ANGSD (Analysis of Next Generation Sequencing Data): commonly used for population genetic analyses when working with low-coverage sequence data. Provides information about SNP positions and their population frequencies.

1. **chromo**: Chromosome or contig identifier (e.g., KN882277.1, KN885472.1) from a genome assembly.
2. **position**: The specific base pair position on the chromosome/contig where the variant is located.
3. **major**: The major allele at this position - the more common nucleotide (G, C, T, A).
4. **minor**: The minor allele - the less common alternative nucleotide.
5. **unknownEM**: Estimated allele frequency of the minor allele as calculated by an Expectation-Maximization (EM) algorithm. Values range from 0-1, with values like 0.332737 suggesting the minor allele frequency is about 33.3%.
6. **pu-EM**: p-value or probability statistic related to the EM algorithm calculation, indicating confidence in the variant call. The very small values (e.g., 3.127339e-03 = 0.0031) suggest high confidence.
7. **nInd**: Number of individuals in which this variant was observed. For example, the first variant was found in 3 individuals, while variants on KN885472.1 were found in 6 individuals.

chromo	position	major	minor	unknownEM	pu-EM	nInd
KN882277.1	41498	G	T	0.332737	3.127339e-03	3
KN885472.1	10712	C	G	0.126253	1.118604e-03	6
KN885472.1	10741	T	A	0.205533	2.729806e-03	6
KN885472.1	10746	C	T	0.113382	1.394211e-03	6
KN894013.1	22082	T	C	0.098327	3.551274e-03	2
KN894013.1	22084	C	T	0.106562	3.241062e-03	2
KN883616.1	31041	C	A	0.422659	2.070393e-03	3
KN883616.1	31042	T	G	0.424129	1.269827e-03	3
KN883758.1	179190	A	T	0.336645	3.103740e-03	3