Appendix A

Some example GAZE configurations

A.1 GAZE_std

```
<?xml version="1.0" encoding="US-ASCII"?>
<gaze>

<declarations>
   <feature id="5ss_0" st_off="1" en_off="1"/>
   <feature id="5ss_1" st_off="1" en_off="1"/>
   <feature id="5ss_2" st_off="1" en_off="1"/>
   <feature id="stop" st_off="3" en_off="0"/>
   <feature id="3ss_0" st_off="1" en_off="1"/>
   <feature id="3ss_1" st_off="1" en_off="1"/>
   <feature id="3ss_2" st_off="1" en_off="1"/>
   <feature id="start" st_off="0" en_off="3"/>
   <feature id="start_rev" st_off="3" en_off="0"/>
   <feature id="3ss_0_rev" st_off="1" en_off="1"/>
   <feature id="3ss_1_rev" st_off="1" en_off="1"/>
   <feature id="3ss_2_rev" st_off="1" en_off="1"/>
   <feature id="stop_rev" st_off="0" en_off="3"/>
   <feature id="5ss_0_rev" st_off="1" en_off="1"/>
   <feature id="5ss_1_rev" st_off="1" en_off="1"/>
   <feature id="5ss_2_rev" st_off="1" en_off="1"/>

   <segment id="coding_seg" scoring="standard_max"/>
   <segment id="coding_seg_rev" scoring="standard_max"/>

   <lengthfunction id="intron_pen"/>
   <lengthfunction id="intergene_pen"/>
   <lengthfunction id="init_ex_pen"/>
   <lengthfunction id="term_ex_pen"/>
   <lengthfunction id="int_ex_pen"/>
   <lengthfunction id="sngl_ex_pen"/>
</declarations>

<gff2gaze>
```

```
   <!-- Features -->

   <gffline feature="atg" source="Genefinder" strand="+">
      <feat id="start"/>
   </gffline>

   <gffline feature="atg" source="Genefinder" strand="-">
      <feat id="start_rev"/>
   </gffline>

   <gffline feature="stop" source="Genefinder" strand="+">
      <feat id="stop"/>
   </gffline>

   <gffline feature="stop" source="Genefinder" strand="-">
      <feat id="stop_rev"/>
   </gffline>

   <gffline feature="splice5" source="Genefinder" strand="+">
      <feat id="5ss_0"/>
      <feat id="5ss_1"/>
      <feat id="5ss_2"/>
   </gffline>

   <gffline feature="splice5" source="Genefinder" strand="-">
      <feat id="5ss_0_rev"/>
      <feat id="5ss_1_rev"/>
      <feat id="5ss_2_rev"/>
   </gffline>

   <gffline feature="splice3" source="Genefinder" strand="+">
      <feat id="3ss_0"/>
      <feat id="3ss_1"/>
      <feat id="3ss_2"/>
   </gffline>

   <gffline feature="splice3" source="Genefinder" strand="-">
      <feat id="3ss_0_rev"/>
      <feat id="3ss_1_rev"/>
      <feat id="3ss_2_rev"/>
   </gffline>

   <!-- Segments -->

   <gffline feature="coding_seg" source="Genefinder" strand="+">
      <seg id="coding_seg"/>
   </gffline>

   <gffline feature="coding_seg" source="Genefinder" strand="-">
      <seg id="coding_seg_rev"/>
   </gffline>
</gff2gaze>


<dna2gaze>
   <dnafeat pattern="atg">
      <feat id="start" score="0.0"/>
   </dnafeat>

   <dnafeat pattern="cat">
      <feat id="start_rev" score="0.0"/>
   </dnafeat>

   <dnafeat pattern="taa">
      <feat id="stop" score="-100.0"/>
```

```
   </dnafeat>
   <dnafeat pattern="tag">
      <feat id="stop" score="-100.0"/>
   </dnafeat>
   <dnafeat pattern="tga">
      <feat id="stop" score="-100.0"/>
   </dnafeat>

   <dnafeat pattern="tta">
      <feat id="stop_rev" score="-100.0"/>
   </dnafeat>
   <dnafeat pattern="cta">
      <feat id="stop_rev" score="-100.0"/>
   </dnafeat>
   <dnafeat pattern="tca">
      <feat id="stop_rev" score="-100.0"/>
   </dnafeat>

   <takedna id="5ss_1" st_off="0" en_off="1"/>
   <takedna id="3ss_1" st_off="1" en_off="-1"/>
   <takedna id="5ss_2" st_off="-1" en_off="1"/>
   <takedna id="3ss_2" st_off="1" en_off="0"/>
   <takedna id="5ss_1_rev" st_off="1" en_off="0"/>
   <takedna id="3ss_1_rev" st_off="-1" en_off="1"/>
   <takedna id="5ss_2_rev" st_off="1" en_off="-1"/>
   <takedna id="3ss_2_rev" st_off="0" en_off="1"/>
</dna2gaze>

<model>
   <target id="END">
      <source id="BEGIN">
         <output feature="no genes"/>
      </source>

      <source id="start">
         <useseg id="coding_seg" source_phase="0"/>
         <killfeat id="stop" source_phase="0"/>
         <output feature="CDS_end_not_found" strand="+" frame="0"/>
      </source>

      <source id="stop">
         <output feature="intergenic"/>
      </source>

      <source id="start_rev" mindis="0">
         <output feature="intergenic"/>
      </source>

      <source id="stop_rev">
         <useseg id="coding_seg_rev" source_phase="0"/>
         <killfeat id="stop_rev" source_phase="0"/>
         <output feature="CDS_start_not_found" strand="-"/>
      </source>

      <source id="3ss_0">
         <useseg id="coding_seg" source_phase="0"/>
         <killfeat id="stop" source_phase="0"/>
         <output feature="CDS_end_not_found" strand="+" frame="0"/>
      </source>

      <source id="3ss_1">
         <useseg id="coding_seg" source_phase="2"/>
         <killfeat id="stop" source_phase="2"/>
         <output feature="CDS_end_not_found" strand="+" frame="1"/>
      </source>
```

```
   <source id="3ss_2">
      <useseg id="coding_seg" source_phase="1"/>
      <killfeat id="stop" source_phase="1"/>
      <output feature="CDS_end_not_found" strand="+" frame="2"/>
   </source>

   <source id="5ss_0" len_fun="intron_pen">
      <output feature="intron_end_not_found" strand="+"/>
   </source>

   <source id="5ss_1" len_fun="intron_pen">
      <output feature="intron_end_not_found" strand="+"/>
   </source>

   <source id="5ss_2" len_fun="intron_pen">
      <output feature="intron_end_not_found" strand="+"/>
   </source>

   <source id="3ss_0_rev" len_fun="intron_pen">
      <output feature="intron_start_not_found" strand="-"/>
   </source>

   <source id="3ss_1_rev" len_fun="intron_pen">
      <output feature="intron_start_not_found" strand="-"/>
   </source>

   <source id="3ss_2_rev" len_fun="intron_pen">
      <output feature="intron_start_not_found" strand="-"/>
   </source>

   <source id="5ss_0_rev">
      <useseg id="coding_seg_rev" source_phase="0"/>
      <killfeat id="stop_rev" source_phase="0"/>
      <output feature="CDS_start_not_found" strand="-"/>
   </source>

   <source id="5ss_1_rev">
      <useseg id="coding_seg_rev" source_phase="1"/>
      <killfeat id="stop_rev" source_phase="1"/>
      <output feature="CDS_start_not_found" strand="-"/>
   </source>

   <source id="5ss_2_rev">
      <useseg id="coding_seg_rev" source_phase="2"/>
      <killfeat id="stop_rev" source_phase="2"/>
      <output feature="CDS_start_not_found" strand="-"/>
   </source>
</target>

<target id="start">
   <source id="BEGIN">
      <output feature="intergenic"/>
   </source>

   <source id="stop" mindis="0" len_fun="intergene_pen">
      <output feature="intergenic"/>
   </source>

   <source id="start_rev" mindis="0" len_fun="intergene_pen">
      <output feature="intergenic"/>
   </source>
</target>

<target id="start_rev">
```

```
   <useseg id="coding_seg_rev" target_phase="0"/>
   <killfeat id="stop_rev" target_phase="0"/>

   <source id="BEGIN">
      <output feature="CDS_end_not_found" strand="-" frame="0"/>
   </source>

   <source id="stop_rev" mindis="6" len_fun="sngl_ex_pen" phase="0">
      <output feature="CDS" strand="-" frame="0"/>
   </source>

   <source id="5ss_0_rev" mindis="3" len_fun="init_ex_pen" phase="0">
      <output feature="CDS" strand="-" frame="0"/>
   </source>

   <source id="5ss_1_rev" mindis="3" len_fun="init_ex_pen" phase="1">
      <output feature="CDS" strand="-" frame="0"/>
   </source>

   <source id="5ss_2_rev" mindis="3" len_fun="init_ex_pen" phase="2">
      <output feature="CDS" strand="-" frame="0"/>
   </source>
</target>

<target id="stop">
   <useseg id="coding_seg" target_phase="0"/>
   <killfeat id="stop" target_phase="0"/>

   <source id="BEGIN">
      <output feature="CDS_start_not_found" strand="+"/>
   </source>

   <source id="start" mindis="6" len_fun="sngl_ex_pen" phase="0">
      <output feature="CDS" strand="+" frame="0"/>
   </source>

   <source id="3ss_0" mindis="3" len_fun="term_ex_pen" phase="0">
      <output feature="CDS" strand="+" frame="0"/>
   </source>

   <source id="3ss_1" mindis="3" len_fun="term_ex_pen" phase="2">
      <output feature="CDS" strand="+" frame="1"/>
   </source>

   <source id="3ss_2" mindis="3" len_fun="term_ex_pen" phase="1">
      <output feature="CDS" strand="+" frame="2"/>
   </source>
</target>

<target id="stop_rev">
   <source id="BEGIN">
      <output feature="intergenic"/>
   </source>

   <source id="start_rev" mindis="0" len_fun="intergene_pen">
      <output feature="intergenic"/>
   </source>

   <source id="stop" mindis="0" len_fun="intergene_pen">
      <output feature="intergenic"/>
   </source>
</target>

<target id="5ss_0">
   <useseg id="coding_seg" target_phase="0"/>
```

```
   <killfeat id="stop" target_phase="0"/>

   <source id="BEGIN">
      <output feature="CDS_start_not_found" strand="+"/>
   </source>

   <source id="start" mindis="3" len_fun="init_ex_pen" phase="0">
      <output feature="CDS" strand="+" frame="0"/>
   </source>

   <source id="3ss_0" mindis="20" len_fun="int_ex_pen" phase="0">
      <output feature="CDS" strand="+" frame="0"/>
   </source>

   <source id="3ss_1" mindis="20" len_fun="int_ex_pen" phase="2">
      <output feature="CDS" strand="+" frame="1"/>
   </source>

   <source id="3ss_2" mindis="20" len_fun="int_ex_pen" phase="1">
      <output feature="CDS" strand="+" frame="2"/>
   </source>
</target>

<target id="5ss_0_rev">
   <source id ="BEGIN" len_fun="intron_pen">
      <output feature="intron_end_not_found" strand="-"/>
   </source>

   <source id="3ss_0_rev" mindis="39" len_fun="intron_pen">
      <output feature="intron" strand="-"/>
   </source>
</target>

<target id="5ss_1">
   <useseg id="coding_seg" target_phase="1"/>
   <killfeat id="stop" target_phase="1"/>

   <source id="BEGIN">
      <output feature="CDS_start_not_found" strand="+"/>
   </source>

   <source id="start" mindis="3"  len_fun="init_ex_pen" phase="1">
      <output feature="CDS" strand="+" frame="0"/>
   </source>

   <source id="3ss_0" mindis="20" len_fun="int_ex_pen" phase="1">
      <output feature="CDS" strand="+" frame="0"/>
   </source>

   <source id="3ss_1" mindis="20" len_fun="int_ex_pen" phase="0">
      <output feature="CDS" strand="+" frame="1"/>
   </source>

   <source id="3ss_2" mindis="20" len_fun="int_ex_pen" phase="2">
      <output feature="CDS" strand="+" frame="2"/>
   </source>
</target>

<target id="5ss_1_rev">
   <source id ="BEGIN" len_fun="intron_pen">
      <output feature="intron_end_not_found" strand="-"/>
   </source>

   <source id="3ss_1_rev" mindis="39" len_fun="intron_pen">
      <killdna source_dna="ct" target_dna="a"/>
```

```
      <killdna source_dna="tc" target_dna="a"/>
      <killdna source_dna="tt" target_dna="a"/>
      <output feature="intron" strand="-"/>
   </source>
</target>

<target id="5ss_2">
   <useseg id="coding_seg" target_phase="2"/>
   <killfeat id="stop" target_phase="2"/>

   <source id ="BEGIN">
      <output feature="CDS_start_not_found" strand="+"/>
   </source>

   <source id="start" mindis="3"  len_fun="init_ex_pen" phase="2">
      <output feature="CDS" strand="+" frame="0"/>
   </source>

   <source id="3ss_0" mindis="20" len_fun="int_ex_pen" phase="2">
      <output feature="CDS" strand="+" frame="0"/>
   </source>

   <source id="3ss_1" mindis="20" len_fun="int_ex_pen" phase="1">
      <output feature="CDS" strand="+" frame="1"/>
   </source>

   <source id="3ss_2" mindis="20" len_fun="int_ex_pen" phase="0">
      <output feature="CDS" strand="+" frame="2"/>
   </source>
</target>

<target id="5ss_2_rev">
   <source id ="BEGIN" len_fun="intron_pen">
      <output feature="intron_end_not_found" strand="-"/>
   </source>
   <source id="3ss_2_rev" mindis="39" len_fun="intron_pen">
      <killdna source_dna="c" target_dna="ta"/>
      <killdna source_dna="t" target_dna="ca"/>
      <killdna source_dna="t" target_dna="ta"/>
      <output feature="intron" strand="-"/>
   </source>
</target>

<target id="3ss_0">
   <source id="BEGIN" len_fun="intron_pen">
      <output feature="intron_start_not_found" strand="+"/>
   </source>
   <source id="5ss_0" mindis="39" len_fun="intron_pen">
      <output feature="intron" strand="+"/>
   </source>
</target>

<target id="3ss_0_rev">
   <useseg id="coding_seg_rev" target_phase="0"/>
   <killfeat id="stop_rev" target_phase="0"/>

   <source id="BEGIN">
      <output feature="CDS_end_not_found" strand="-" frame="0"/>
   </source>

   <source id="stop_rev" mindis="3" len_fun="term_ex_pen" phase="0">
      <output feature="CDS" strand="-" frame="0"/>
   </source>

   <source id="5ss_0_rev" mindis="20" len_fun="int_ex_pen" phase="0">
```

```
      <output feature="CDS" strand="-" frame="0"/>
   </source>

   <source id="5ss_1_rev" mindis="20" len_fun="int_ex_pen" phase="1">
      <output feature="CDS" strand="-" frame="0"/>
   </source>

   <source id="5ss_2_rev" mindis="20" len_fun="int_ex_pen" phase="2">
      <output feature="CDS" strand="-" frame="0"/>
   </source>
</target>

<target id="3ss_1">
   <source id="BEGIN" len_fun="intron_pen">
      <output feature="intron_start_not_found" strand="+"/>
   </source>
   <source id="5ss_1" mindis="39" len_fun="intron_pen">
      <killdna source_dna="t" target_dna="aa"/>
      <killdna source_dna="t" target_dna="ag"/>
      <killdna source_dna="t" target_dna="ga"/>
      <output feature="intron" strand="+"/>
   </source>
</target>

<target id="3ss_1_rev">
   <useseg id="coding_seg_rev" target_phase="2"/>
   <killfeat id="stop_rev" target_phase="2"/>

   <source id="BEGIN">
      <output feature="CDS_end_not_found" strand="-" frame="1"/>
   </source>

   <source id="stop_rev" mindis="3"  len_fun="term_ex_pen" phase="2">
      <output feature="CDS" strand="-" frame="1"/>
   </source>

   <source id="5ss_0_rev" mindis="20" len_fun="int_ex_pen" phase="2">
      <output feature="CDS" strand="-" frame="1"/>
   </source>

   <source id="5ss_1_rev" mindis="20" len_fun="int_ex_pen" phase="0">
      <output feature="CDS" strand="-" frame="1"/>
   </source>

   <source id="5ss_2_rev" mindis="20" len_fun="int_ex_pen" phase="1">
      <output feature="CDS" strand="-" frame="1"/>
   </source>
</target>

<target id="3ss_2">
   <source id="BEGIN" len_fun="intron_pen">
      <output feature="intron_start_not_found" strand="+"/>
   </source>
   <source id="5ss_2" mindis="39" len_fun="intron_pen">
      <killdna source_dna="ta" target_dna="a"/>
      <killdna source_dna="ta" target_dna="g"/>
      <killdna source_dna="tg" target_dna="a"/>
      <output feature="intron" strand="+"/>
   </source>
</target>

<target id="3ss_2_rev">
   <useseg id="coding_seg_rev" target_phase="1"/>
   <killfeat id="stop_rev" target_phase="1"/>
```

```
      <source id ="BEGIN">
         <output feature="CDS_end_not_found" strand="-" frame="2"/>
      </source>

      <source id="stop_rev" mindis="3" len_fun="term_ex_pen" phase="1">
         <output feature="CDS" strand="-" frame="2"/>
      </source>

      <source id="5ss_0_rev" mindis="20" len_fun="int_ex_pen" phase="1">
         <output feature="CDS" strand="-" frame="2"/>
      </source>

      <source id="5ss_1_rev" mindis="20" len_fun="int_ex_pen" phase="2">
         <output feature="CDS" strand="-" frame="2"/>
      </source>

      <source id="5ss_2_rev" mindis="20" len_fun="int_ex_pen" phase="0">
         <output feature="CDS" strand="-" frame="2"/>
      </source>
   </target>
</model>

<lengthfunctions>
   <lengthfunc id="intron_pen" file="/tables/intron_penalty.klh"/>
   <lengthfunc id="init_ex_pen" file="/tables/exon_penalty.initial.klh"/>
   <lengthfunc id="term_ex_pen" file="/tables/exon_penalty.terminal.klh"/>
   <lengthfunc id="int_ex_pen" file="/tables/exon_penalty.internal.klh"/>

   <lengthfunc id="sngl_ex_pen">
      <point x="0" y="4"/>
      <point x="1" y="4"/>
   </lengthfunc>

   <lengthfunc id="intergene_pen">
     <point x="0" y="4"/>
     <point x="1" y="4"/>
   </lengthfunc>
</lengthfunctions>

</gaze>
```

A.2 GAZE_EST

```
<?xml version="1.0" encoding="US-ASCII"?>
<gaze>

<declarations>
   <feature id="trans_start" st_off="0" en_off="1"/>
   <feature id="5ss_0" st_off="1" en_off="1"/>
   <feature id="5ss_1" st_off="1" en_off="1"/>
   <feature id="5ss_2" st_off="1" en_off="1"/>
   <feature id="stop" st_off="3" en_off="0"/>
   <feature id="t_splice" st_off="1" en_off="1"/>
   <feature id="3ss_0" st_off="1" en_off="1"/>
   <feature id="3ss_1" st_off="1" en_off="1"/>
   <feature id="3ss_2" st_off="1" en_off="1"/>
   <feature id="start" st_off="0" en_off="3"/>
   <feature id="trans_stop" st_off="1" en_off="0"/>
   <feature id="trans_stop_rev" st_off="0" en_off="1"/>
   <feature id="start_rev" st_off="3" en_off="0"/>
   <feature id="3ss_0_rev" st_off="1" en_off="1"/>
   <feature id="3ss_1_rev" st_off="1" en_off="1"/>
   <feature id="3ss_2_rev" st_off="1" en_off="1"/>
```

```
   <feature id="t_splice_rev" st_off="1" en_off="1"/>
   <feature id="stop_rev" st_off="0" en_off="3"/>
   <feature id="5ss_0_rev" st_off="1" en_off="1"/>
   <feature id="5ss_1_rev" st_off="1" en_off="1"/>
   <feature id="5ss_2_rev" st_off="1" en_off="1"/>
   <feature id="trans_start_rev" st_off="1" en_off="0"/>

   <segment id="coding_seg" scoring="standard_max"/>
   <segment id="est_seg" mul="0.01"/>
   <segment id="est_intron" mul="0.05"/>
   <segment id="coding_seg_rev" scoring="standard_max"/>
   <segment id="est_seg_rev" mul="0.01"/>
   <segment id="est_intron_rev" mul="0.05"/>
   <segment id="est_span" mul="-1000.0"/>

   <lengthfunction id="intron_pen"/>
   <lengthfunction id="intergene_pen"/>
   <lengthfunction id="tsplice_pen"/>
   <lengthfunction id="init_ex_pen"/>
   <lengthfunction id="term_ex_pen"/>
   <lengthfunction id="int_ex_pen"/>
   <lengthfunction id="sngl_ex_pen"/>
</declarations>

<gff2gaze>
   <!-- Features -->

   <gffline feature="atg" source="Genefinder" strand="+">
      <feat id="start"/>
   </gffline>

   <gffline feature="atg" source="Genefinder" strand="-">
      <feat id="start_rev"/>
   </gffline>

   <gffline feature="stop" source="Genefinder" strand="+">
      <feat id="stop"/>
   </gffline>

   <gffline feature="stop" source="Genefinder" strand="-">
      <feat id="stop_rev"/>
   </gffline>

   <gffline feature="splice5" source="Genefinder" strand="+">
      <feat id="5ss_0"/>
      <feat id="5ss_1"/>
      <feat id="5ss_2"/>
   </gffline>

   <gffline feature="splice5" source="Genefinder" strand="-">
      <feat id="5ss_0_rev"/>
      <feat id="5ss_1_rev"/>
      <feat id="5ss_2_rev"/>
   </gffline>

   <gffline feature="splice3" source="Genefinder" strand="+">
      <feat id="3ss_0"/>
      <feat id="3ss_1"/>
      <feat id="3ss_2"/>
      <feat id="t_splice"/>
   </gffline>

   <gffline feature="splice3" source="Genefinder" strand="-">
      <feat id="3ss_0_rev"/>
      <feat id="3ss_1_rev"/>
```

```
   <feat id="3ss_2_rev"/>
   <feat id="t_splice_rev"/>
</gffline>

<!-- The following features will be added by the pre-processor to the GFF
     file, using the est_span objects. But perhaps there should be more
     expressiveness in the GFF2GAZE section to allow for the creation of
     features corresponding to the ends of the region given by the GFF line -->

<gffline feature="transcript_start" source="EST_derived" strand="+">
    <feat id="trans_start"/>
</gffline>

<gffline feature="transcript_start" source="BLAT_mRNA_BEST_derived" strand="+">
    <feat id="trans_start"/>
</gffline>

<gffline feature="transcript_start" source="EST_derived" strand="-">
    <feat id="trans_start_rev"/>
</gffline>

<gffline feature="transcript_start" source="BLAT_mRNA_BEST_derived" strand="-">
    <feat id="trans_start_rev"/>
</gffline>

<gffline feature="transcript_stop" source="EST_derived" strand="+">
    <feat id="trans_stop"/>
</gffline>

<gffline feature="transcript_stop" source="BLAT_mRNA_BEST_derived" strand="+">
    <feat id="trans_stop"/>
</gffline>

<gffline feature="transcript_stop" source="EST_derived" strand="-">
    <feat id="trans_stop_rev"/>
</gffline>

<gffline feature="transcript_stop" source="BLAT_mRNA_BEST_derived" strand="-">
    <feat id="trans_stop_rev"/>
</gffline>

<!-- Segments -->

<gffline feature="coding_seg" source="Genefinder" strand="+">
   <seg id="coding_seg"/>
</gffline>

<gffline feature="coding_seg" source="Genefinder" strand="-">
   <seg id="coding_seg_rev"/>
</gffline>

<!-- The following segments are derived by the pre-processor -->

<gffline feature="similarity" source="EST_GENOME_strand" strand="+">
   <seg id="est_seg"/>
</gffline>

<gffline feature="similarity" source="EST_GENOME_strand" strand="-">
   <seg id="est_seg_rev"/>
</gffline>

<gffline feature="intron" source="EST_derived" strand="+">
   <seg id="est_intron"/>
</gffline>
```

```
   <gffline feature="intron" source="EST_derived" strand="-">
      <seg id="est_intron_rev"/>
   </gffline>

   <gffline feature="EST_span">
      <seg id="est_span"/>
   </gffline>
</gff2gaze>

<dna2gaze>
   <dnafeat pattern="atg">
      <feat id="start" score="0.0"/>
   </dnafeat>

   <dnafeat pattern="cat">
      <feat id="start_rev" score="0.0"/>
   </dnafeat>

   <dnafeat pattern="taa">
      <feat id="stop" score="-100.0"/>
   </dnafeat>
   <dnafeat pattern="tag">
      <feat id="stop" score="-100.0"/>
   </dnafeat>
   <dnafeat pattern="tga">
      <feat id="stop" score="-100.0"/>
   </dnafeat>

   <dnafeat pattern="tta">
      <feat id="stop_rev" score="-100.0"/>
   </dnafeat>
   <dnafeat pattern="cta">
      <feat id="stop_rev" score="-100.0"/>
   </dnafeat>
   <dnafeat pattern="tca">
      <feat id="stop_rev" score="-100.0"/>
   </dnafeat>

   <takedna id="5ss_1" st_off="0" en_off="1"/>
   <takedna id="3ss_1" st_off="1" en_off="-1"/>
   <takedna id="5ss_2" st_off="-1" en_off="1"/>
   <takedna id="3ss_2" st_off="1" en_off="0"/>
   <takedna id="5ss_1_rev" st_off="1" en_off="0"/>
   <takedna id="3ss_1_rev" st_off="-1" en_off="1"/>
   <takedna id="5ss_2_rev" st_off="1" en_off="-1"/>
   <takedna id="3ss_2_rev" st_off="0" en_off="1"/>
</dna2gaze>

<model>
   <target id="END">
      <source id="BEGIN">
         <output feature="no genes"/>
      </source>

      <source id="start">
         <useseg id="coding_seg" source_phase="0"/>
         <useseg id="est_seg"/>
         <killfeat id="stop" source_phase="0"/>
         <output feature="CDS_end_not_found" strand="+" frame="0"/>
      </source>

      <source id="stop">
         <useseg id="est_span"/>
         <output feature="intergenic"/>
      </source>
```

```
<source id="start_rev" mindis="0">
   <useseg id="est_span"/>
   <output feature="intergenic"/>
</source>

<source id="stop_rev">
   <useseg id="coding_seg_rev" source_phase="0"/>
   <useseg id="est_seg_rev"/>
   <killfeat id="stop_rev" source_phase="0"/>
   <output feature="CDS_start_not_found" strand="-"/>
</source>

<source id="3ss_0">
   <useseg id="coding_seg" source_phase="0"/>
   <useseg id="est_seg"/>
   <killfeat id="stop" source_phase="0"/>
   <output feature="CDS_end_not_found" strand="+" frame="0"/>
</source>

<source id="3ss_1">
   <useseg id="coding_seg" source_phase="2"/>
   <useseg id="est_seg"/>
   <killfeat id="stop" source_phase="2"/>
   <output feature="CDS_end_not_found" strand="+" frame="1"/>
</source>

<source id="3ss_2">
   <useseg id="coding_seg" source_phase="1"/>
   <useseg id="est_seg"/>
   <killfeat id="stop" source_phase="1"/>
   <output feature="CDS_end_not_found" strand="+" frame="2"/>
</source>

<source id="5ss_0" len_fun="intron_pen">
   <useseg id="est_intron" exact="source"/>
   <output feature="intron_end_not_found" strand="+"/>
</source>

<source id="5ss_1" len_fun="intron_pen">
   <useseg id="est_intron" exact="source"/>
   <output feature="intron_end_not_found" strand="+"/>
</source>

<source id="5ss_2" len_fun="intron_pen">
   <useseg id="est_intron" exact="source"/>
   <output feature="intron_end_not_found" strand="+"/>
</source>

<source id="3ss_0_rev" len_fun="intron_pen">
   <useseg id="est_intron_rev" exact="source"/>
   <output feature="intron_start_not_found" strand="-"/>
</source>

<source id="3ss_1_rev" len_fun="intron_pen">
   <useseg id="est_intron_rev" exact="source"/>
   <output feature="intron_start_not_found" strand="-"/>
</source>

<source id="3ss_2_rev" len_fun="intron_pen">
   <useseg id="est_intron_rev" exact="source"/>
   <output feature="intron_start_not_found" strand="-"/>
</source>

<source id="5ss_0_rev">
```

```
      <useseg id="coding_seg_rev" source_phase="0"/>
      <useseg id="est_seg_rev"/>
      <killfeat id="stop_rev" source_phase="0"/>
      <output feature="CDS_start_not_found" strand="-"/>
   </source>

   <source id="5ss_1_rev">
      <useseg id="coding_seg_rev" source_phase="1"/>
      <useseg id="est_seg_rev"/>
      <killfeat id="stop_rev" source_phase="1"/>
      <output feature="CDS_start_not_found" strand="-"/>
   </source>

   <source id="5ss_2_rev">
      <useseg id="coding_seg_rev" source_phase="2"/>
      <useseg id="est_seg_rev"/>
      <killfeat id="stop_rev" source_phase="2"/>
      <output feature="CDS_start_not_found" strand="-"/>
   </source>

   <source id="trans_start">
      <useseg id="est_seg"/>
      <output feature="UTR5_end_not_found" strand="+"/>
   </source>

   <source id="trans_stop">
      <useseg id="est_span"/>
      <output feature="intergenic"/>
   </source>

   <source id="trans_stop_rev">
      <useseg id="est_seg_rev"/>
      <output feature="UTR3_start_not_found" strand="-"/>
   </source>

   <source id="trans_start_rev">
      <useseg id="est_span"/>
      <output feature="intergenic"/>
   </source>

   <source id="t_splice" mindis="0" maxdis="50" len_fun="tsplice_pen">
      <useseg id="est_seg"/>
      <output feature="trans_splice_UTR5_end_not_found" strand="+"/>
   </source>

   <source id="t_splice_rev">
      <useseg id="est_span"/>
      <output feature="intergenic"/>
   </source>
</target>

<target id="start">
   <source id="BEGIN">
      <useseg id="est_span"/>
      <output feature="intergenic"/>
   </source>

   <source id="t_splice" mindis="0" maxdis="50" len_fun="tsplice_pen">
      <useseg id="est_seg"/>
      <output feature="trans_splice_UTR5" strand="+"/>
   </source>

   <source id="trans_start" mindis="0">
      <useseg id="est_seg"/>
      <output feature="UTR5" strand="+"/>
```

```
   </source>

   <source id="trans_stop" mindis="0" len_fun="intergene_pen">
      <useseg id="est_span"/>
      <output feature="intergenic"/>
   </source>

   <source id="stop" mindis="0" len_fun="intergene_pen">
      <useseg id="est_span"/>
      <output feature="intergenic"/>
   </source>

   <source id="trans_start_rev" mindis="0" len_fun="intergene_pen">
      <useseg id="est_span"/>
      <output feature="intergenic"/>
   </source>

   <source id="t_splice_rev" mindis="0" len_fun="intergene_pen">
      <useseg id="est_span"/>
      <output feature="intergenic"/>
   </source>

   <source id="start_rev" mindis="0" len_fun="intergene_pen">
      <useseg id="est_span"/>
      <output feature="intergenic"/>
   </source>
</target>

<target id="start_rev">
   <useseg id="coding_seg_rev" target_phase="0"/>
   <useseg id="est_seg_rev"/>
   <killfeat id="stop_rev" target_phase="0"/>

   <source id="BEGIN">
      <output feature="CDS_end_not_found" strand="-" frame="0"/>
   </source>

   <source id="stop_rev" mindis="6" len_fun="sngl_ex_pen" phase="0">
      <output feature="CDS" strand="-" frame="0"/>
   </source>

   <source id="5ss_0_rev" mindis="3" len_fun="init_ex_pen" phase="0">
      <output feature="CDS" strand="-" frame="0"/>
   </source>

   <source id="5ss_1_rev" mindis="3" len_fun="init_ex_pen" phase="1">
      <output feature="CDS" strand="-" frame="0"/>
   </source>

   <source id="5ss_2_rev" mindis="3" len_fun="init_ex_pen" phase="2">
      <output feature="CDS" strand="-" frame="0"/>
   </source>
</target>

<target id="stop">
   <useseg id="coding_seg" target_phase="0"/>
   <useseg id="est_seg"/>
   <killfeat id="stop" target_phase="0"/>

   <source id="BEGIN">
      <output feature="CDS_start_not_found" strand="+"/>
   </source>

   <source id="start" mindis="6" len_fun="sngl_ex_pen" phase="0">
      <output feature="CDS" strand="+" frame="0"/>
```

```
   </source>

   <source id="3ss_0" mindis="3" len_fun="term_ex_pen" phase="0">
      <output feature="CDS" strand="+" frame="0"/>
   </source>

   <source id="3ss_1" mindis="3" len_fun="term_ex_pen" phase="2">
      <output feature="CDS" strand="+" frame="1"/>
   </source>

   <source id="3ss_2" mindis="3" len_fun="term_ex_pen" phase="1">
      <output feature="CDS" strand="+" frame="2"/>
   </source>
</target>

<target id="stop_rev">
   <source id="BEGIN">
      <useseg id="est_span"/>
      <output feature="intergenic"/>
   </source>

   <source id="trans_stop_rev" mindis="0">
      <useseg id="est_seg_rev"/>
      <output feature="UTR3" strand="-"/>
   </source>

   <source id="trans_start_rev" mindis="0" len_fun="intergene_pen">
      <useseg id="est_span"/>
      <output feature="intergenic"/>
   </source>

   <source id="t_splice_rev" mindis="0" len_fun="intergene_pen">
      <useseg id="est_span"/>
      <output feature="intergenic"/>
   </source>

   <source id="start_rev" mindis="0" len_fun="intergene_pen">
      <useseg id="est_span"/>
      <output feature="intergenic"/>
   </source>

   <source id="trans_stop" mindis="0" len_fun="intergene_pen">
      <useseg id="est_span"/>
      <output feature="intergenic"/>
   </source>

   <source id="stop" mindis="0" len_fun="intergene_pen">
      <useseg id="est_span"/>
      <output feature="intergenic"/>
   </source>
</target>

<target id="5ss_0">
   <useseg id="coding_seg" target_phase="0"/>
   <useseg id="est_seg"/>
   <killfeat id="stop" target_phase="0"/>

   <source id="BEGIN">
      <output feature="CDS_start_not_found" strand="+"/>
   </source>

   <source id="start" mindis="3" len_fun="init_ex_pen" phase="0">
      <output feature="CDS" strand="+" frame="0"/>
   </source>
```

```
   <source id="3ss_0" mindis="20" len_fun="int_ex_pen" phase="0">
      <output feature="CDS" strand="+" frame="0"/>
   </source>

   <source id="3ss_1" mindis="20" len_fun="int_ex_pen" phase="2">
      <output feature="CDS" strand="+" frame="1"/>
   </source>

   <source id="3ss_2" mindis="20" len_fun="int_ex_pen" phase="1">
      <output feature="CDS" strand="+" frame="2"/>
   </source>
</target>


<target id="5ss_0_rev">
   <source id ="BEGIN" len_fun="intron_pen">
      <useseg id="est_intron_rev" exact="target"/>
      <output feature="intron_end_not_found" strand="-"/>
   </source>

   <source id="3ss_0_rev" mindis="39" len_fun="intron_pen">
      <useseg id="est_intron_rev" exact="both"/>
      <output feature="intron" strand="-"/>
   </source>
</target>

<target id="5ss_1">
   <useseg id="coding_seg" target_phase="1"/>
   <useseg id="est_seg"/>
   <killfeat id="stop" target_phase="1"/>

   <source id="BEGIN">
      <output feature="CDS_start_not_found" strand="+"/>
   </source>

   <source id="start" mindis="3"  len_fun="init_ex_pen" phase="1">
      <output feature="CDS" strand="+" frame="0"/>
   </source>

   <source id="3ss_0" mindis="20" len_fun="int_ex_pen" phase="1">
      <output feature="CDS" strand="+" frame="0"/>
   </source>

   <source id="3ss_1" mindis="20" len_fun="int_ex_pen" phase="0">
      <output feature="CDS" strand="+" frame="1"/>
   </source>

   <source id="3ss_2" mindis="20" len_fun="int_ex_pen" phase="2">
      <output feature="CDS" strand="+" frame="2"/>
   </source>
</target>

<target id="5ss_1_rev">
   <source id ="BEGIN" len_fun="intron_pen">
      <useseg id="est_intron_rev" exact="target"/>
      <output feature="intron_end_not_found" strand="-"/>
   </source>

   <source id="3ss_1_rev" mindis="39" len_fun="intron_pen">
      <useseg id="est_intron_rev" exact="both"/>
      <killdna source_dna="ct" target_dna="a"/>
      <killdna source_dna="tc" target_dna="a"/>
      <killdna source_dna="tt" target_dna="a"/>
      <output feature="intron" strand="-"/>
   </source>
```

```
</target>

<target id="5ss_2">
   <useseg id="coding_seg" target_phase="2"/>
   <useseg id="est_seg"/>
   <killfeat id="stop" target_phase="2"/>

   <source id ="BEGIN">
      <output feature="CDS_start_not_found" strand="+"/>
   </source>

   <source id="start" mindis="3"  len_fun="init_ex_pen" phase="2">
      <output feature="CDS" strand="+" frame="0"/>
   </source>

   <source id="3ss_0" mindis="20" len_fun="int_ex_pen" phase="2">
      <output feature="CDS" strand="+" frame="0"/>
   </source>

   <source id="3ss_1" mindis="20" len_fun="int_ex_pen" phase="1">
      <output feature="CDS" strand="+" frame="1"/>
   </source>

   <source id="3ss_2" mindis="20" len_fun="int_ex_pen" phase="0">
      <output feature="CDS" strand="+" frame="2"/>
   </source>
</target>

<target id="5ss_2_rev">
   <source id ="BEGIN" len_fun="intron_pen">
      <useseg id="est_intron_rev" exact="target"/>
      <output feature="intron_end_not_found" strand="-"/>
   </source>
   <source id="3ss_2_rev" mindis="39" len_fun="intron_pen">
      <useseg id="est_intron_rev" exact="both"/>
      <killdna source_dna="c" target_dna="ta"/>
      <killdna source_dna="t" target_dna="ca"/>
      <killdna source_dna="t" target_dna="ta"/>
      <output feature="intron" strand="-"/>
   </source>
</target>

<target id="3ss_0">
   <source id="BEGIN" len_fun="intron_pen">
      <useseg id="est_intron" exact="target"/>
      <output feature="intron_start_not_found" strand="+"/>
   </source>
   <source id="5ss_0" mindis="39" len_fun="intron_pen">
      <useseg id="est_intron" exact="both"/>
      <output feature="intron" strand="+"/>
   </source>
</target>

<target id="3ss_0_rev">
   <useseg id="coding_seg_rev" target_phase="0"/>
   <useseg id="est_seg_rev"/>
   <killfeat id="stop_rev" target_phase="0"/>

   <source id="BEGIN">
      <output feature="CDS_end_not_found" strand="-" frame="0"/>
   </source>

   <source id="stop_rev" mindis="3" len_fun="term_ex_pen" phase="0">
      <output feature="CDS" strand="-" frame="0"/>
   </source>
```

```
   <source id="5ss_0_rev" mindis="20" len_fun="int_ex_pen" phase="0">
      <output feature="CDS" strand="-" frame="0"/>
   </source>

   <source id="5ss_1_rev" mindis="20" len_fun="int_ex_pen" phase="1">
      <output feature="CDS" strand="-" frame="0"/>
   </source>

   <source id="5ss_2_rev" mindis="20" len_fun="int_ex_pen" phase="2">
      <output feature="CDS" strand="-" frame="0"/>
   </source>
</target>

<target id="3ss_1">
   <source id="BEGIN" len_fun="intron_pen">
      <useseg id="est_intron" exact="target"/>
      <output feature="intron_start_not_found" strand="+"/>
   </source>
   <source id="5ss_1" mindis="39" len_fun="intron_pen">
      <useseg id="est_intron" exact="both"/>
      <killdna source_dna="t" target_dna="aa"/>
      <killdna source_dna="t" target_dna="ag"/>
      <killdna source_dna="t" target_dna="ga"/>
      <output feature="intron" strand="+"/>
   </source>
</target>

<target id="3ss_1_rev">
   <useseg id="coding_seg_rev" target_phase="2"/>
   <useseg id="est_seg_rev"/>
   <killfeat id="stop_rev" target_phase="2"/>

   <source id="BEGIN">
      <output feature="CDS_end_not_found" strand="-" frame="1"/>
   </source>

   <source id="stop_rev" mindis="3"  len_fun="term_ex_pen" phase="2">
      <output feature="CDS" strand="-" frame="1"/>
   </source>

   <source id="5ss_0_rev" mindis="20" len_fun="int_ex_pen" phase="2">
      <output feature="CDS" strand="-" frame="1"/>
   </source>

   <source id="5ss_1_rev" mindis="20" len_fun="int_ex_pen" phase="0">
      <output feature="CDS" strand="-" frame="1"/>
   </source>

   <source id="5ss_2_rev" mindis="20" len_fun="int_ex_pen" phase="1">
      <output feature="CDS" strand="-" frame="1"/>
   </source>
</target>

<target id="3ss_2">
   <source id="BEGIN" len_fun="intron_pen">
      <useseg id="est_intron" exact="target"/>
      <output feature="intron_start_not_found" strand="+"/>
   </source>
   <source id="5ss_2" mindis="39" len_fun="intron_pen">
      <useseg id="est_intron" exact="both"/>
      <killdna source_dna="ta" target_dna="a"/>
      <killdna source_dna="ta" target_dna="g"/>
      <killdna source_dna="tg" target_dna="a"/>
      <output feature="intron" strand="+"/>
```

```
   </source>
</target>

<target id="3ss_2_rev">
   <useseg id="coding_seg_rev" target_phase="1"/>
   <useseg id="est_seg_rev"/>
   <killfeat id="stop_rev" target_phase="1"/>

   <source id ="BEGIN">
      <output feature="CDS_end_not_found" strand="-" frame="2"/>
   </source>

   <source id="stop_rev" mindis="3" len_fun="term_ex_pen" phase="1">
      <output feature="CDS" strand="-" frame="2"/>
   </source>

   <source id="5ss_0_rev" mindis="20" len_fun="int_ex_pen" phase="1">
      <output feature="CDS" strand="-" frame="2"/>
   </source>

   <source id="5ss_1_rev" mindis="20" len_fun="int_ex_pen" phase="2">
      <output feature="CDS" strand="-" frame="2"/>
   </source>

   <source id="5ss_2_rev" mindis="20" len_fun="int_ex_pen" phase="0">
      <output feature="CDS" strand="-" frame="2"/>
   </source>
</target>

<target id="trans_start">
   <useseg id="est_span"/>

   <source id="BEGIN">
      <output feature="intergenic"/>
   </source>

   <source id="trans_stop" mindis="0" len_fun="intergene_pen">
      <output feature="intergenic"/>
   </source>

   <source id="stop" mindis="0" len_fun="intergene_pen">
      <output feature="intergenic"/>
   </source>

   <source id="trans_start_rev" mindis="0" len_fun="intergene_pen">
      <output feature="intergenic"/>
   </source>

   <source id="t_splice_rev" mindis="0" len_fun="intergene_pen">
      <output feature="intergenic"/>
   </source>

   <source id="start_rev" mindis="0" len_fun="intergene_pen">
      <output feature="intergenic"/>
   </source>
</target>

<target id="trans_stop">
   <useseg id="est_seg"/>

   <source id="BEGIN">
      <output feature="UTR3_start_not_found" strand="+"/>
   </source>

   <source id="stop" mindis="0" >
```

```
      <output feature="UTR3" strand="+"/>
   </source>
</target>

<target id="trans_start_rev">
   <useseg id="est_seg_rev"/>

   <source id="BEGIN">
      <output feature="UTR5_end_not_found" strand="-"/>
   </source>

   <source id="t_splice_rev" mindis="0">
      <output feature="TSL_UTR5" strand="-"/>
   </source>

   <source id="start_rev" mindis="0">
      <output feature="UTR5" strand="-"/>
   </source>
</target>

<target id="trans_stop_rev">
   <useseg id="est_span"/>

   <source id="BEGIN">
      <output feature="intergenic"/>
   </source>

   <source id="start_rev" mindis="0" len_fun="intergene_pen">
      <output feature="intergenic"/>
   </source>

   <source id="t_splice_rev" mindis="0" len_fun="intergene_pen">
      <output feature="intergenic"/>
   </source>

   <source id="trans_start_rev" mindis="0" len_fun="intergene_pen">
      <output feature="intergenic"/>
   </source>

   <source id="stop" mindis="0" len_fun="intergene_pen">
      <output feature="intergenic"/>
   </source>

   <source id="trans_stop" mindis="0" len_fun="intergene_pen">
      <output feature="intergenic"/>
   </source>
</target>

<target id="t_splice">
   <source id="BEGIN">
      <useseg id="est_span"/>
      <output feature="intergenic"/>
   </source>

   <source id="trans_start" mindis="0">
      <useseg id="est_seg"/>
      <output feature="TSL_UTR5" strand="+"/>
   </source>

   <source id="trans_stop" mindis="0" len_fun="intergene_pen">
      <useseg id="est_span"/>
      <output feature="intergenic"/>
   </source>

   <source id="stop" mindis="0" len_fun="intergene_pen">
```

```
         <useseg id="est_span"/>
         <output feature="intergenic"/>
      </source>

      <source id="trans_start_rev" mindis="0" len_fun="intergene_pen">
         <useseg id="est_span"/>
         <output feature="intergenic"/>
      </source>

      <source id="t_splice_rev" mindis="0" len_fun="intergene_pen">
         <useseg id="est_span"/>
         <output feature="intergenic"/>
      </source>

      <source id="start_rev" mindis="0" len_fun="intergene_pen">
         <useseg id="est_span"/>
         <output feature="intergenic"/>
      </source>
   </target>

   <target id="t_splice_rev">
      <useseg id="est_seg_rev"/>

      <source id="BEGIN"  mindis="0" maxdis="50" len_fun="tsplice_pen">
         <output feature="trans_splice_UTR5_end_not_found" strand="-"/>
      </source>

      <source id="start_rev" mindis="0" maxdis="50" len_fun="tsplice_pen">
         <output feature="trans_splice_UTR5" strand="-"/>
      </source>
   </target>
</model>

<lengthfunctions>
   <lengthfunc id="intron_pen" file="/tables/intron_penalty.klh"/>
   <lengthfunc id="init_ex_pen" file="/tables/exon_penalty.initial.klh"/>
   <lengthfunc id="term_ex_pen" file="/tables/exon_penalty.terminal.klh"/>
   <lengthfunc id="int_ex_pen" file="/tables/exon_penalty.internal.klh"/>
   <lengthfunc id="tsplice_pen" file="/tables/trans_splice_penalty.klh"/>

   <lengthfunc id="sngl_ex_pen">
      <point x="0" y="4"/>
      <point x="1" y="4"/>
   </lengthfunc>

   <lengthfunc id="intergene_pen">
     <point x="0" y="4"/>
     <point x="1" y="4"/>
   </lengthfunc>
</lengthfunctions>

</gaze>
```

A.3 GAZE_GeneID

```
<?xml version="1.0" encoding="US-ASCII"?>
<gaze>

<declarations>
   <feature id="5ss_0" st_off="1" en_off="1" mul="0.6"/>
   <feature id="5ss_1" st_off="1" en_off="1" mul="0.6"/>
   <feature id="5ss_2" st_off="1" en_off="1" mul="0.6"/>
   <feature id="stop" st_off="3" en_off="3" mul="0.6"/>
```

```
   <feature id="3ss_0" st_off="1" en_off="1" mul="0.6"/>
   <feature id="3ss_1" st_off="1" en_off="1" mul="0.6"/>
   <feature id="3ss_2" st_off="1" en_off="1" mul="0.6"/>
   <feature id="start" st_off="0" en_off="3" mul="0.6"/>
   <feature id="start_rev" st_off="3" en_off="0" mul="0.6"/>
   <feature id="3ss_0_rev" st_off="1" en_off="1" mul="0.6"/>
   <feature id="3ss_1_rev" st_off="1" en_off="1" mul="0.6"/>
   <feature id="3ss_2_rev" st_off="1" en_off="1" mul="0.6"/>
   <feature id="stop_rev" st_off="3" en_off="3" mul="0.6"/>
   <feature id="5ss_0_rev" st_off="1" en_off="1" mul="0.6"/>
   <feature id="5ss_1_rev" st_off="1" en_off="1" mul="0.6"/>
   <feature id="5ss_2_rev" st_off="1" en_off="1" mul="0.6"/>

   <segment id="cod_ini_0" scoring="standard_sum" partial="FALSE" mul="0.4"/>
   <segment id="cod_ini_1" scoring="standard_sum" partial="FALSE" mul="0.4"/>
   <segment id="cod_ini_2" scoring="standard_sum" partial="FALSE" mul="0.4"/>
   <segment id="cod_ini_rev_0" scoring="standard_sum" partial="FALSE" mul="0.4"/>
   <segment id="cod_ini_rev_1" scoring="standard_sum" partial="FALSE" mul="0.4"/>
   <segment id="cod_ini_rev_2" scoring="standard_sum" partial="FALSE" mul="0.4"/>
   <segment id="cod_tr_0" scoring="standard_sum" partial="FALSE" mul="0.4"/>
   <segment id="cod_tr_1" scoring="standard_sum" partial="FALSE" mul="0.4"/>
   <segment id="cod_tr_2" scoring="standard_sum" partial="FALSE" mul="0.4"/>
   <segment id="cod_tr_rev_0" scoring="standard_sum" partial="FALSE" mul="0.4"/>
   <segment id="cod_tr_rev_1" scoring="standard_sum" partial="FALSE" mul="0.4"/>
   <segment id="cod_tr_rev_2" scoring="standard_sum" partial="FALSE" mul="0.4"/>

   <lengthfunction id="intron_pen" mul="0.0"/>
   <lengthfunction id="intergene_pen" mul="0.0"/>
   <lengthfunction id="init_ex_pen" mul="1.0"/>
   <lengthfunction id="term_ex_pen" mul="1.0"/>
   <lengthfunction id="int_ex_pen" mul="1.0"/>
   <lengthfunction id="sngl_ex_pen" mul="1.0"/>
</declarations>


<gff2gaze>
   <!-- Features -->

   <gffline feature="Start" source="geneid_v1.0" strand="+">
      <feat id="start"/>
   </gffline>

   <gffline feature="Start" source="geneid_v1.0" strand="-">
      <feat id="start_rev"/>
   </gffline>

   <gffline feature="Stop" source="geneid_v1.0" strand="+">
      <feat id="stop"/>
   </gffline>

   <gffline feature="Stop" source="geneid_v1.0" strand="-">
      <feat id="stop_rev"/>
   </gffline>

   <gffline feature="Donor" source="geneid_v1.0" strand="+">
      <feat id="5ss_0"/>
      <feat id="5ss_1"/>
      <feat id="5ss_2"/>
   </gffline>

   <gffline feature="Donor" source="geneid_v1.0" strand="-">
      <feat id="5ss_0_rev"/>
      <feat id="5ss_1_rev"/>
      <feat id="5ss_2_rev"/>
   </gffline>
```

```
   <gffline feature="Acceptor" source="geneid_v1.0" strand="+">
      <feat id="3ss_0"/>
      <feat id="3ss_1"/>
      <feat id="3ss_2"/>
   </gffline>

   <gffline feature="Acceptor" source="geneid_v1.0" strand="-">
      <feat id="3ss_0_rev"/>
      <feat id="3ss_1_rev"/>
      <feat id="3ss_2_rev"/>
   </gffline>

   <!-- Segments -->

   <gffline feature="cod_ini" source="GENEID" strand="+" frame="0">
      <seg id="cod_ini_0"/>
   </gffline>

   <gffline feature="cod_ini" source="GENEID" strand="+" frame="1">
      <seg id="cod_ini_1"/>
   </gffline>

   <gffline feature="cod_ini" source="GENEID" strand="+" frame="2">
      <seg id="cod_ini_2"/>
   </gffline>

   <gffline feature="cod_ini" source="GENEID" strand="-" frame="0">
      <seg id="cod_ini_rev_0"/>
   </gffline>

   <gffline feature="cod_ini" source="GENEID" strand="-" frame="1">
      <seg id="cod_ini_rev_1"/>
   </gffline>

   <gffline feature="cod_ini" source="GENEID" strand="-" frame="2">
      <seg id="cod_ini_rev_2"/>
   </gffline>

   <gffline feature="cod_tr" source="GENEID" strand="+" frame="0">
      <seg id="cod_tr_0"/>
   </gffline>

   <gffline feature="cod_tr" source="GENEID" strand="+" frame="1">
      <seg id="cod_tr_1"/>
   </gffline>

   <gffline feature="cod_tr" source="GENEID" strand="+" frame="2">
      <seg id="cod_tr_2"/>
   </gffline>

   <gffline feature="cod_tr" source="GENEID" strand="-" frame="0">
      <seg id="cod_tr_rev_0"/>
   </gffline>

   <gffline feature="cod_tr" source="GENEID" strand="-" frame="1">
      <seg id="cod_tr_rev_1"/>
   </gffline>

   <gffline feature="cod_tr" source="GENEID" strand="-" frame="2">
      <seg id="cod_tr_rev_2"/>
   </gffline>
</gff2gaze>

<dna2gaze>
```

```
   <dnafeat pattern="taa">
      <feat id="stop" score="-100"/>
   </dnafeat>
   <dnafeat pattern="tag">
      <feat id="stop" score="-100"/>
   </dnafeat>
   <dnafeat pattern="tga">
      <feat id="stop" score="-100"/>
   </dnafeat>

   <dnafeat pattern="tta">
      <feat id="stop_rev" score="-100"/>
   </dnafeat>
   <dnafeat pattern="cta">
      <feat id="stop_rev" score="-100"/>
   </dnafeat>
   <dnafeat pattern="tca">
      <feat id="stop_rev" score="-100"/>
   </dnafeat>

   <takedna id="5ss_1" st_off="0" en_off="1"/>
   <takedna id="3ss_1" st_off="1" en_off="-1"/>
   <takedna id="5ss_2" st_off="-1" en_off="1"/>
   <takedna id="3ss_2" st_off="1" en_off="0"/>
   <takedna id="5ss_1_rev" st_off="1" en_off="0"/>
   <takedna id="3ss_1_rev" st_off="-1" en_off="1"/>
   <takedna id="5ss_2_rev" st_off="1" en_off="-1"/>
   <takedna id="3ss_2_rev" st_off="0" en_off="1"/>
</dna2gaze>

<model>
   <target id="END">
      <source id="BEGIN">
         <output feature="no genes"/>
      </source>

      <source id="stop">
         <output feature="intergenic"/>
      </source>

      <source id="start_rev" mindis="0">
         <output feature="intergenic"/>
      </source>

      <source id="3ss_0_rev">
         <output feature="intron" strand="-"/>
      </source>

      <source id="3ss_1_rev">
         <output feature="intron" strand="-"/>
      </source>

      <source id="3ss_2_rev">
         <output feature="intron" strand="-"/>
      </source>

      <source id="5ss_0">
         <output feature="intron" strand="+"/>
      </source>

      <source id="5ss_1">
         <output feature="intron" strand="+"/>
      </source>

      <source id="5ss_2">
```

```
      <output feature="intron" strand="+"/>
   </source>
</target>

<target id="start">
   <source id="BEGIN">
      <output feature="intergenic"/>
   </source>

   <source id="stop" mindis="2000" len_fun="intergene_pen">
      <output feature="intergenic"/>
   </source>

   <source id="start_rev" mindis="2000" len_fun="intergene_pen">
      <output feature="intergenic"/>
   </source>
</target>

<target id="start_rev">
   <useseg id="cod_ini_rev_0" exact="target" />
   <useseg id="cod_tr_rev_0" target_phase="0" />
   <useseg id="cod_tr_rev_1" target_phase="1" />
   <useseg id="cod_tr_rev_2" target_phase="2" />

   <killfeat id="stop_rev" target_phase="0"/>

   <source id="stop_rev" mindis="60" len_fun="sngl_ex_pen" phase="0">
      <output feature="CDS_term" strand="-" frame="0"/>
   </source>

   <source id="5ss_0_rev" mindis="3" len_fun="init_ex_pen" phase="0">
      <output feature="CDS" strand="-" frame="0"/>
   </source>

   <source id="5ss_1_rev" mindis="3" len_fun="init_ex_pen" phase="1">
      <output feature="CDS" strand="-" frame="0"/>
   </source>

   <source id="5ss_2_rev" mindis="3" len_fun="init_ex_pen" phase="2">
      <output feature="CDS" strand="-" frame="0"/>
   </source>
</target>

<target id="stop">
   <useseg id="cod_tr_0" target_phase="0" />
   <useseg id="cod_tr_2" target_phase="1" />
   <useseg id="cod_tr_1" target_phase="2" />

   <killfeat id="stop" target_phase="0"/>

   <source id="start" mindis="60" len_fun="sngl_ex_pen" phase="0">
      <useseg id="cod_ini_0" exact="source" />
      <output feature="CDS_term" strand="+" frame="0"/>
   </source>

   <source id="3ss_0" mindis="0" len_fun="term_ex_pen" phase="0">
      <useseg id="cod_ini_0" exact="source" />
      <output feature="CDS_term" strand="+" frame="0"/>
   </source>

   <source id="3ss_1" mindis="0" len_fun="term_ex_pen" phase="2">
      <useseg id="cod_ini_1" exact="source" />
      <output feature="CDS_term" strand="+" frame="1"/>
   </source>
```

```
   <source id="3ss_2" mindis="0" len_fun="term_ex_pen" phase="1">
      <useseg id="cod_ini_2" exact="source" />
      <output feature="CDS_term" strand="+" frame="2"/>
   </source>
</target>

<target id="stop_rev">
   <source id="BEGIN">
      <output feature="intergenic"/>
   </source>

   <source id="start_rev" mindis="2000" len_fun="intergene_pen">
      <output feature="intergenic"/>
   </source>

   <source id="stop" mindis="2000" len_fun="intergene_pen">
      <output feature="intergenic"/>
   </source>
</target>

<target id="5ss_0">
   <useseg id="cod_tr_0" target_phase="0" />
   <useseg id="cod_tr_2" target_phase="1" />
   <useseg id="cod_tr_1" target_phase="2" />

   <killfeat id="stop" target_phase="0"/>

   <source id="start" mindis="3" len_fun="init_ex_pen" phase="0">
      <useseg id="cod_ini_0" exact="source" />
      <output feature="CDS" strand="+" frame="0"/>
   </source>

   <source id="3ss_0" mindis="18" len_fun="int_ex_pen" phase="0">
      <useseg id="cod_ini_0" exact="source" />
      <output feature="CDS" strand="+" frame="0"/>
   </source>

   <source id="3ss_1" mindis="18" len_fun="int_ex_pen" phase="2">
      <useseg id="cod_ini_1" exact="source" />
      <output feature="CDS" strand="+" frame="1"/>
   </source>

   <source id="3ss_2" mindis="18" len_fun="int_ex_pen" phase="1">
      <useseg id="cod_ini_2" exact="source" />
      <output feature="CDS" strand="+" frame="2"/>
   </source>
</target>

<target id="5ss_0_rev">
   <source id="BEGIN">
      <output feature="intron" strand="-"/>
   </source>

   <source id="3ss_0_rev" mindis="20" maxdis="25000" len_fun="intron_pen">
      <output feature="intron" strand="-"/>
   </source>
</target>

<target id="5ss_1">
   <useseg id="cod_tr_1" target_phase="0" />
   <useseg id="cod_tr_0" target_phase="1" />
   <useseg id="cod_tr_2" target_phase="2" />

   <killfeat id="stop" target_phase="1"/>
```

```
   <source id="start" mindis="3"  len_fun="init_ex_pen" phase="1">
      <useseg id="cod_ini_0" exact="source" />
      <output feature="CDS" strand="+" frame="0"/>
   </source>

   <source id="3ss_0" mindis="18" len_fun="int_ex_pen" phase="1">
      <useseg id="cod_ini_0" exact="source" />
      <output feature="CDS" strand="+" frame="0"/>
   </source>

   <source id="3ss_1" mindis="18" len_fun="int_ex_pen" phase="0">
      <useseg id="cod_ini_1" exact="source" />
      <output feature="CDS" strand="+" frame="1"/>
   </source>

   <source id="3ss_2" mindis="18" len_fun="int_ex_pen" phase="2">
      <useseg id="cod_ini_2" exact="source" />
      <output feature="CDS" strand="+" frame="2"/>
   </source>
</target>

<target id="5ss_1_rev">
   <source id="BEGIN">
      <output feature="intron" strand="-"/>
   </source>

   <source id="3ss_1_rev" mindis="20" maxdis="25000" len_fun="intron_pen">
      <killdna source_dna="ct" target_dna="a"/>
      <killdna source_dna="tc" target_dna="a"/>
      <killdna source_dna="tt" target_dna="a"/>
      <output feature="intron" strand="-"/>
   </source>
</target>

<target id="5ss_2">
   <useseg id="cod_tr_2" target_phase="0" />
   <useseg id="cod_tr_1" target_phase="1" />
   <useseg id="cod_tr_0" target_phase="2" />

   <killfeat id="stop" target_phase="2"/>

   <source id="start" mindis="3"  len_fun="init_ex_pen" phase="2">
      <useseg id="cod_ini_0" exact="source" />
      <output feature="CDS" strand="+" frame="0"/>
   </source>

   <source id="3ss_0" mindis="18" len_fun="int_ex_pen" phase="2">
      <useseg id="cod_ini_0" exact="source" />
      <output feature="CDS" strand="+" frame="0"/>
   </source>

   <source id="3ss_1" mindis="18" len_fun="int_ex_pen" phase="1">
      <useseg id="cod_ini_1" exact="source" />
      <output feature="CDS" strand="+" frame="1"/>
   </source>

   <source id="3ss_2" mindis="18" len_fun="int_ex_pen" phase="0">
      <useseg id="cod_ini_2" exact="source" />
      <output feature="CDS" strand="+" frame="2"/>
   </source>
</target>

<target id="5ss_2_rev">
   <source id="BEGIN">
      <output feature="intron" strand="-"/>
```

```
   </source>

   <source id="3ss_2_rev" mindis="20" maxdis="25000" len_fun="intron_pen">
      <killdna source_dna="c" target_dna="ta"/>
      <killdna source_dna="t" target_dna="ca"/>
      <killdna source_dna="t" target_dna="ta"/>
      <output feature="intron" strand="-"/>
   </source>
</target>

<target id="3ss_0">
   <source id="BEGIN">
      <output feature="intron" strand="+"/>
   </source>

   <source id="5ss_0" mindis="20" maxdis="25000" len_fun="intron_pen">
      <output feature="intron" strand="+"/>
   </source>
</target>

<target id="3ss_0_rev">
   <useseg id="cod_ini_rev_0" exact="target" />
   <useseg id="cod_tr_rev_0" target_phase="0" />
   <useseg id="cod_tr_rev_1" target_phase="1" />
   <useseg id="cod_tr_rev_2" target_phase="2" />

   <killfeat id="stop_rev" target_phase="0"/>

   <source id="stop_rev" mindis="0" len_fun="term_ex_pen" phase="0">
      <output feature="CDS_term" strand="-" frame="0"/>
   </source>

   <source id="5ss_0_rev" mindis="18" len_fun="int_ex_pen" phase="0">
      <output feature="CDS" strand="-" frame="0"/>
   </source>

   <source id="5ss_1_rev" mindis="18" len_fun="int_ex_pen" phase="1">
      <output feature="CDS" strand="-" frame="0"/>
   </source>

   <source id="5ss_2_rev" mindis="18" len_fun="int_ex_pen" phase="2">
      <output feature="CDS" strand="-" frame="0"/>
   </source>
</target>

<target id="3ss_1">
   <source id="BEGIN">
      <output feature="intron" strand="+"/>
   </source>

   <source id="5ss_1" mindis="20" maxdis="25000" len_fun="intron_pen">
      <killdna source_dna="t" target_dna="aa"/>
      <killdna source_dna="t" target_dna="ag"/>
      <killdna source_dna="t" target_dna="ga"/>
      <output feature="intron" strand="+"/>
   </source>
</target>

<target id="3ss_1_rev">
   <useseg id="cod_ini_rev_1" exact="target" />
   <useseg id="cod_tr_rev_1" target_phase="0" />
   <useseg id="cod_tr_rev_2" target_phase="1" />
   <useseg id="cod_tr_rev_0" target_phase="2" />

   <killfeat id="stop_rev" target_phase="2"/>
```

```
      <source id="stop_rev" mindis="0"  len_fun="term_ex_pen" phase="2">
         <output feature="CDS_term" strand="-" frame="1"/>
      </source>

      <source id="5ss_0_rev" mindis="18" len_fun="int_ex_pen" phase="2">
         <output feature="CDS" strand="-" frame="1"/>
      </source>

      <source id="5ss_1_rev" mindis="18" len_fun="int_ex_pen" phase="0">
         <output feature="CDS" strand="-" frame="1"/>
      </source>

      <source id="5ss_2_rev" mindis="18" len_fun="int_ex_pen" phase="1">
         <output feature="CDS" strand="-" frame="1"/>
      </source>
   </target>

   <target id="3ss_2">
      <source id="BEGIN">
         <output feature="intron" strand="+"/>
      </source>

      <source id="5ss_2" mindis="20" maxdis="25000" len_fun="intron_pen">
         <killdna source_dna="ta" target_dna="a"/>
         <killdna source_dna="ta" target_dna="g"/>
         <killdna source_dna="tg" target_dna="a"/>
         <output feature="intron" strand="+"/>
      </source>
   </target>

   <target id="3ss_2_rev">
      <useseg id="cod_ini_rev_2" exact="target" />
      <useseg id="cod_tr_rev_2" target_phase="0" />
      <useseg id="cod_tr_rev_0" target_phase="1" />
      <useseg id="cod_tr_rev_1" target_phase="2" />

      <killfeat id="stop_rev" target_phase="1"/>

      <source id="stop_rev" mindis="0" len_fun="term_ex_pen" phase="1">
         <output feature="CDS_term" strand="-" frame="2"/>
      </source>

      <source id="5ss_0_rev" mindis="18" len_fun="int_ex_pen" phase="1">
         <output feature="CDS" strand="-" frame="2"/>
      </source>

      <source id="5ss_1_rev" mindis="18" len_fun="int_ex_pen" phase="2">
         <output feature="CDS" strand="-" frame="2"/>
      </source>

      <source id="5ss_2_rev" mindis="18" len_fun="int_ex_pen" phase="0">
         <output feature="CDS" strand="-" frame="2"/>
      </source>
   </target>
</model>


<lengthfunctions>
   <lengthfunc id="intron_pen">
      <point x="0" y="1.0"/>
      <point x="1" y="1.0"/>
   </lengthfunc>

   <lengthfunc id="intergene_pen">
```

```
     <point x="0" y="1.0"/>
     <point x="1" y="1.0"/>
   </lengthfunc>

   <lengthfunc id="init_ex_pen">
      <point x="0" y="4.5"/>
      <point x="1" y="4.5"/>
   </lengthfunc>

   <lengthfunc id="int_ex_pen">
      <point x="0" y="4.5"/>
      <point x="1" y="4.5"/>
   </lengthfunc>

   <lengthfunc id="term_ex_pen">
      <point x="0" y="4.5"/>
      <point x="1" y="4.5"/>
   </lengthfunc>

   <lengthfunc id="sngl_ex_pen">
      <point x="0" y="4.5"/>
      <point x="1" y="4.5"/>
   </lengthfunc>
</lengthfunctions>

</gaze>
```