```
##fileformat=VCFv4.1
##fileDate=20140311
##source=rvd2
##Somatic test in cancer-normal-paired sample.
##Somatic status determining threshold in cancer-normal-paired sample = (0.05,0.75)
##contig=<ID=7,length=44716>
##INFO=<ID=COAF,Number=1,Type=Float,Description="Control Allele Frequency">
##INFO=<ID=CAAF,Number=1,Type=Float,Description="Case Allele Frequency">
##FORMAT=<ID=AU,Number=1,Type=Integer,Description="Number of 'A' alleles used in fitting the model">
##FORMAT=<ID=CU,Number=1,Type=Integer,Description="Number of 'C' alleles used in fitting the model">
##FORMAT=<ID=GU,Number=1,Type=Integer,Description="Number of 'G' alleles used in fitting the model">
##FORMAT=<ID=TU,Number=1,Type=Integer,Description="Number of 'T' alleles used in fitting the model">
```

#CHROM	POS	REF	SOMATIC	FORMAT	Normal	Case
chr7	154743899	C	Germline:homo-homo	AU:CU:GU:TU	0:0:0:45	0:0:0:71
chr7	154749704	G	LOH1:heter-ref	AU:CU:GU:TU	8:0:36:0	2:0:42:0
chr7	154753635	T	Germline:homo-homo	AU:CU:GU:TU	0:38:0:0	0:63:0:1
chr7	154754371	T	LOH2: heter-homo	AU:CU:GU:TU	0:19:0:31	0:61:0:0
chr7	154757241	A	Somatic:ref-heter	AU:CU:GU:TU	34:0:1:0	54:4:0:0
chr7	154758813	G	LOH2: heter-homo	AU:CU:GU:TU	14:0:28:0	54:0:0:0
chr7	154760439	A	Somatic:ref-homo	AU:CU:GU:TU	37:0:0:0	0:38:0:0
chr7	154766700	C	Germline:heter-heter	AU:CU:GU:TU	4:21:0:0	10:42:0:0
chr7	154766732	T	Somatic:ref-heter	AU:CU:GU:TU	0:0:0:35	0:0:5:44
chr7	154766832	A	Somatic:ref-heter	AU:CU:GU:TU	34:0:0:0	42:4:0:0
chr7	154777118	A	Somatic:ref-heter	AU:CU:GU:TU	46:0:0:0	31:4:0:0
chr7	154780960	C	Germline:homo-homo	AU:CU:GU:TU	0:0:0:42	0:0:0:56
chr7	154781769	G	LOH1:heter-ref	AU:CU:GU:TU	0:0:21:4	0:0:31:2