:14:17	JZ			HG001/NA12878	NISTv3.3.2	693453597.TTTCTCTCTCTC50PASScallable=CS_HiSeqPE300xGATK_callable;callsetnames=HiSeqPE300xGATK,HiSeqPE300xfreebayes;callsets=2;datasetr						Manual inspection of read	No		Pedigree consistent and clear in illuminaf		Yes, variant and genotype	Yes, tandem repeat	
12/20/2016 9:16:57	JZ			HG001/NA12878	NISTv3.3.2	1677447704.GGAAA,GAAAA50PASScallable=CS_HiSeqPE300xGATK_callable;callsetnames=HiSeqPE300xGATK,CGnormal,HiSeqPE300xfreebayes;callse						Manual inspection of read	No		Clear in illumina and pedigree consistent		Yes, variant and genotype	Yes, homopolymer	
12/20/2016 9:50:18	JZ			HG001/NA12878	NISTv3.3.2	1934936340rs67809236CTC50PASScallable=CS_HiSeqPE300xGATK_callable;callsetnames=HiSeqPE300xGATK,HiSeqPE300xfreebayes;callsets=2;datase						Manual inspection of read	No		Clean homvar in illumina data crossing homopolyme		Yes, variant and genotype	Yes, homopolymer	
12/20/2016 9:53:12	JZ			HG001/NA12878	NISTv3.3.2	2147251322.CAAAAAACAAAAAAA,C50PASScallable=CS_HiSeqPE300xGATK_callable;callsetnames=HiSeqPE300xGATK,HiSeqPE300xfreebayes;callsets						Manual inspection of read	No		Clear compound het in illumina and supported by 10		Yes, variant and genotype	Yes, homopolymer	
12/20/2016 9:55:12	JZ			HG001/NA12878	NISTv3.3.2	5159645468.CCTTT,CTTTT50PASScallable=CS_HiSeqPE300xGATK_callable;callsetnames=HiSeqPE300xGATK,HiSeqPE300xfreebayes;callsets=2;datase						Manual inspection of read	No		clear compound het in illumina and pedigree consist		Yes, variant and genotype	Yes, homopolymer	
12/20/2016 9:57:18	JZ			HG001/NA12878	NISTv3.3.2	271935012.CGTGTGTCGT,C50PASScallable=CS_HiSeqPE300xGATK_callable;callsetnames=HiSeqPE300xGATK,HiSeqPE300xfreebayes,10XGATKhaplo;						Manual inspection of read	No		Clear compound het in illumina and pedigree consis		Yes, variant and genotype	Yes, tandem repeat	
12/20/2016 10:24:03	JZ			HG001/NA12878	NISTv3.3.2	4173044651.AAT,ATTTT50PASScallable=CS_HiSeqPE300xGATK_callable;callsetnames=HiSeqPE300xGATK,HiSeqPE300xfreebayes;callsets=2;datasetnar						Manual inspection of read	No		Clear in illumina, pedigree consistent, and mostly co		Yes, variant and genotype	Yes, homopolymer	
12/20/2016 10:30:01	JZ			HG001/NA12878	NISTv3.3.2	428399167rs4580640TG50PASSplatforms=3;platformnames=Illumina,CG,10X;datasets=3;datasetnames=HiSeqPE300x,CGnormal,10XChromium;callsets=4 428399199.GGT50PASSplatforms=2;platformnames=Illumina,10X;datasets=2;datasetnames=HiSeqPE300x,10XChromium;callsets=2;callsetnames=HiSeqP 428399209rs60535451GGTT50PASSplatforms=3;platformnames=Illumina,CG,10X;datasets=3;datasetnames=HiSeqPE300x,CGnormal,10XChromium;callse 428399362rs34550165CTC50PASSplatforms=3;platformnames=Illumina,CG,10X;datasets=3;datasetnames=HiSeqPE300x,CGnormal,10XChromium;callsets						Manual inspection of read	Yes	several phased variants ir	in pedigree and one 10X haplotype. partial call from		Yes, variant and genotype	Yes, homopolymer	
12/20/2016 10:31:46	JZ			HG001/NA12878	NISTv3.3.2	576314690.TTAC,TACAC50PASSplatforms=1;platformnames=Illumina;datasets=1;datasetnames=HiSeqPE300x;callsets=2;callsetnames=HiSeqPE300xGAT						Manual inspection of read	No		phased in pedigree and 10X		Yes, variant and genotype	Yes, tandem repeat	
12/20/2016 10:34:11	JZ			HG001/NA12878	NISTv3.3.2	896823069.TTTGTG,TTGTGTG50PASSplatforms=2;platformnames=Illumina,10X;datasets=2;datasetnames=HiSeqPE300x,10XChromium;callsets=3;callset						Manual inspection of read	No		phased in pedigree and 10X		Yes, variant and genotype	Yes, tandem repeat	
12/20/2016 10:41:08	JZ			HG001/NA12878	NISTv3.3.2	675010330.CTATATATACACACATATGTATGTGTATATATGTTTATGTACTATATATACACATACATATGTGTGC..BS=75010331;Regions=CONF,HG001allgenome						Manual inspection of read	No		Appears likely to be an alignment error in long unit T		It is unclear	Yes, tandem repeat	
12/20/2016 10:45:55	JZ			HG001/NA12878	NISTv3.3.2	19 29138419 rs61602483 T TACAC 50 PASS platforms=3;platformnames=Illumina,CG,10X;datasets=3;datasetnames=HiSeqPE300x,CC 19 29138437 . T TACAC 50 PASS platforms=1;platformnames=Illumina;datasets=1;datasetnames=HiSeqPE300x;callsets=1;callsetnam						Manual inspection of read	Yes		Complex var in tandem repeat partially called in sen		Yes, variant and genotype	Yes, tandem repeat	
12/20/2016 10:49:34	JZ			HG001/NA12878	NISTv3.3.2	2 228488421 rs199776812 G T 50 PASS platforms=3;platformnames=Illumina,CG,10X;datasets=3;datasetnames=HiSeqPE300x,CGn 2 228488422 . AGC A 50 PASS platforms=3;platformnames=Illumina,CG,10X;datasets=3;datasetnames=HiSeqPE300x,CGnormal,10X 2 228488425 . T TA 50 PASS platforms=3;platformnames=Illumina,CG,10X;datasets=3;datasetnames=HiSeqPE300x,CGnormal,10XC 2 228488426 rs200953868 C CA 50 PASS platforms=3;platformnames=Illumina,CG,10X;datasets=3;datasetnames=HiSeqPE300x,CGr						Manual inspection of read	Yes		Can also be represented as 5 snps within 6bp		Yes, variant and genotype	No	
12/20/2016 10:52:01	JZ			HG001/NA12878	NISTv3.3.2	1044183850.TGGTG,T50PASSplatforms=2;platformnames=Illumina,CG;datasets=2;datasetnames=HiSeqPE300x,CGnormal;callsets=3;callsetnames=HiSeq						Manual inspection of read	No		compound het clear in illumina and CG and pedigree		Yes, variant and genotype	Yes, homopolymer	
12/20/2016 10:55:50	JZ			HG001/NA12878	NISTv3.3.2	6 47964175 . C G 50 PASS platforms=2;platformnames=CG,Illumina;datasets=2;datasetnames=CGnormal,HiSeqPE300x;callsets=2; 6 47964176 . T G 50 PASS platforms=2;platformnames=CG,Illumina;datasets=2;datasetnames=CGnormal,HiSeqPE300x;callsets=2; 6 47964177 . CCCC G 50 PASS platforms=2;platformnames=CG,Illumina;datasets=2;datasetnames=CGnormal,HiSeqPE300x;callsets						Manual inspection of read	Yes		complex variant; pedigree consistent but hom var		Yes, variant and genotype	No	

Timestamp	Your name	Your email (if this is your f	Your Institution (if this is y	GAB Genome	Version of high-confidence	Optionally, enter the vcf is	Chromosome number	Start Position on chromos	True Reference base(s) - 2	True Alternate base(s) - 2	Genotype in VCF format	What evidence do you ha	Did you find any other var	If yes, please give some i	Is there any additional info	number of the variant if	Does the GIAB call appear	Is this a repetitive region?	Reference assembly
12/20/2016 11:04:18	JZ			HG001/NA12878	NISTv3.3.2	16	24230870	rs200555220	CA	C	50	PASS	platforms=2;platformnames=Illumina,10X;datasets=2;datasetnames=HiSeqPE300,10XChr							
12/23/2016 15:25:18	JZ			HG001/NA12878	NISTv3.3.2	16	24230870	CACACACA	C	CACA,C	50	PASS	platforms=2;platformnames=Illumina,10X;datasets=2;datasetnames=HiSeqPE300,10XChr	Manual inspection of read	Yes	Complex compound het in TR; clear in Illumina and 10x	Yes, variant and genotype	Yes, tandem repeat	
12/23/2016 15:25:18	JZ			HG001/NA12878	NISTv3.3.2	X	72180299	r148994585;CTS0PASSplatforms=1;platformnames=10X;datasets=1;datasetnames=10XChromium;callsets=1;callsetnames=10XGATKhapcdsb			Manual inspection of read	Yes				In PacBio, but high cov. In half of reads in one 10X hit is unclear		No		
12/23/2016 15:28:32	JZ			HG001/NA12878	NISTv3.3.2	X	74616992	rs70513633;CGSPASSplatforms=1;platformnames=10X;datasets=1;datasetnames=10XChromium;callsets=1;callsetnames=10XGATKhapcdsb			Manual inspection of read	Yes				In PacBio, but high cov. In all reads in one 10X hapl	Yes, variant and genotype	No		
12/23/2016 15:27:18	JZ			HG001/NA12878	NISTv3.3.2	X	152255126	r145869945;CGSPASSplatforms=1;platformnames=10X;datasets=1;datasetnames=10XChromium;callsets=1;callsetnames=10XGATKhapcdsb			Manual inspection of read	Yes				In PacBio, but high cov. In all reads in one 10X hapl	Yes, variant and genotype	No		
12/20/2017 14:41:30	JZ			HG001/NA12878	NISTv3.3.2	1	1120088932	AGTCTATC	A	GTCTATCA	50	PASS	platforms=2;platformnames=Illumina,10X;datasets=2;datasetnames=HiSeqPE300,10XChromium	Manual inspection of read	Yes	en in GATK	Yes, variant and genotype	Yes, tandem repeat	
12/20/2017 14:42:13	JZ			HG001/NA12878	NISTv3.3.2	1	2100388581	TAAAAATAAAAT	AAT	TAGTATCTAGA	50	PASS	platforms=2;platformnames=Illumina,10X;datasets=2;datasetnames=HiSeqPE300,10XChromium	Manual inspection of read	Yes	en in GATK	Yes, variant and genotype	Yes, homopolymer	
12/20/2017 14:43:02	JZ			HG001/NA12878	NISTv3.3.2	1	3197159486	GCACACACACACACA	G	,GCACACACACACACA	50	PASS	platforms=2;platformnames=Illumina,10X;datasets=2;datasetnames=HiSeqPE300,10XChromium	Manual inspection of read	Yes	en in GATK	Yes, variant and genotype	Yes, tandem repeat	
12/20/2017 14:43:45	JZ			HG001/NA12878	NISTv3.3.2	1	6481938	TTTCTCTCTC	TTCTCTCTCTCTC	,TTCTCTCTCTCTC	50	PASS	platforms=2;platformnames=Illumina,10X;datasets=2;datasetnames=HiSeqPE300,10XChromium	Manual inspection of read	Yes	en in GATK	Yes, variant and genotype	Yes, tandem repeat	
12/20/2017 14:44:24	JZ			HG001/NA12878	NISTv3.3.2	1	6225203613	TAAAAATAAAAAAT	T	,GTAGTAGTAGTAGTA	50	PASS	platforms=2;platformnames=Illumina,10X;datasets=2;datasetnames=HiSeqPE300,10XChromium	Manual inspection of read	Yes	en in GATK	Yes, variant and genotype	Yes, homopolymer	
12/20/2017 14:45:03	JZ			HG001/NA12878	NISTv3.3.2	1	10952092	ATTTTATTTTA	ATTTTATTTTATTTTA	,GSS0922322	50	PASS	platforms=2;platformnames=Illumina,10X;datasets=2;datasetnames=HiSeqPE300,10XChromium	Manual inspection of read	Yes	en in GATK	Yes, variant and genotype	Yes, tandem repeat	
12/20/2017 16:40:11	JZ			HG001/NA12878	NISTv3.3.2	1	14100452118	CAAAAAAAACAAAAAAAA	C	,ES=10942011	50	PASS	platforms=2;platformnames=Illumina,10X;datasets=2;datasetnames=HiSeqPE300,10XChromium	Manual inspection of read	Yes	en in GATK	Yes, variant and genotype	Yes, homopolymer	
12/20/2017 16:41:25	JZ			HG001/NA12878	NISTv3.3.2	1	17607494	AGTCTATCTATCTAT