A screen shot of a computer

Description automatically generated

Gene name is sema4f and from supporting evidence there is similarity to 10 other proteins, and there is 89% coverage of the annotated genomic feature by RNAseq alignments. This gene encodes a transmembrane class IV semaphorin family protein, which plays a role in neural development. The genes product has sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F. The gene has 15 exons, upstream of the start of the gene we can see multiple regions of open chromatin however some of the are non-coding elements which might be potential regulators of said gene. There are potential differences in the expression of this gene in larval and diapause stages because the RNAseq data for the diapause stage is showing fewer peaks, meaning there is less RNA for this specific gene in the diapause stage compared to the larval stage. ATACseq data is also showing less peaks for this region of interest during diapause stage. Peak 583, peak 584, 585, 586, 587 (representing open regions of chromatin which are non-coding) are present in the larval stage and are not present in the diapause stage. This could indicate that these regions are up-regulators of gene sema4f or regulate a different gene during the larval stage development. Peak 587 NCOC is in the intron of the gene and could also act as the gene transcription regulator. Gene spans from 36195 to 36295kb meaning the gene has around 100kb and it is located on the first chromosome. SEMA4F, ssemaphorin 4F in humans (Homo sapiens) has 18 exons. This gene may be involved in neurogenesis in prostate cancer, the development of neurofibromas, and breast cancer tumorigenesis in humans. Alternative splicing results in multiple transcript variants, some variants by excluding exons.