##fileformat=VCFv4.1

##contenttype=HumanOmni25M-8v1-1\_B.bpm

##sourcereport=FinalReport\_HumanOmni25M-8v1-1\_PG0001217-BLD.txt

##genomemap=HumanOmni25M-8v1-1.NCBI37.map.txt

##contig=<ID=NA,length=0,Description="Contig undetermined-for genotyped alleles that do not map to the reference.">

##INFO=<ID=AL,Number=1,Type=String,Description="Array Alleles">

##INFO=<ID=ST,Number=1,Type=String,Description="ProbeStrand">

##FILTER=<ID=GTEX,Description="Genotype excluded from reference sequence mapping.">

##FILTER=<ID=NOCALL,Description="Genotype not called on array.">

##FORMAT=<ID=GC,Number=1,Type=Float,Description="GencallScore">

##FORMAT=<ID=GT,Number=1,Type=String,Description="Genotype">

##workflow\_type=Illumina\_GenotypingToVCF

##workflow\_version=v1.4

#CHROM POS ID REF ALT QUAL FILTER INFO FORMAT WG0231131-DNAD01-PG0001217-BLD

chr7 117149177 rs78655421 A G . PASS AL=A/G;ST=- GT:GC 0/1:0.9120

chr7 117509123 rs2572886 A G . PASS AL=A/G;ST=- GT:GC 0/1:0.9120

chr7 117509123 rs1143674 A G . PASS AL=A/G;ST=- GT:GC 0/1:0.9120

chr7 117509123 rs4800773 A G . PASS AL=A/G;ST=- GT:GC 0/1:0.9120

chr7 117509123 rs2042959 A G . PASS AL=A/G;ST=- GT:GC 0/1:0.9120

chr7 117509123 rs80359806 A G . PASS AL=A/G;ST=- GT:GC 0/1:0.9120

chr7 117509123 rs2337193 A G . PASS AL=A/G;ST=- GT:GC 0/1:0.9120

chr7 117509123 rs2153271 A G . PASS AL=A/G;ST=- GT:GC 0/1:0.9120