Oncogene exome analysis of iPSC vs donor PBMCs

- 1590_101, no cancerous mutations in clone
- 1590_103, no cancerous mutations in clone
- 1590_104, no cancerous mutations in clone; seven sequence changes in clone
- 1592_101, no cancerous mutations in clone; one heterozygous splicing chnage in DNTM3A. This variant is present at a frequency of 0.012 (43 / 3743) in the PBMC donor.
- 1592_122, no cancerous mutations in clone
- 1592_123, no cancerous mutations in clone
- 1620_102, no cancerous mutations in clone; one variant with a one base pair deletion with 0.0261 frequency in the clone and 0.0268 frequency in the donor PBMC
- 1620_104, no cancerous mutations in clone

TUTE predicted deleterious mutations novel in the clones

1590_101, no cancerous mutations in clone

Code

Show 10 **entries** **Search:**

	CHROM	POS	REF	ALT	GT.x	GT.y	AF.x	AF.y	DP.x	INFO.x
No data available in table										

Showing 0 to 0 of 0 entries Previous Next

1590_103, no cancerous mutations in clone

Code

Show 10 **entries** **Search:**

	CHROM	POS	REF	ALT	GT.x	GT.y	AF.x	AF.y	DP.x	INFO.x
No data available in table										

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1590_104, no cancerous mutations in clone; seven new changes in clone

Code

Show 10 **entries** **Search:**

	CHROM	POS	REF	ALT	GT.x	GT.y	AF.x	AF.y	DP.x	
1	1	156848918	C	T	0|1		0.441		4358	VC=SNV;Func=exonic;Gene=NTRK1;ExonicFunc=missense;FullAA=NTRK1:NM_(pathogenic;ClinVar_DIS=Familial_medullary_thyroid_carcinoma|Hereditary_inse
2	14	81606214	A	G	0|1		0.238		4195	VC=SNV;Func=splicing;Gene=TSHR;Transcript=NM_000369.2;NucleotideChange=
3	16	89842176	C	G	0|1		0.196		3007	VC=SNV;Func=exonic;Gene=FANCA;ExonicFunc=missense;FullAA=FANCA:NM_
4	3	189455550	T	G	0|1		0.205		4929	VC=SNV;Func=exonic;Gene=TP63;ExonicFunc=missense;FullAA=TP63:NM_00111
5	4	55129831	C	T	0|1		0.184		3848	VC=SNV;Func=splicing;Gene=PDGFRA;Transcript=NM_006206.4;NucleotideChan
6	7	140434574	C	CA	0|1		0.18		1314	VC=INDEL;Func=splicing;Gene=BRAF;Transcript=NM_004333.4;NucleotideChang
7	X	39911657	C	A	0|1		0.298		1758	VC=SNV;Func=splicing;Gene=BCOR;Transcript=NM_001123385.1;NucleotideChan

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1592_101, no cancerous mutations in clone; one heterozygous splicing change in DNTM3A. This variant is present at a frequency of 0.012 (43 / 3743) in the PBMC donor.

Code

Show 10 **entries** **Search:**

	CHROM	POS	REF	ALT	GT.x	GT.y	AF.x	AF.y	DP.x	
1	2	25470029	T	C	0|1		0.499		5439	VC=SNV;Func=splicing;Gene=DNMT3A;Transcript=NM_175629.2;NucleotideChan 2A>G;MutTaster=1.000;MutTaster_Pred=D;GERP++_RS=4.0;phyloP46way_placenta

Showing 1 to 1 of 1 entries Previous 1 Next

1592_122, no cancerous mutations in clone

Code

Show 10 **entries** **Search:**

CHROM	POS	REF	ALT	GT.x	GT.y	AF.x	AF.y	DP.x	INFO.x
No data available in table									

Showing 0 to 0 of 0 entries Previous Next

1592_123, no cancerous mutations in clone

Code

Show 10 **entries** **Search:**

CHROM	POS	REF	ALT	GT.x	GT.y	AF.x	AF.y	DP.x	INFO.x
No data available in table									

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1620_102, no cancerous mutations in clone; one variant with a one base pair deletion with 0.0261 frequency in the clone and 0.0268 frequency in the donor PBMC

Code

Show 10 **entries** **Search:**

	CHROM	POS	REF	ALT	GT.x	GT.y	AF.x	AF.y	DP.x	
1	5	131931451	TA	T	0|1		0.0261		2945	VC=INDEL;Func=exonic;Gene=RAD50;ExonicFunc=frame shift;FullAA=RAD50:NM_005732.3:exon13:c.2157delA:p.L719fs;Transcript=NM_00

Showing 1 to 1 of 1 entries Previous 1 Next

1620_104, no cancerous mutations in clone

Code

Show 10 **entries** **Search:**

CHROM	POS	REF	ALT	GT.x	GT.y	AF.x	AF.y	DP.x	INFO.x
No data available in table									

Showing 0 to 0 of 0 entries Previous Next