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. Below is the explanation of the .mafs output file, which gives information on the estimates of the minor allele frequencies (mafs).

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