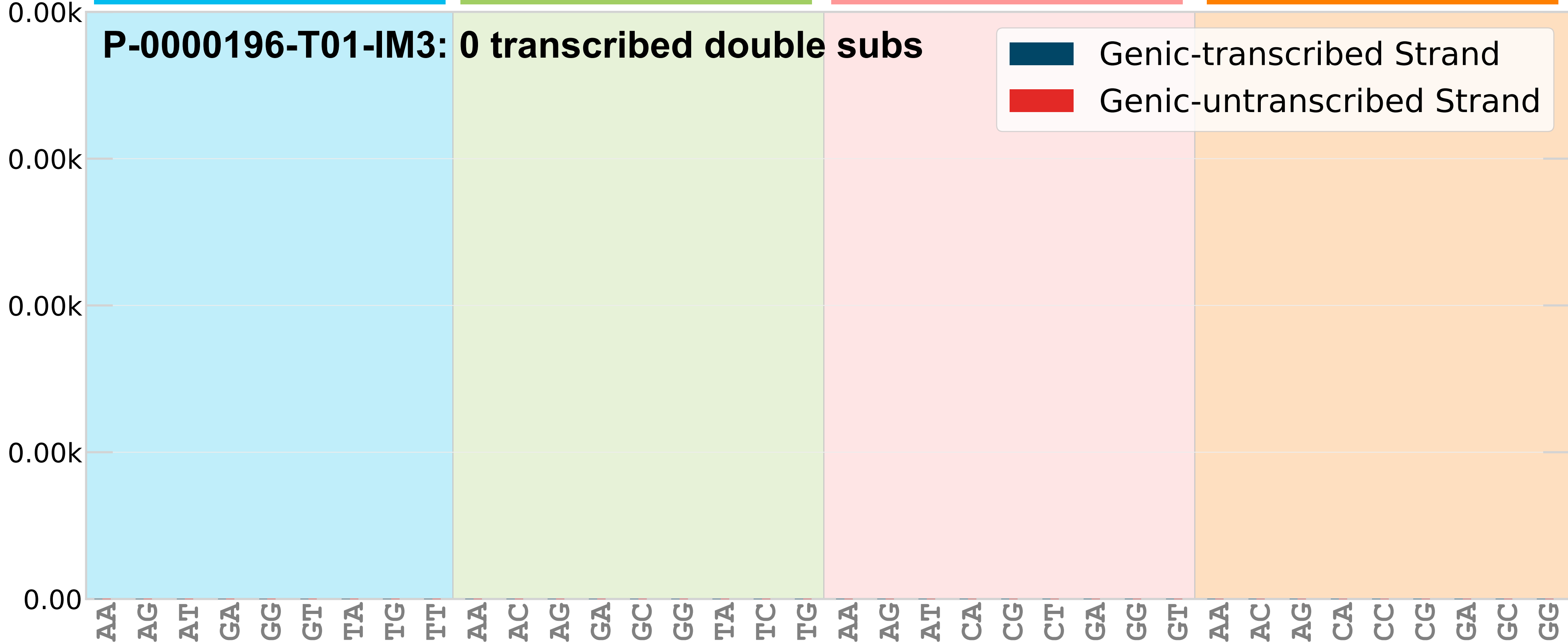
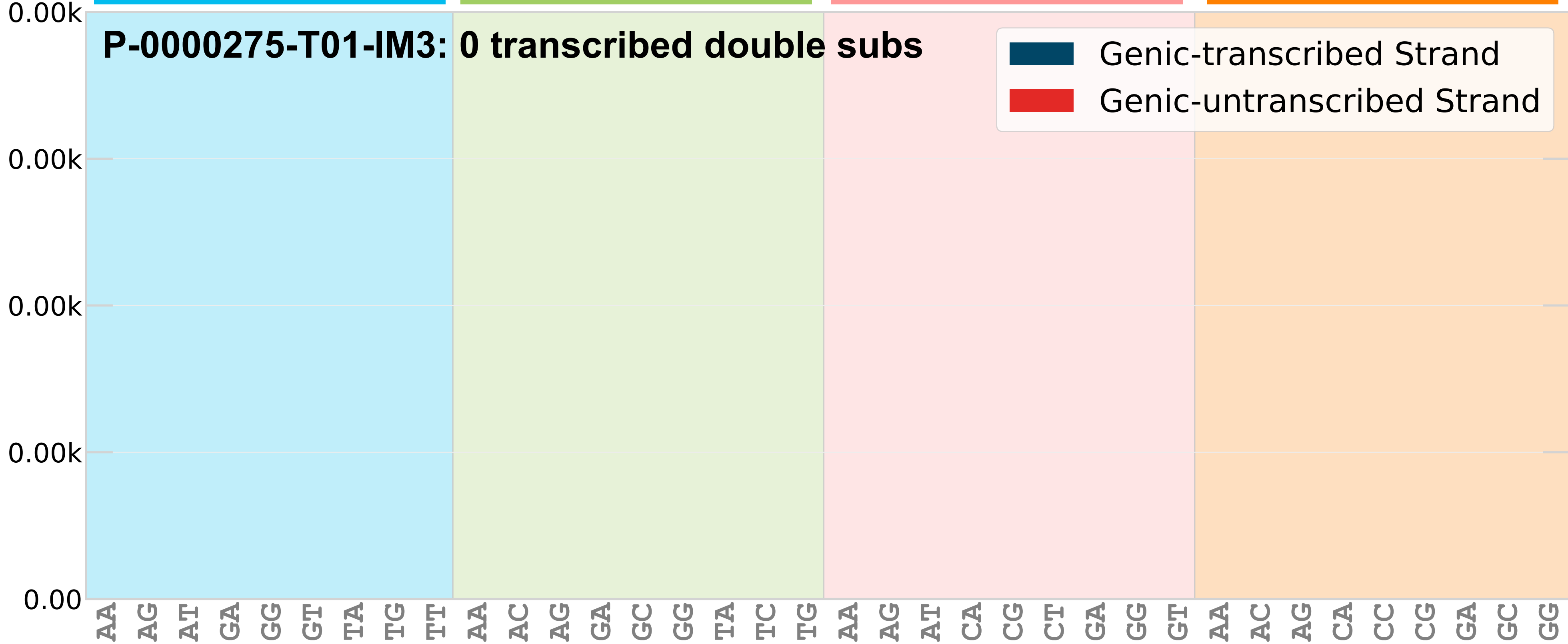
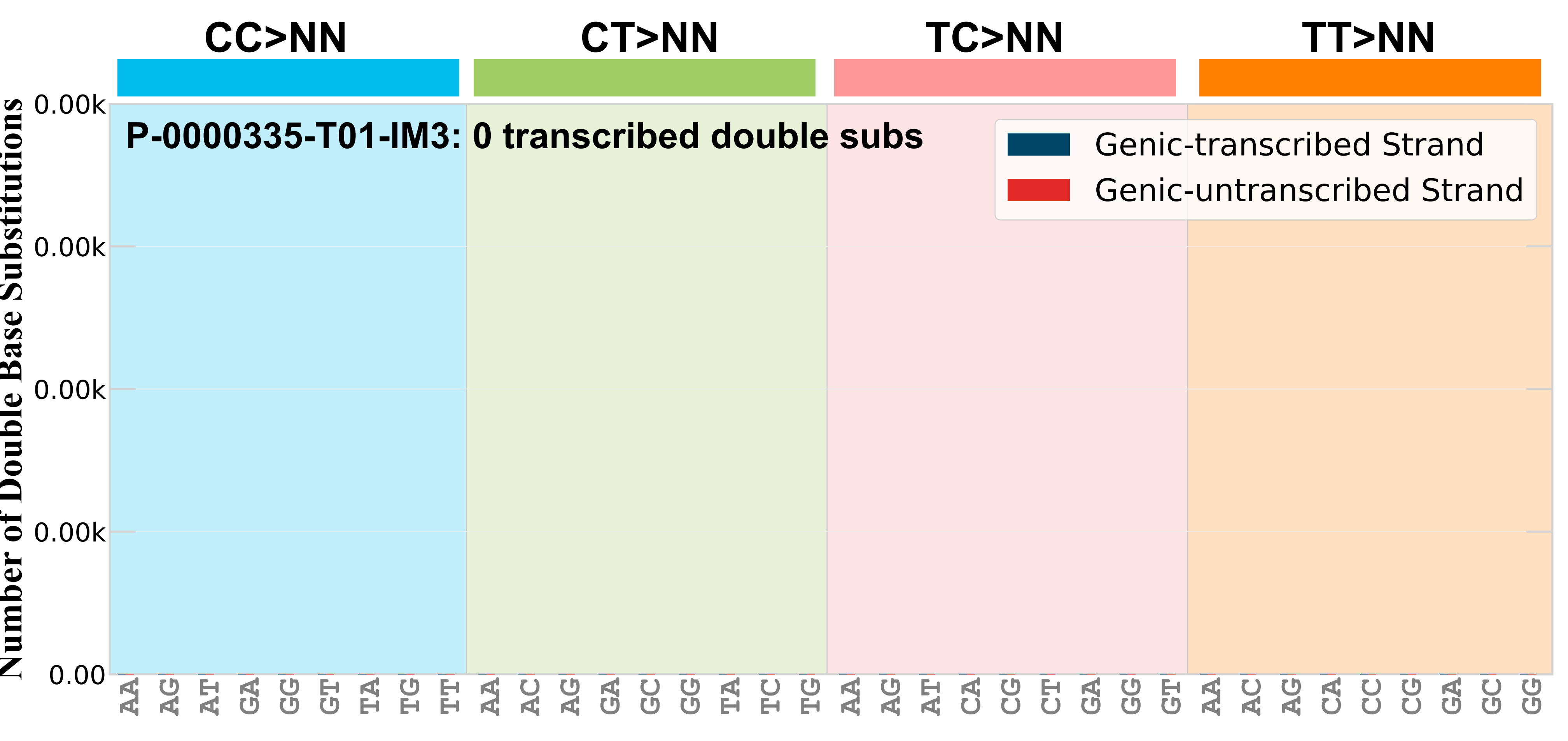


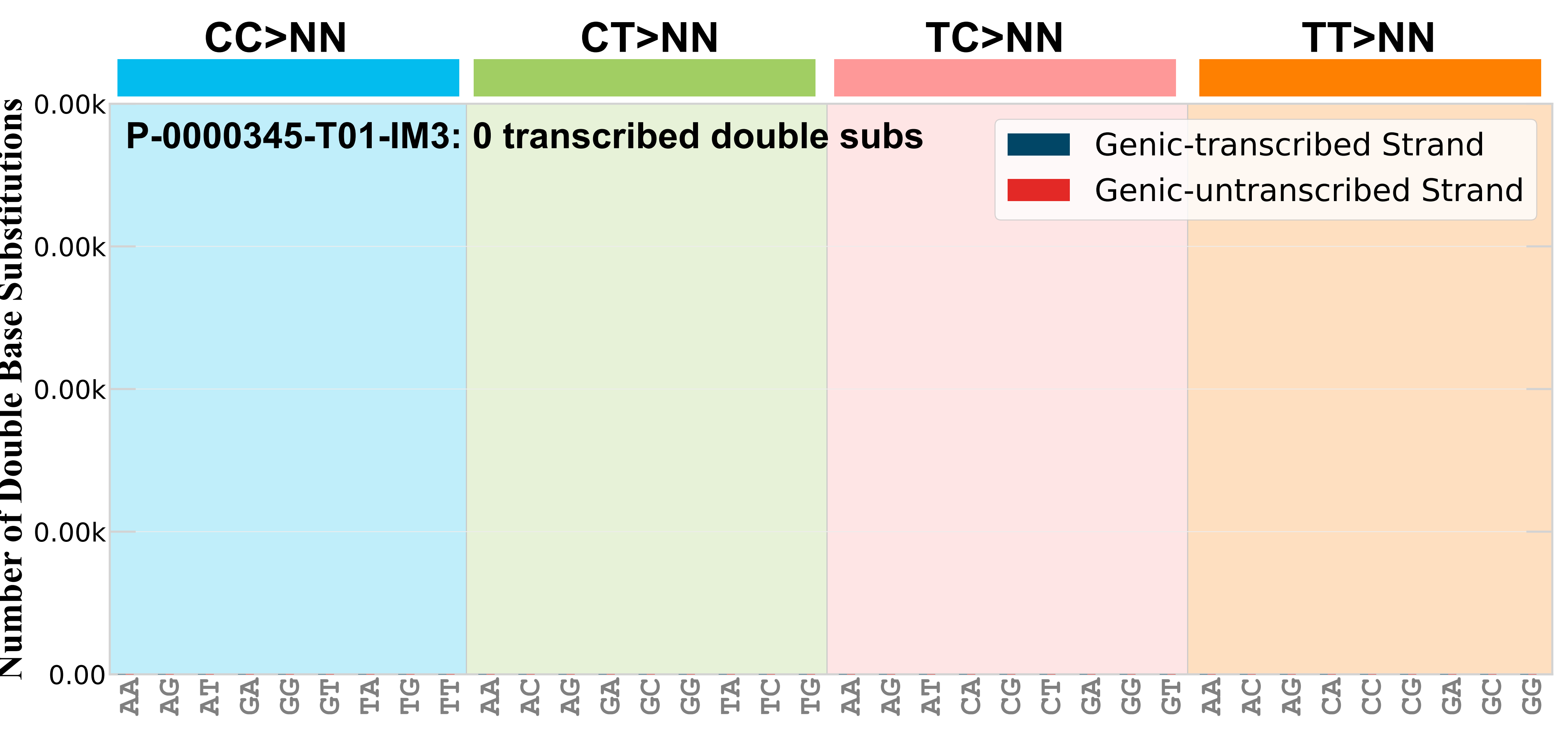
TT>NN

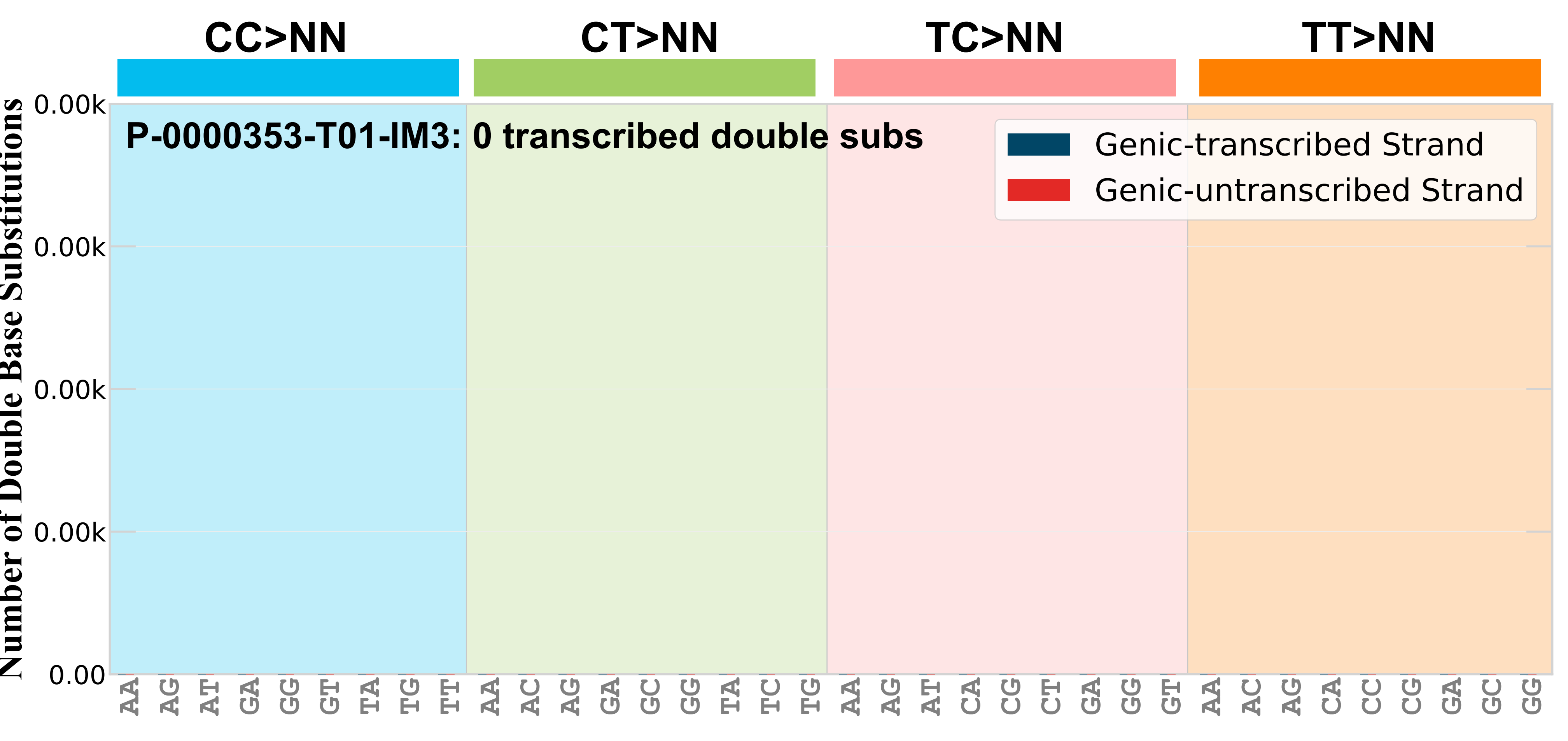


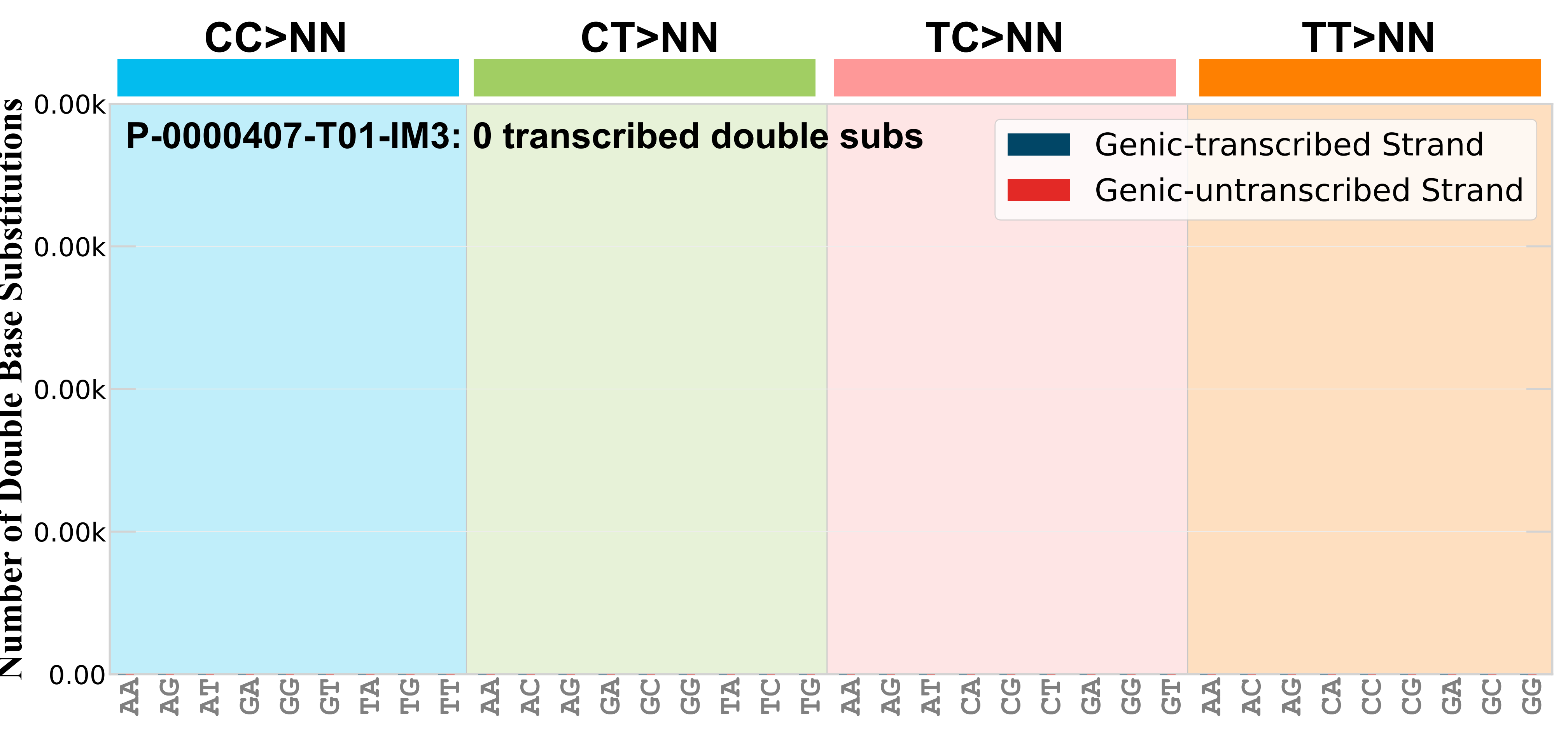
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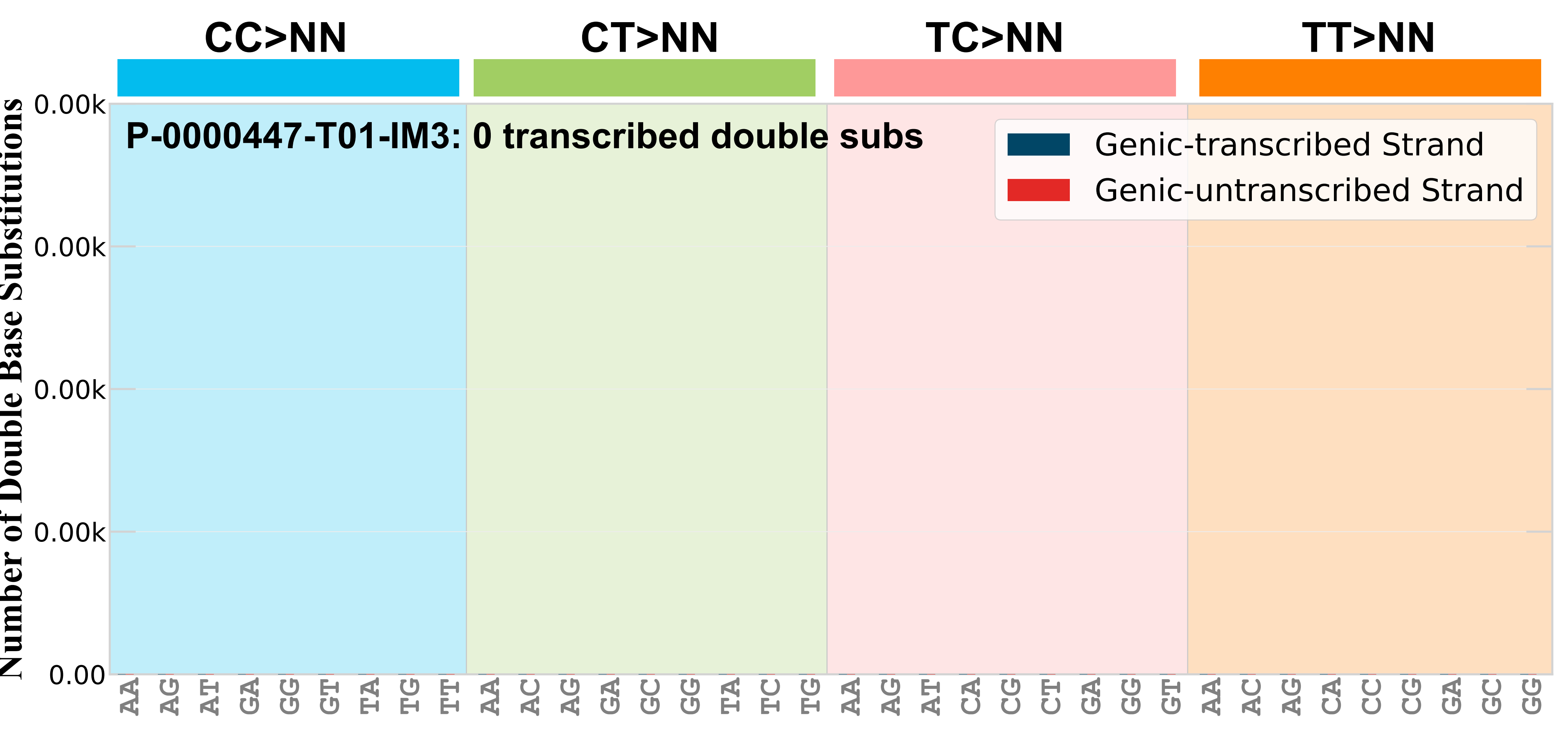


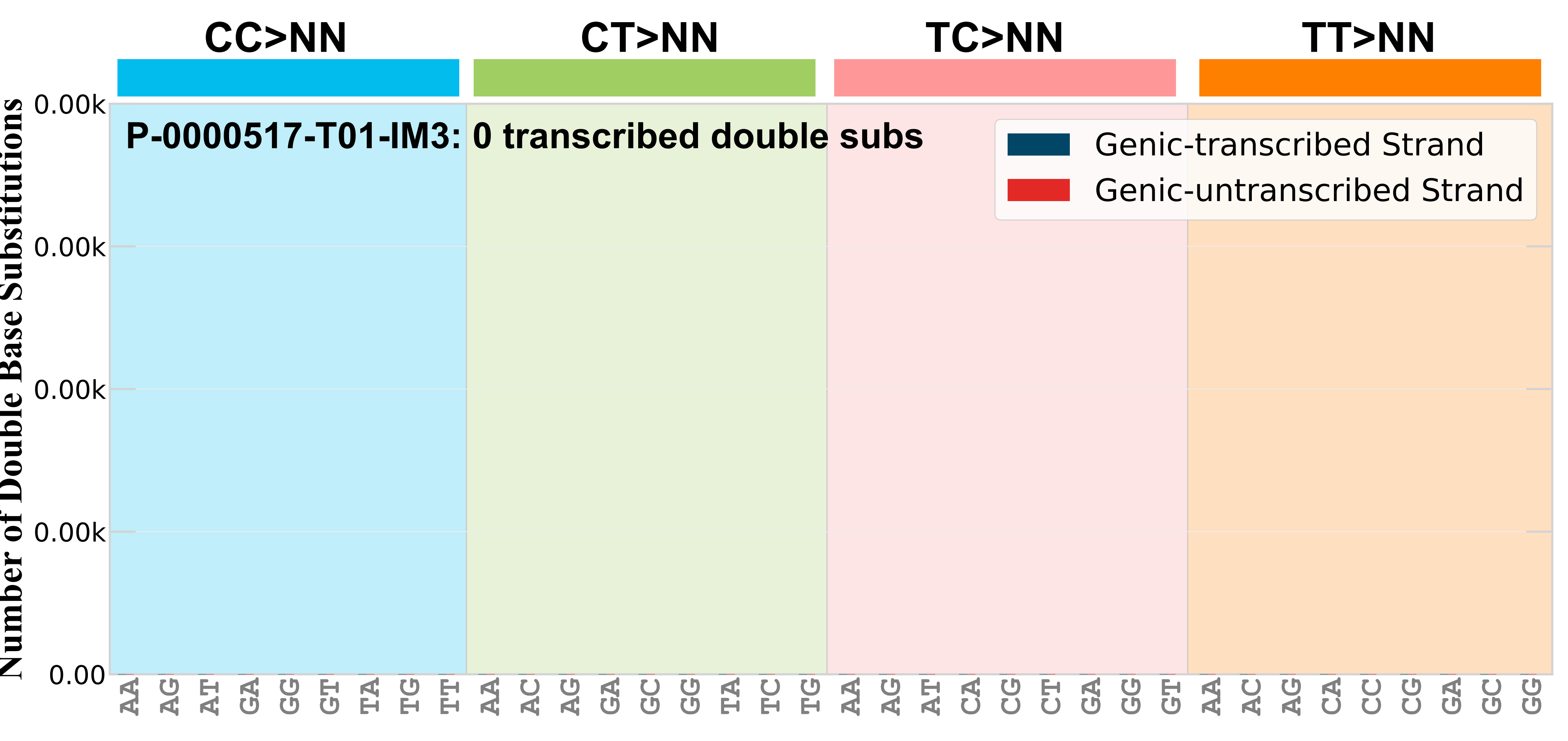




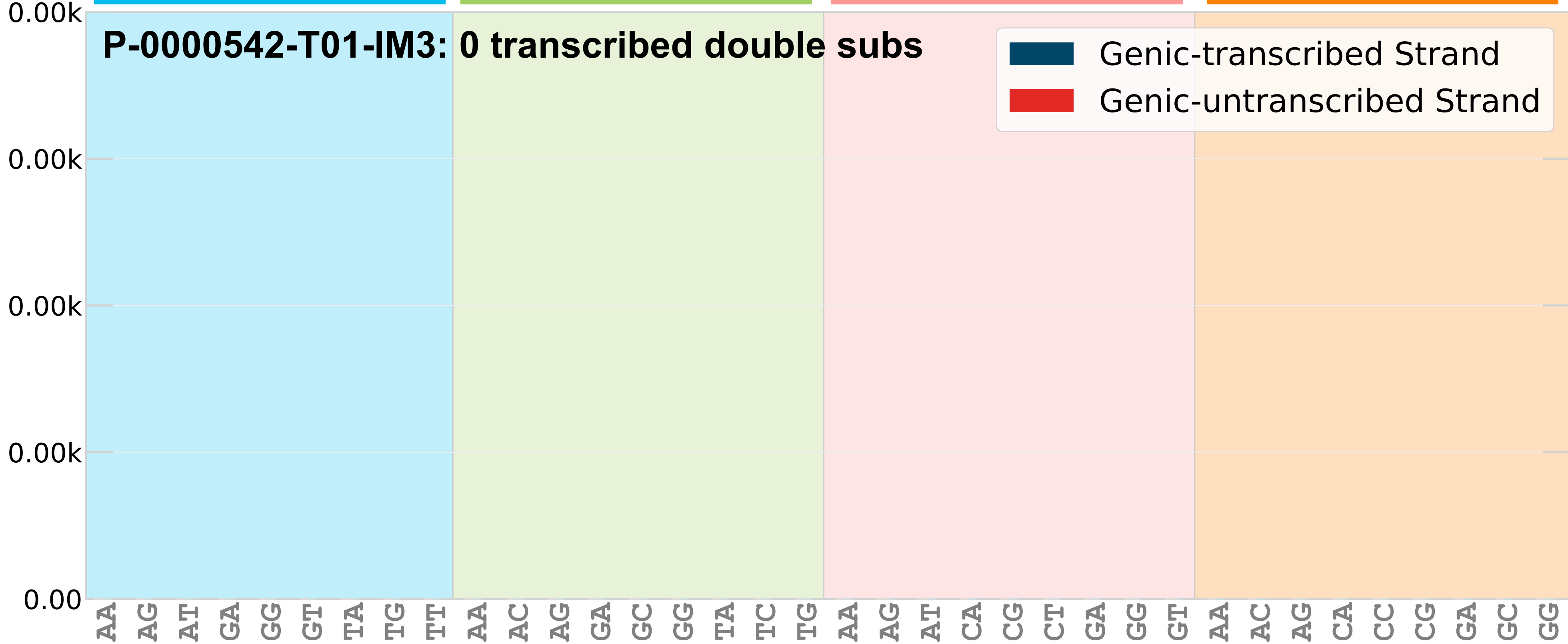




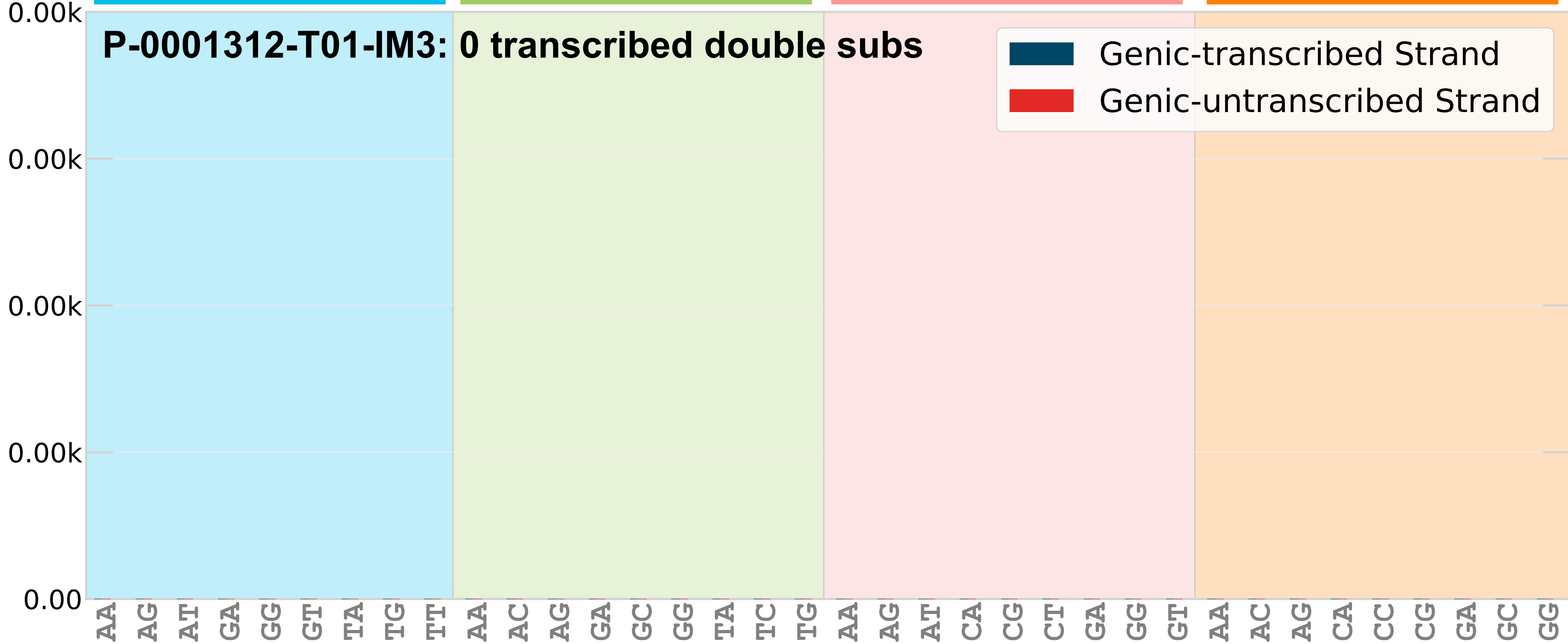




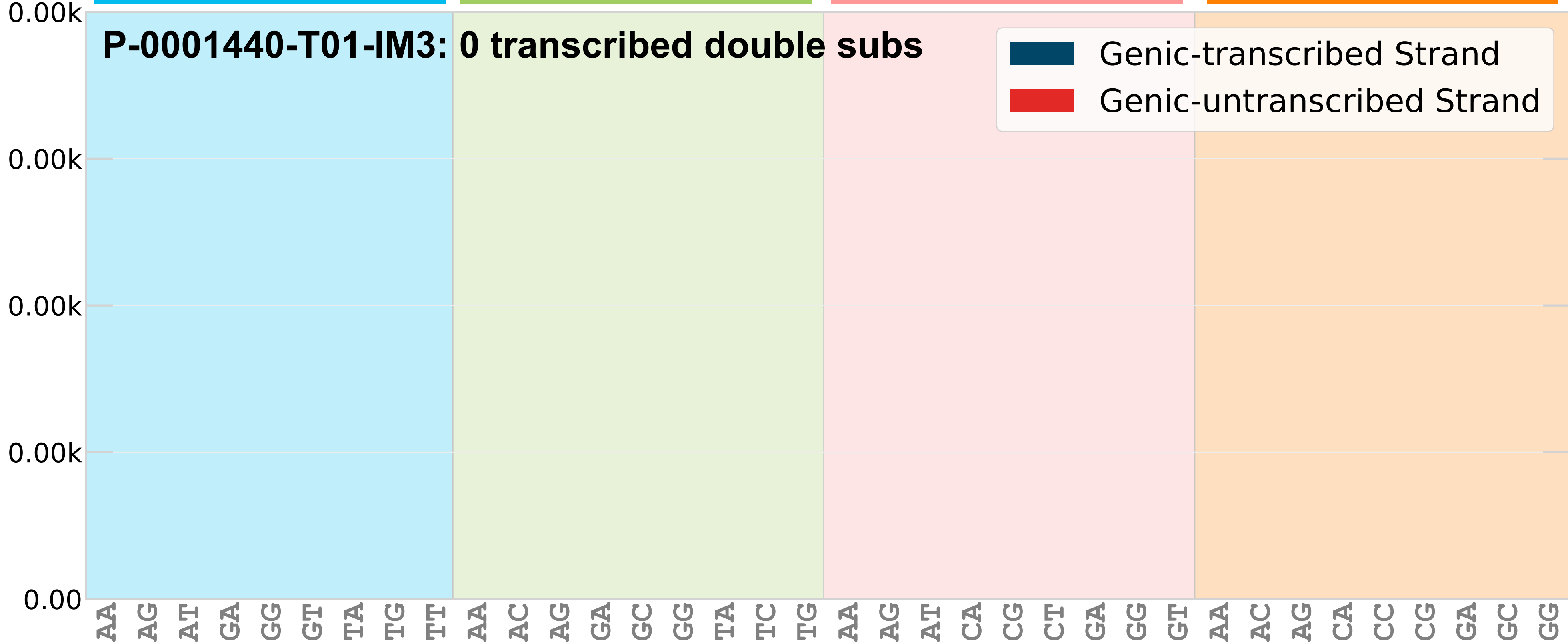
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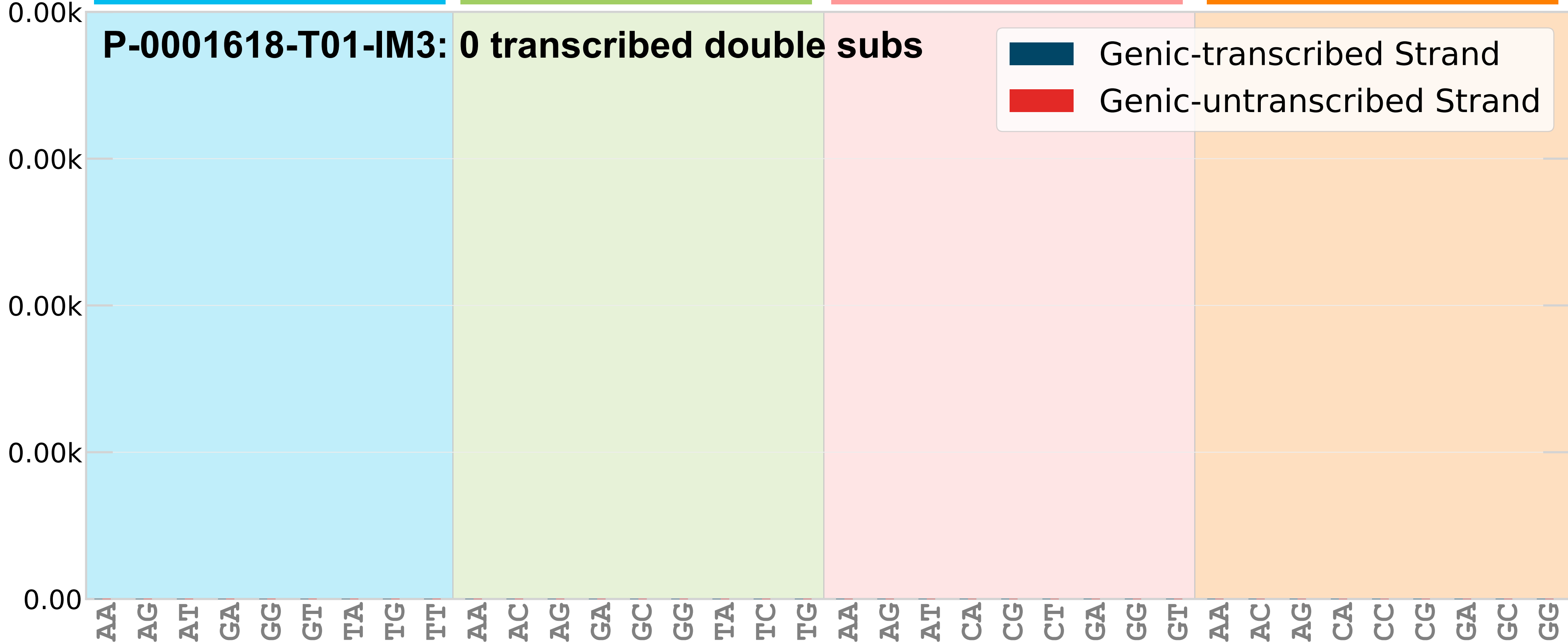
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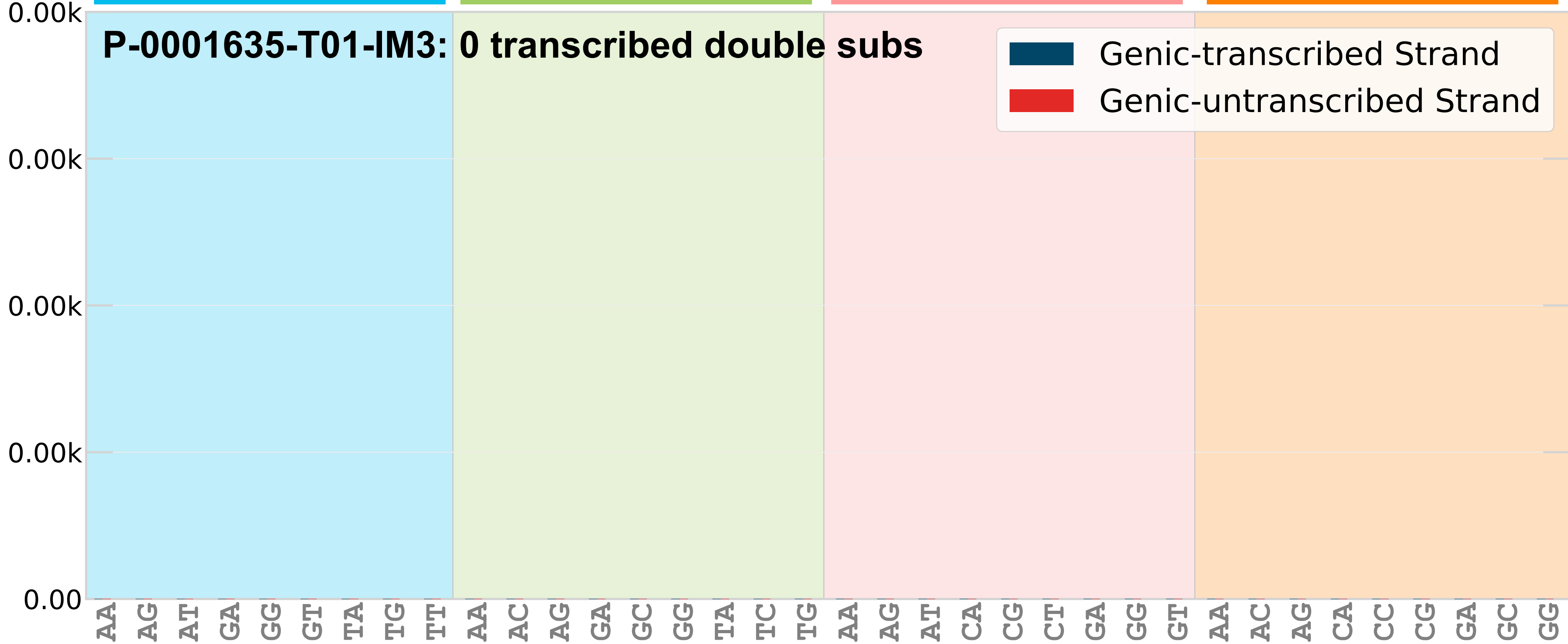
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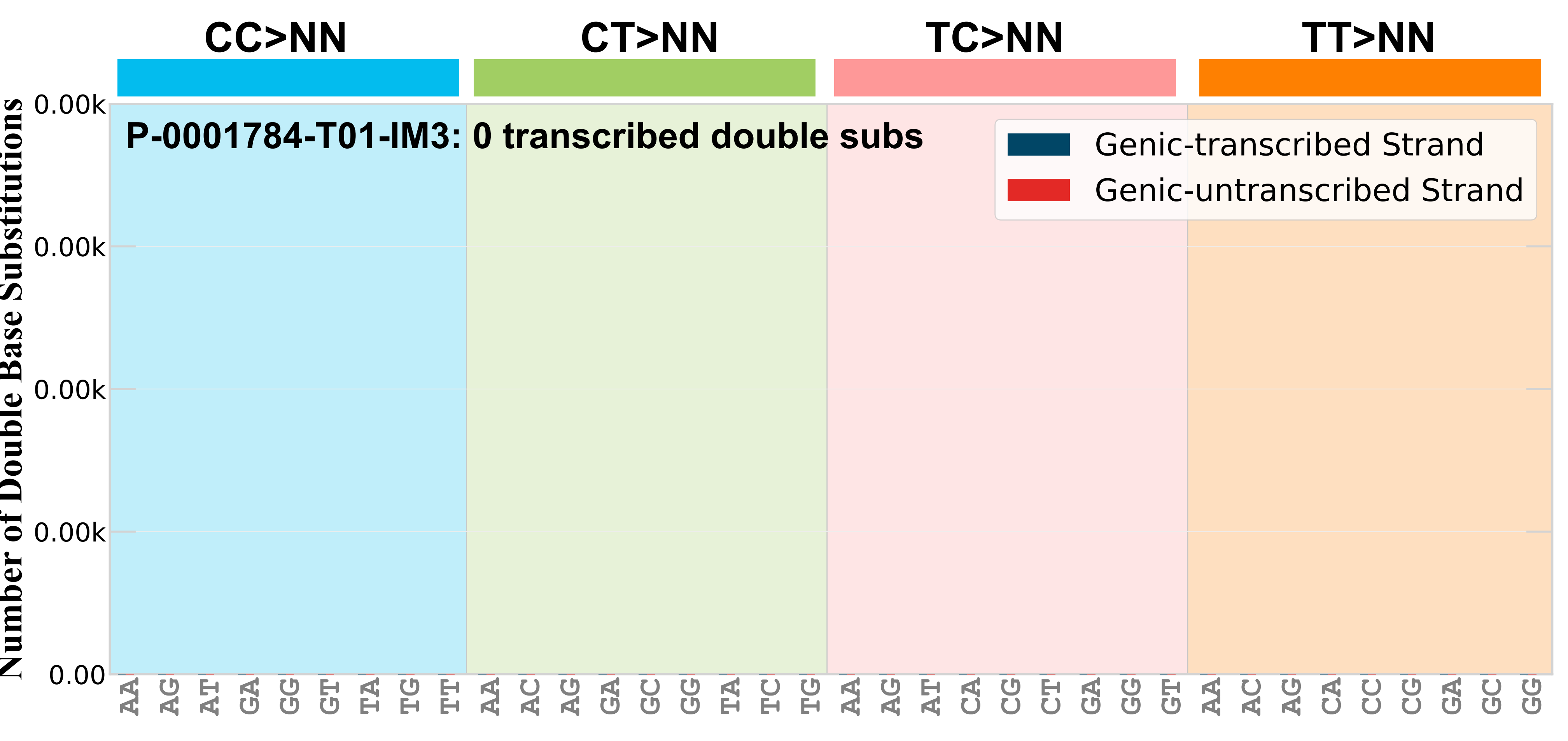


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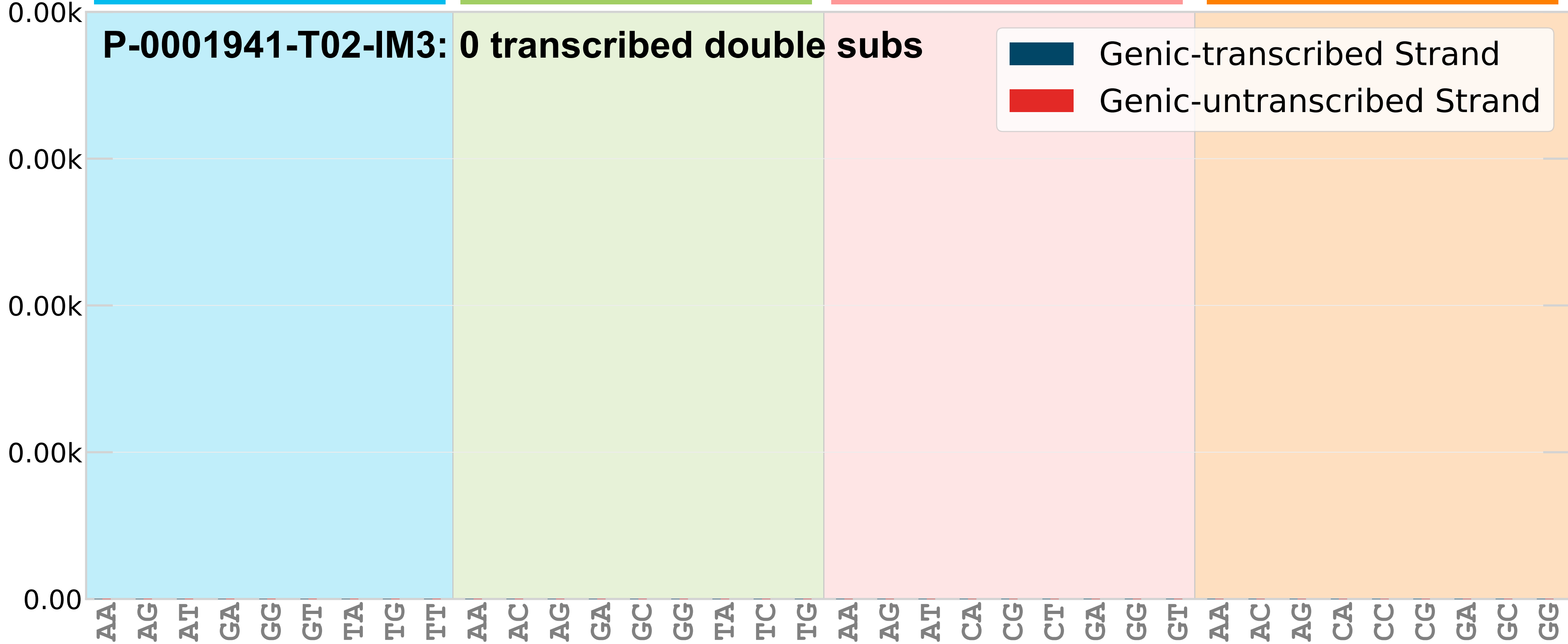


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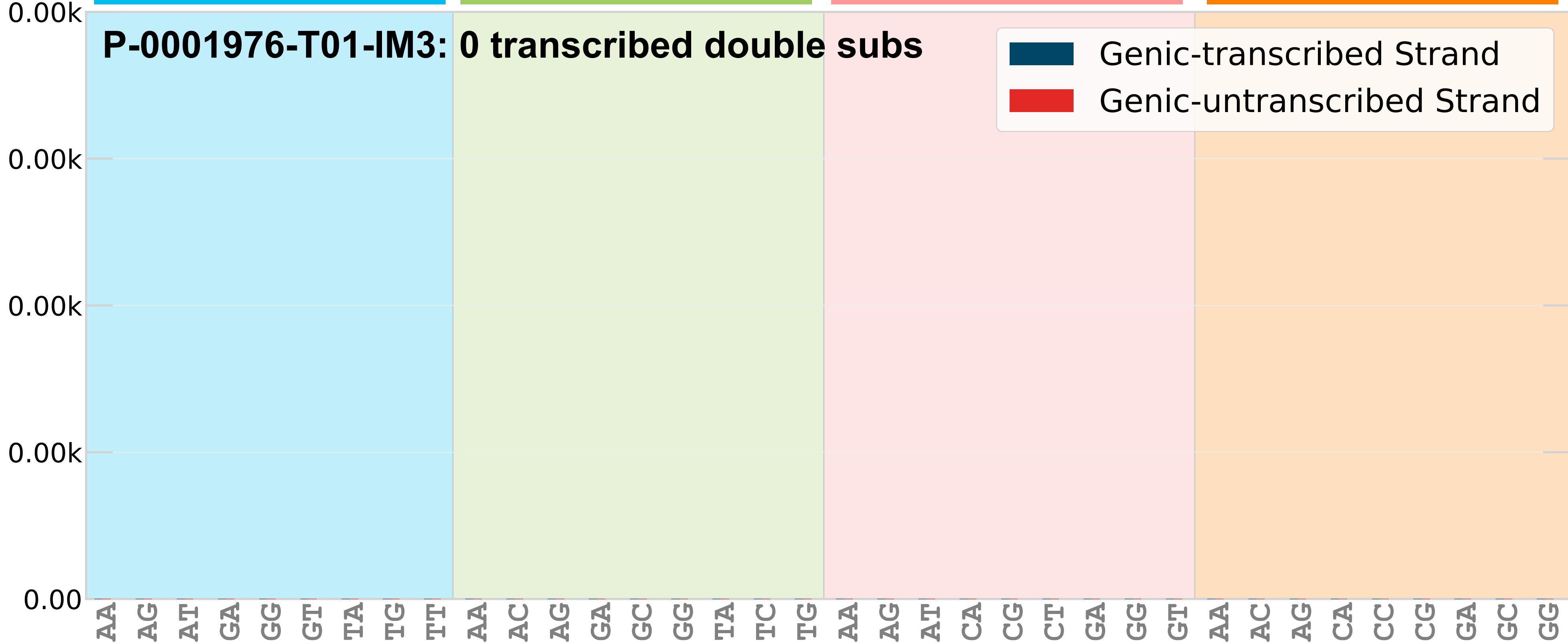




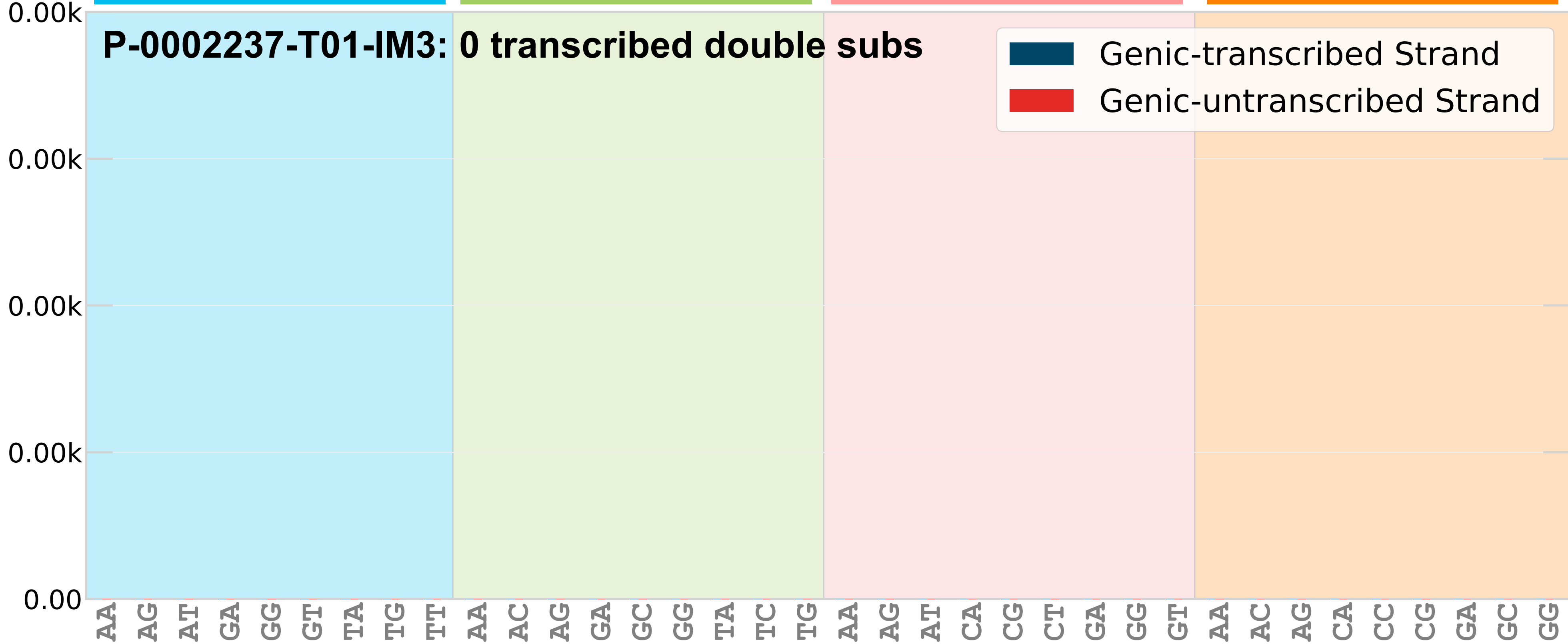
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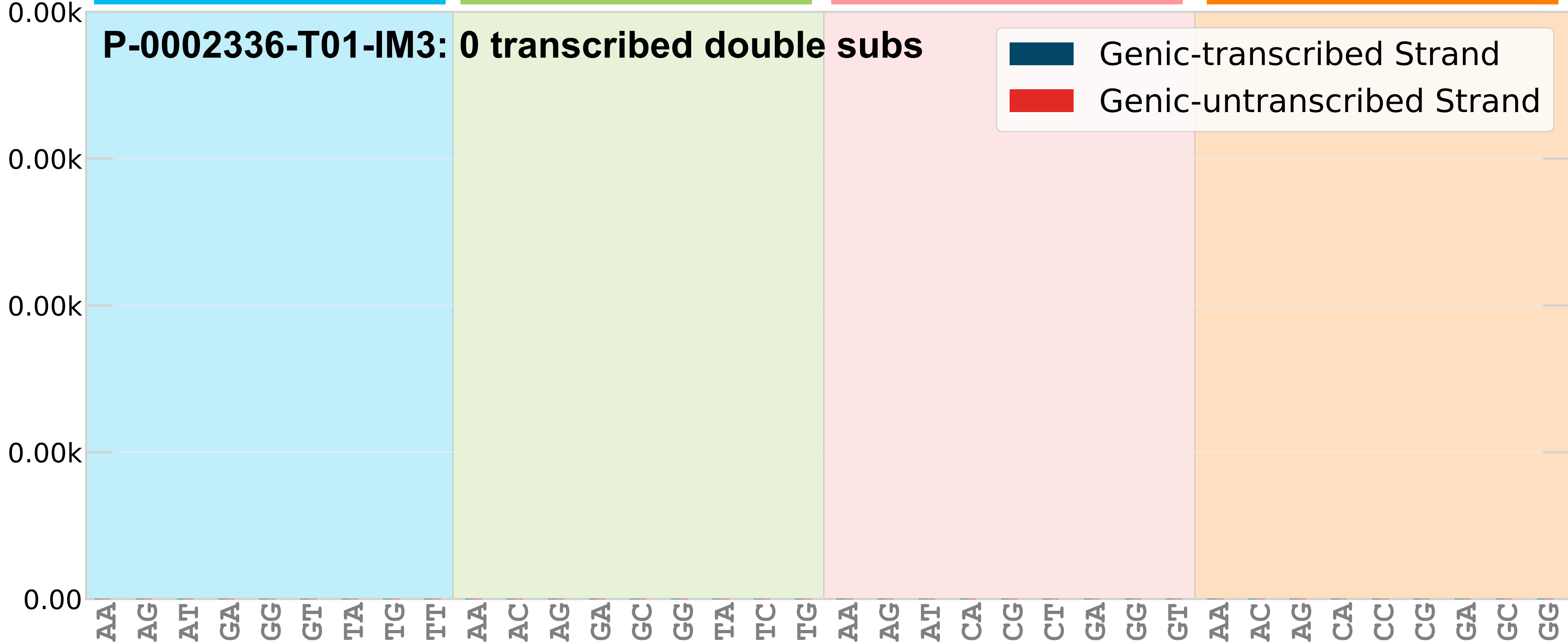
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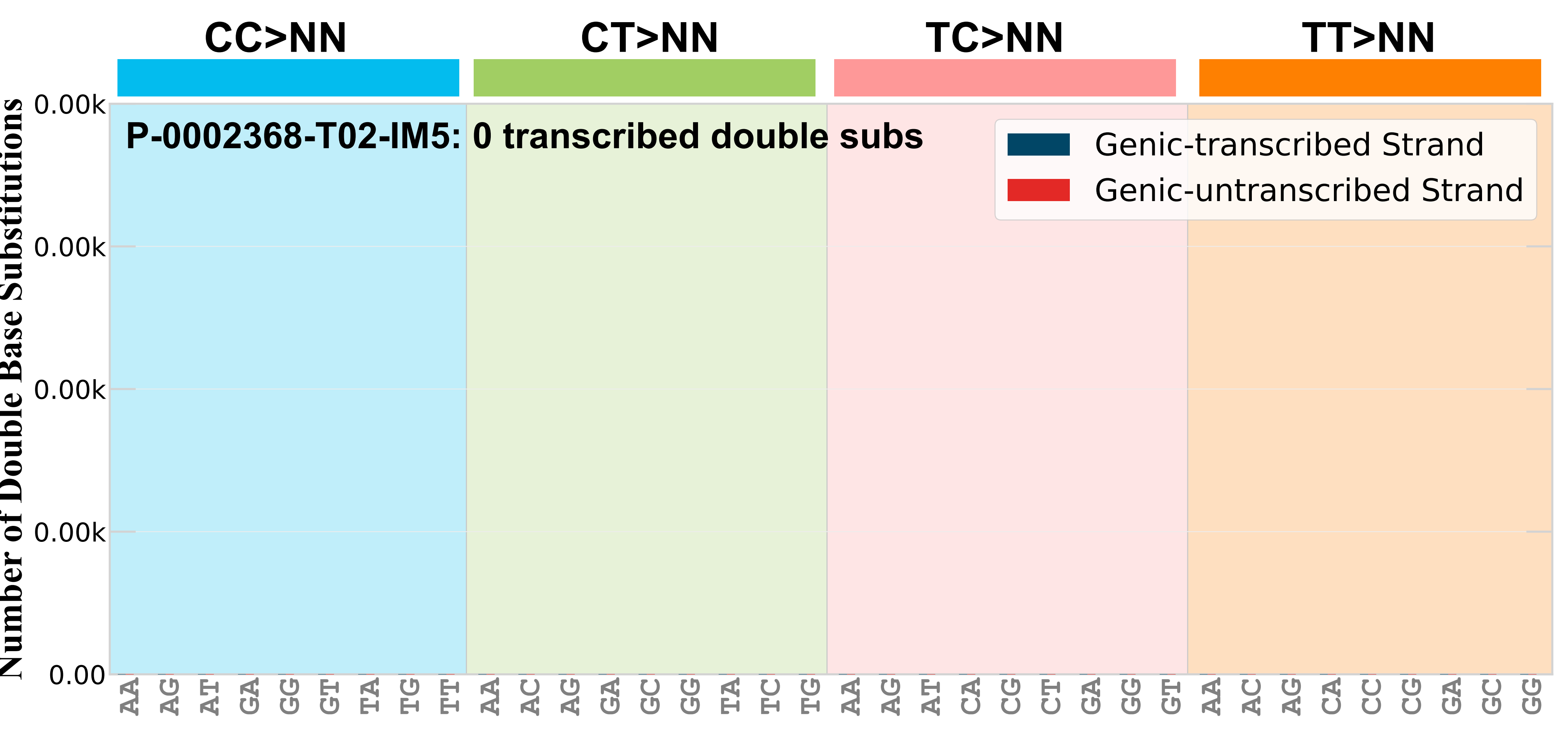


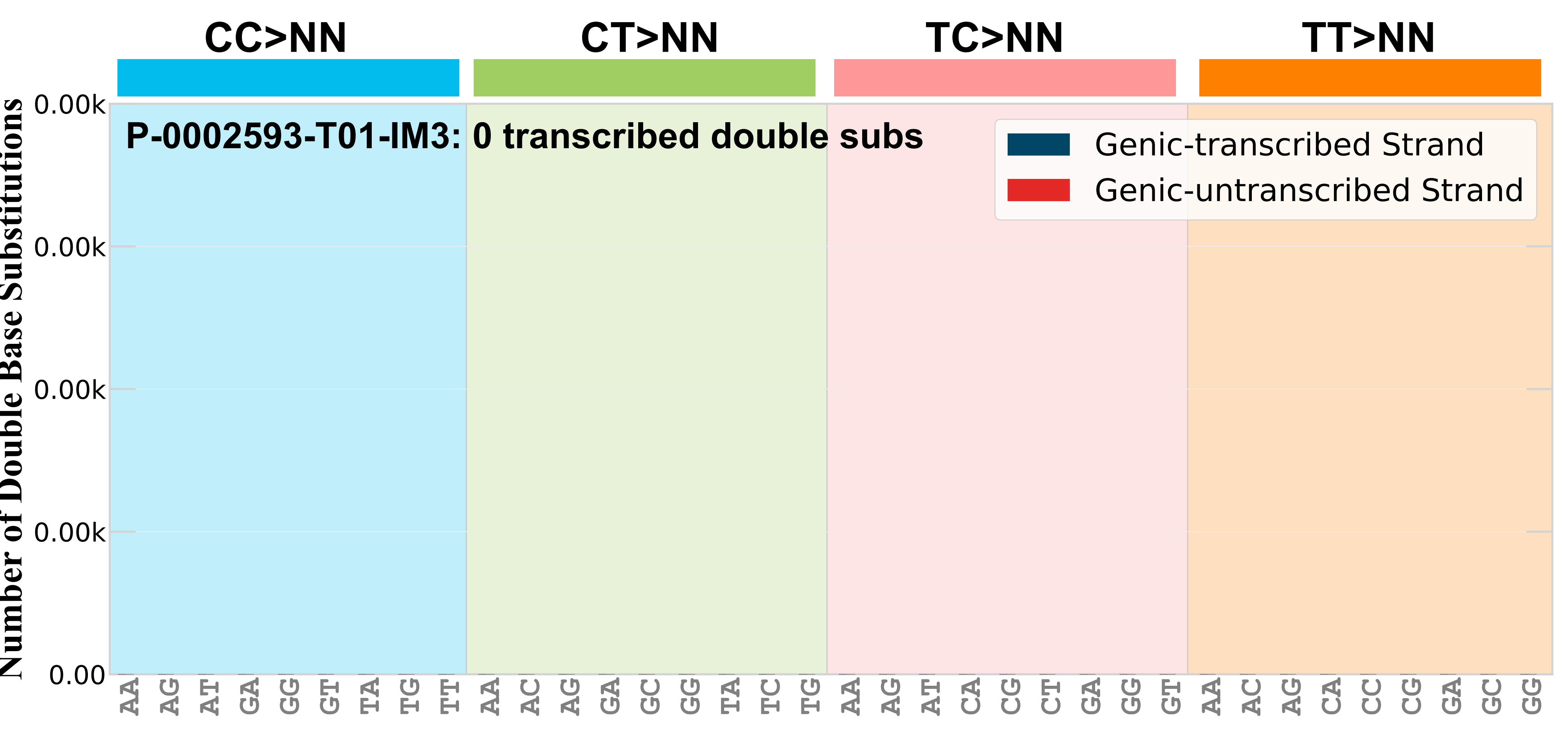
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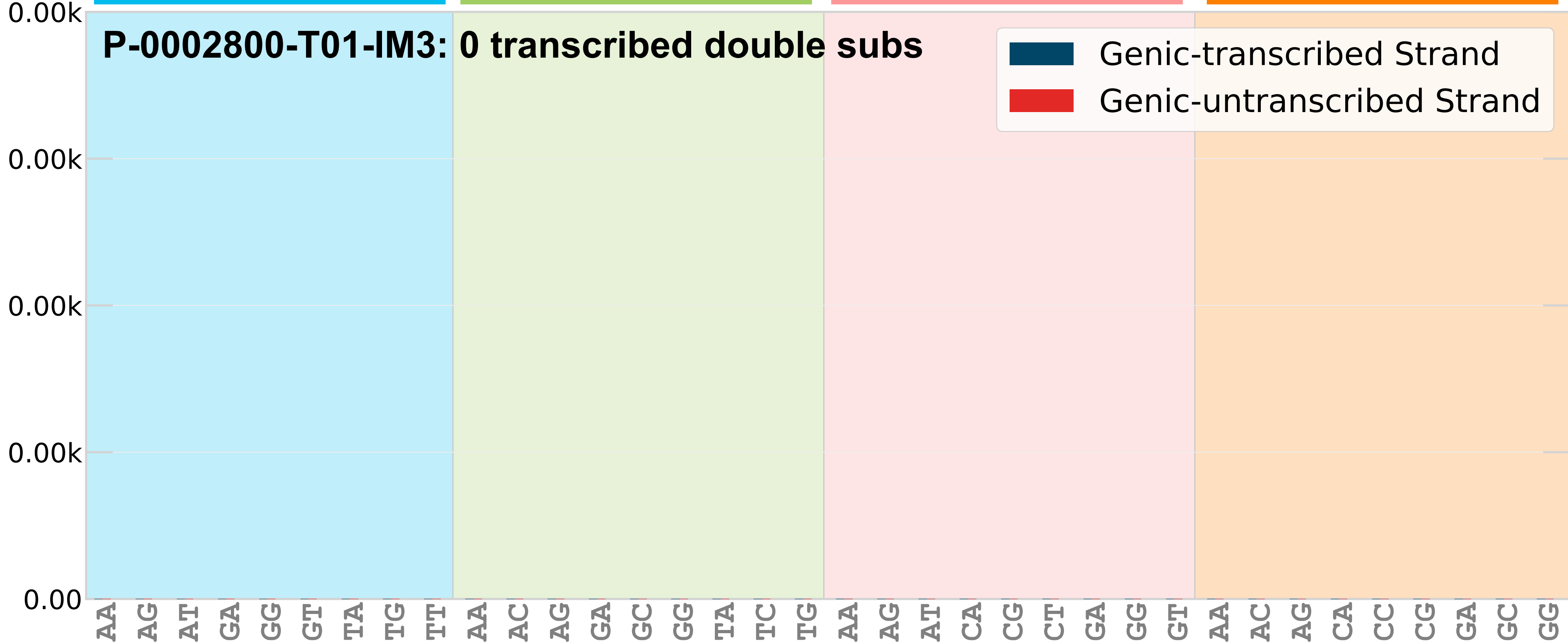
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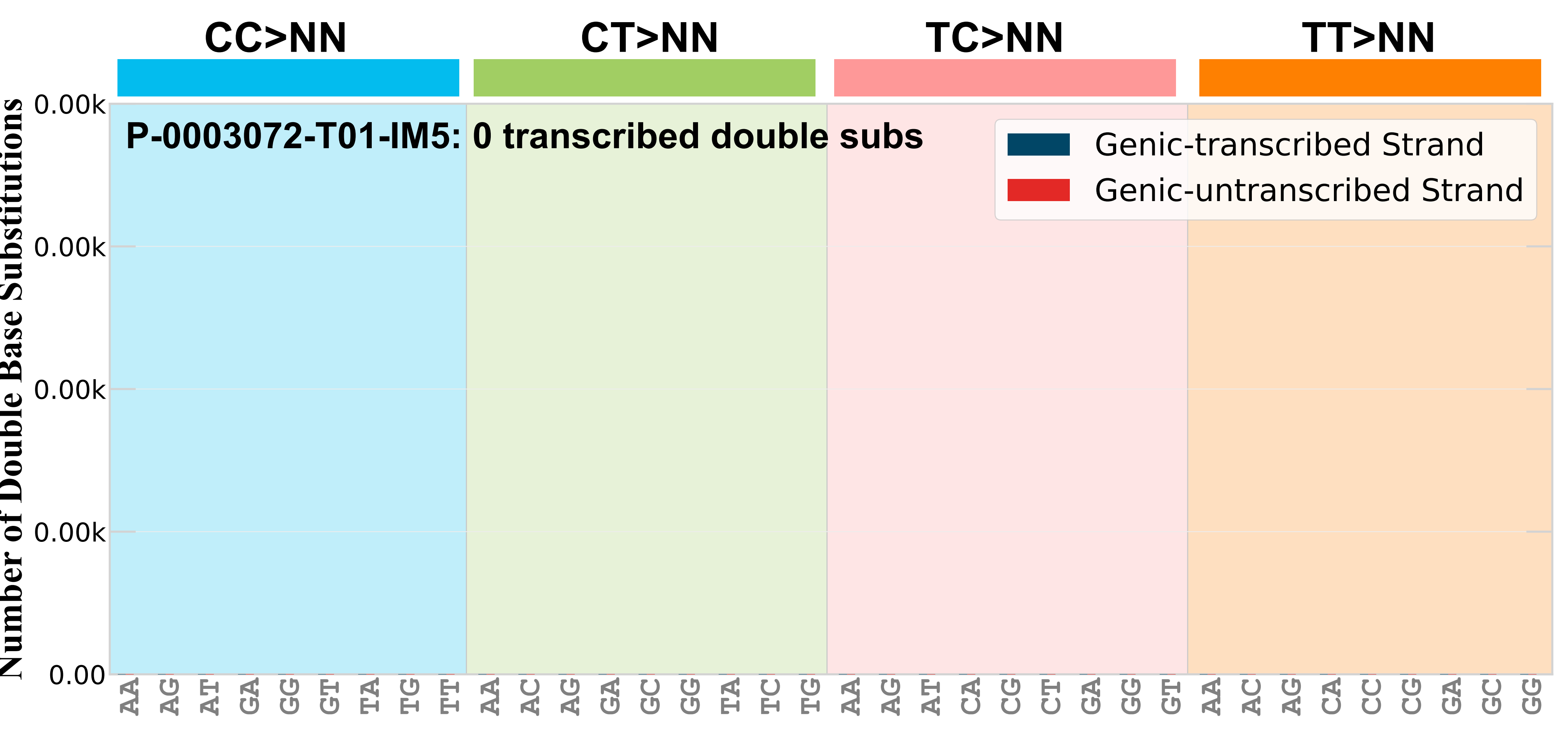




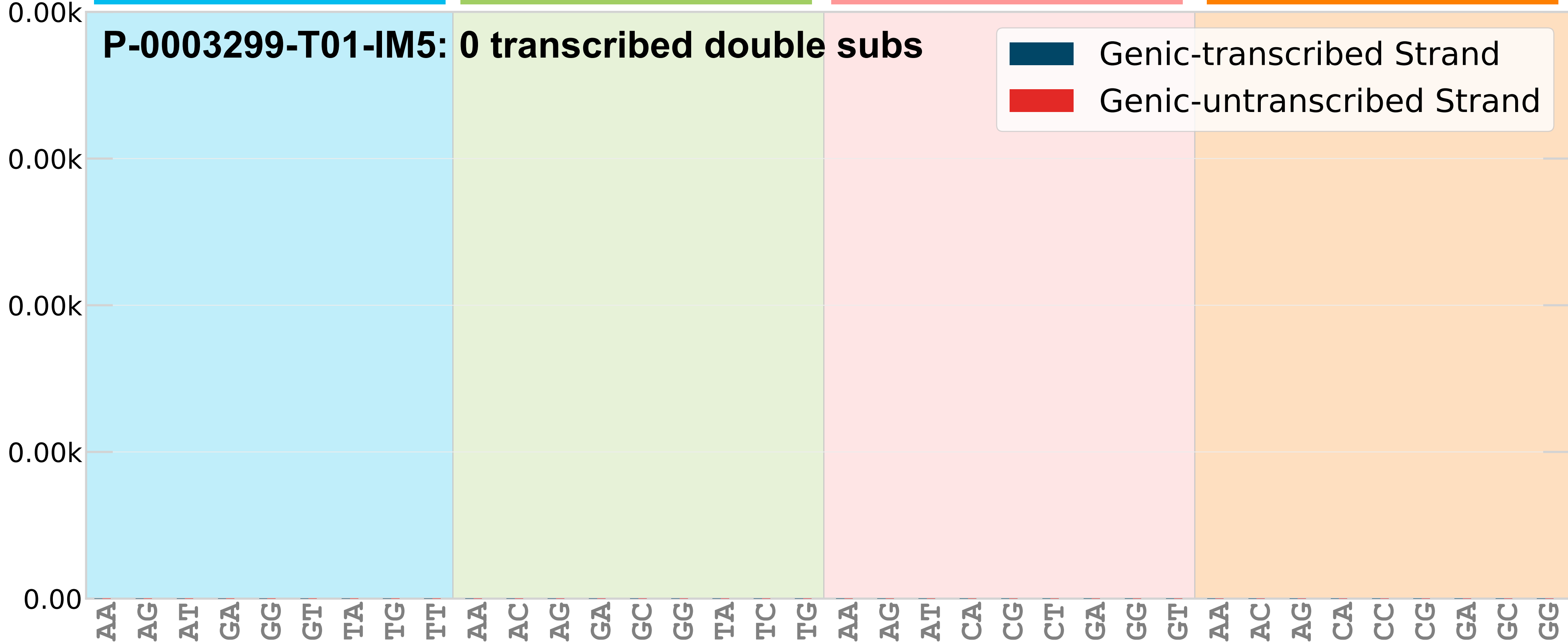


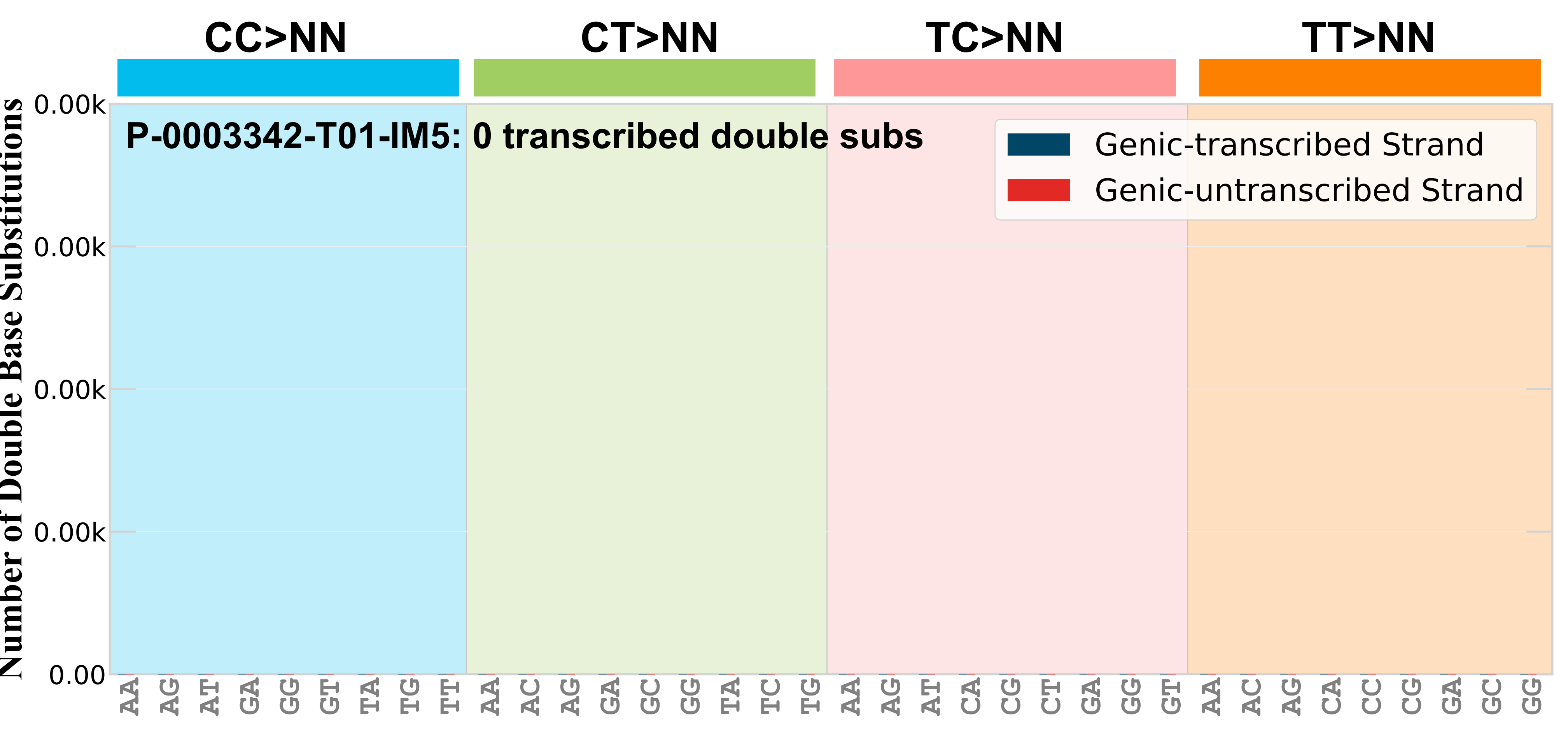
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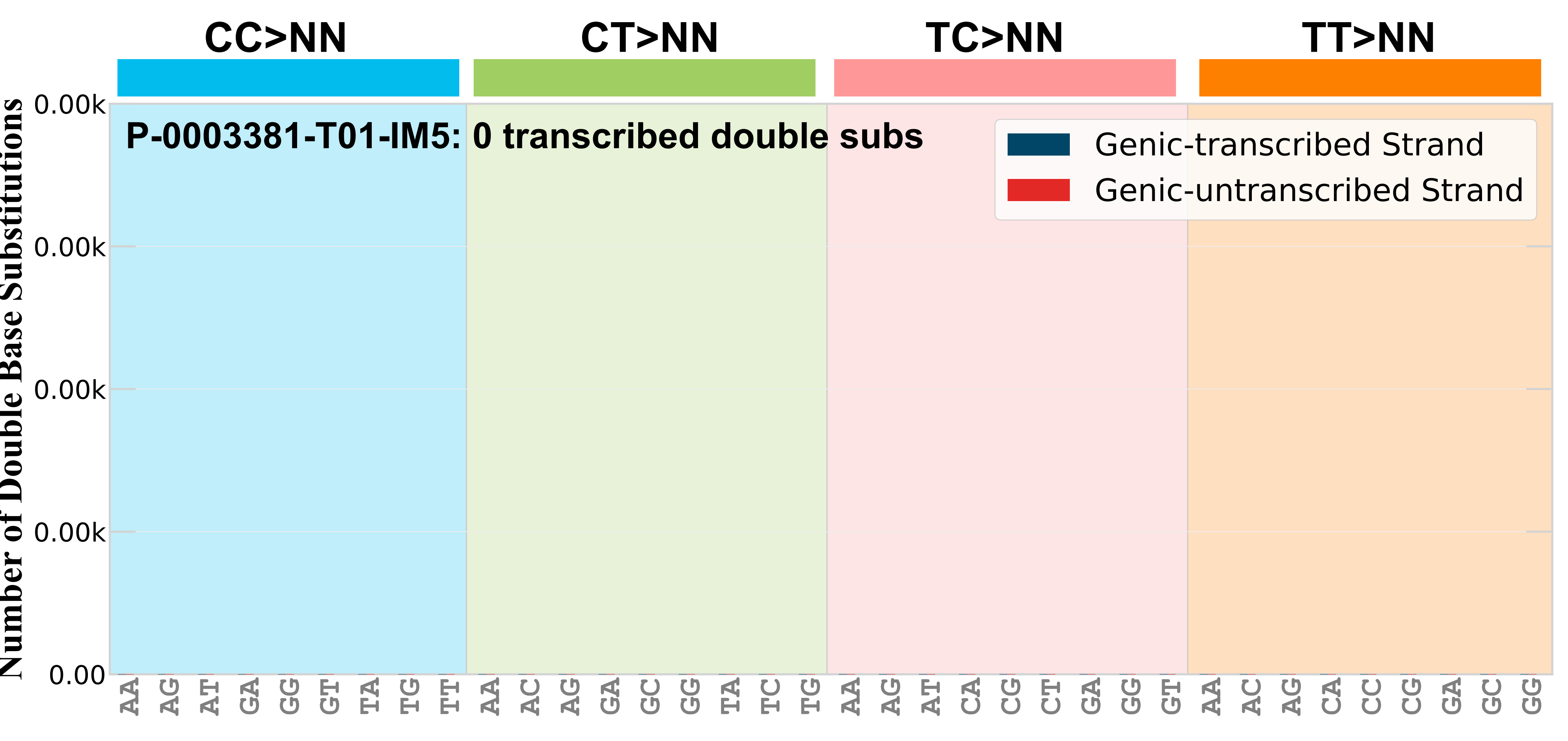


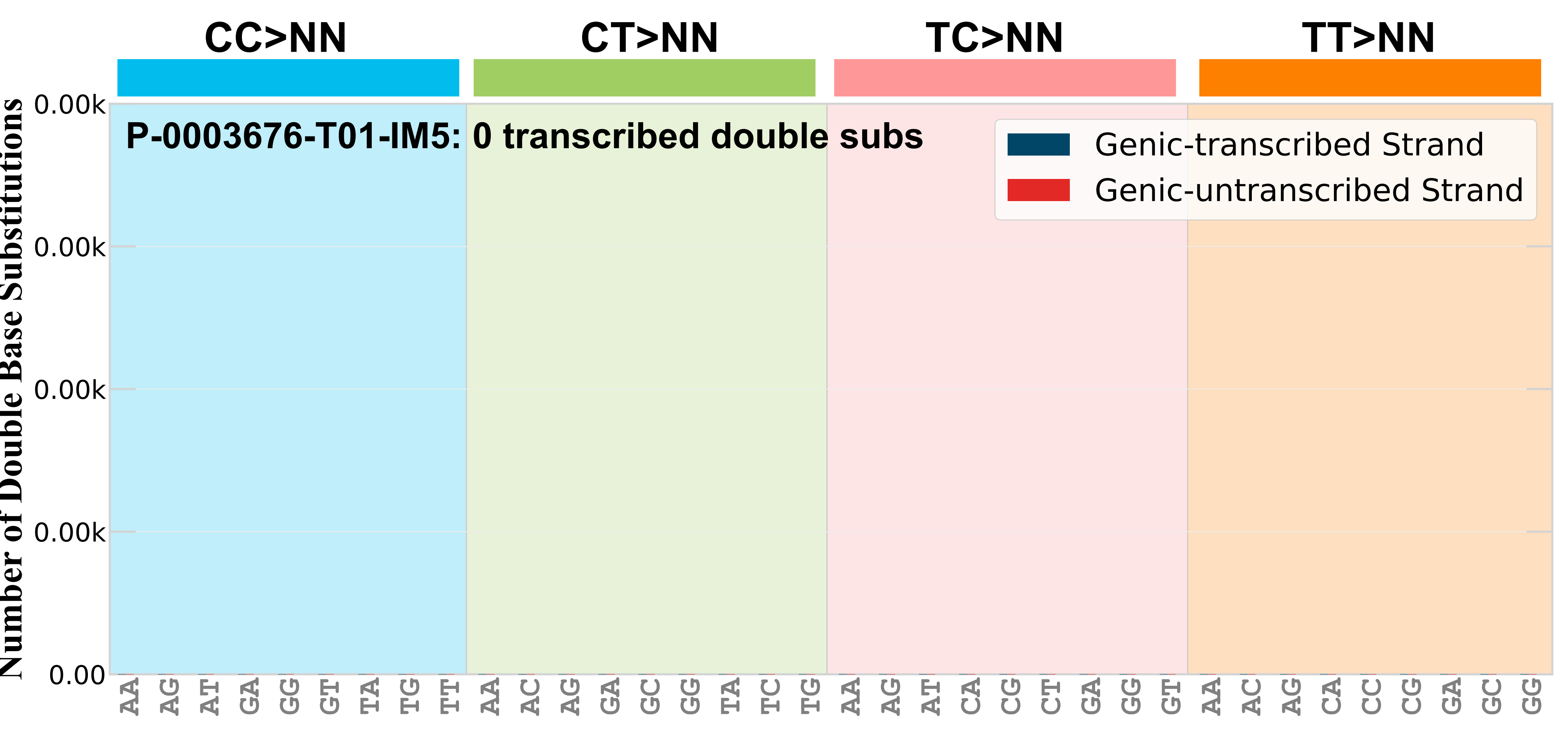


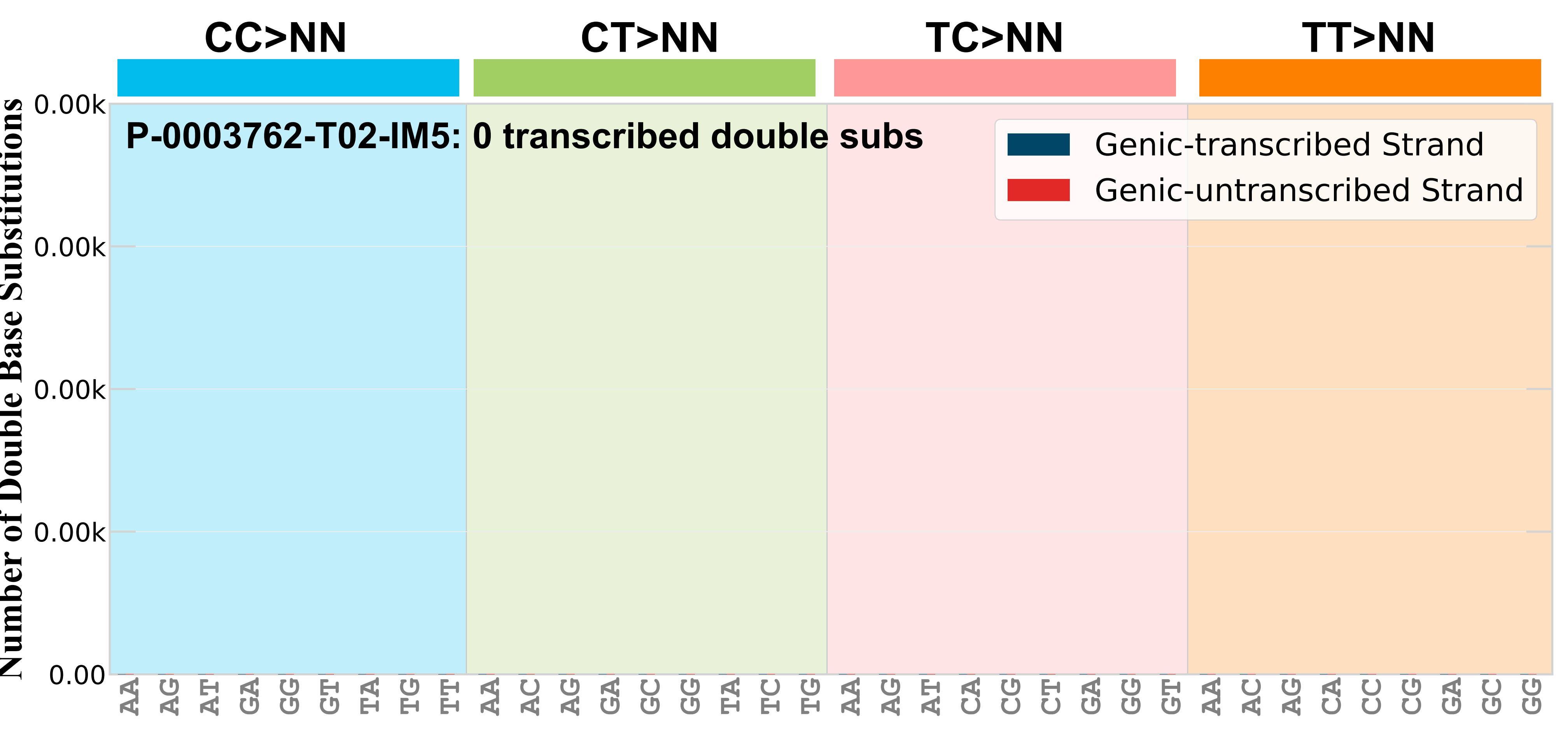
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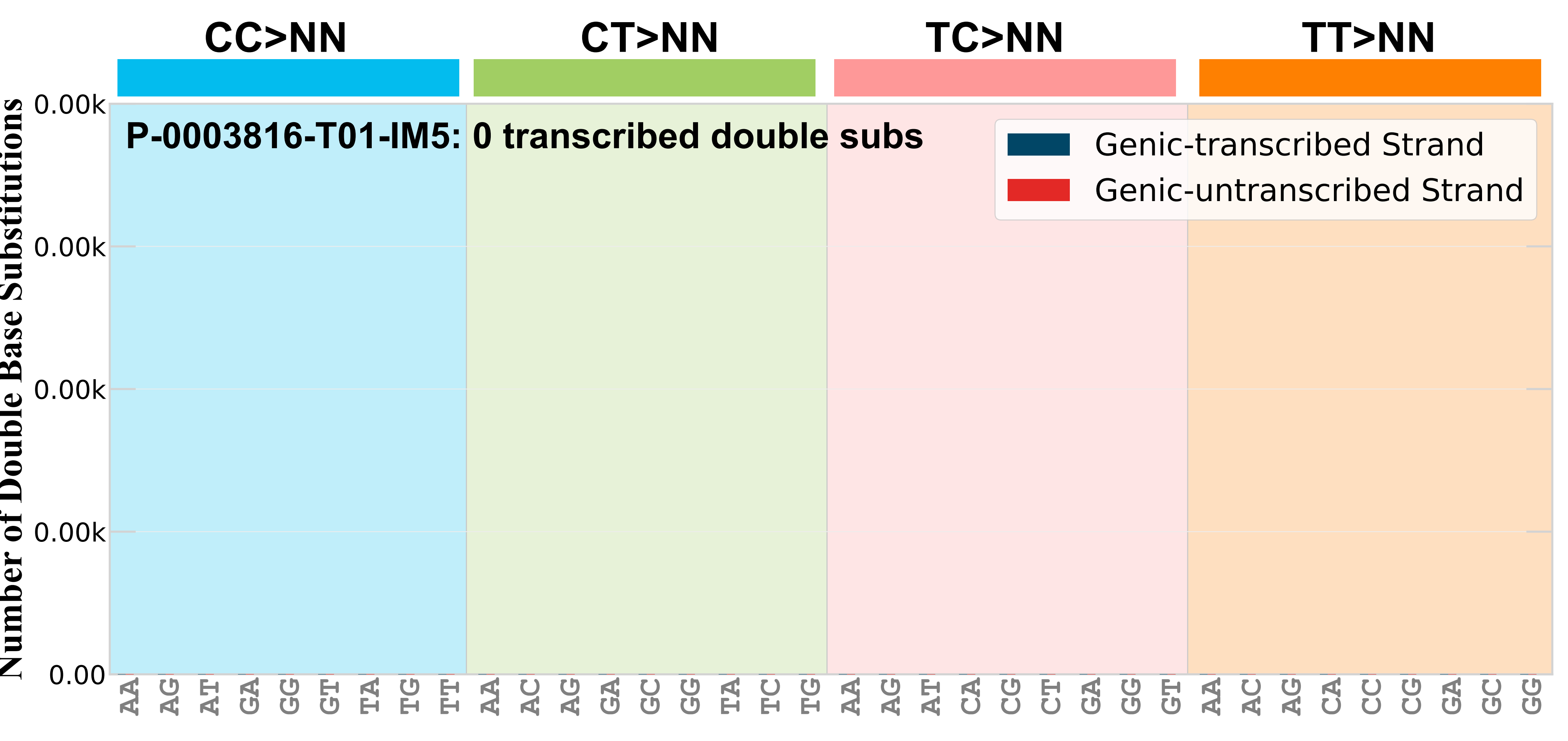


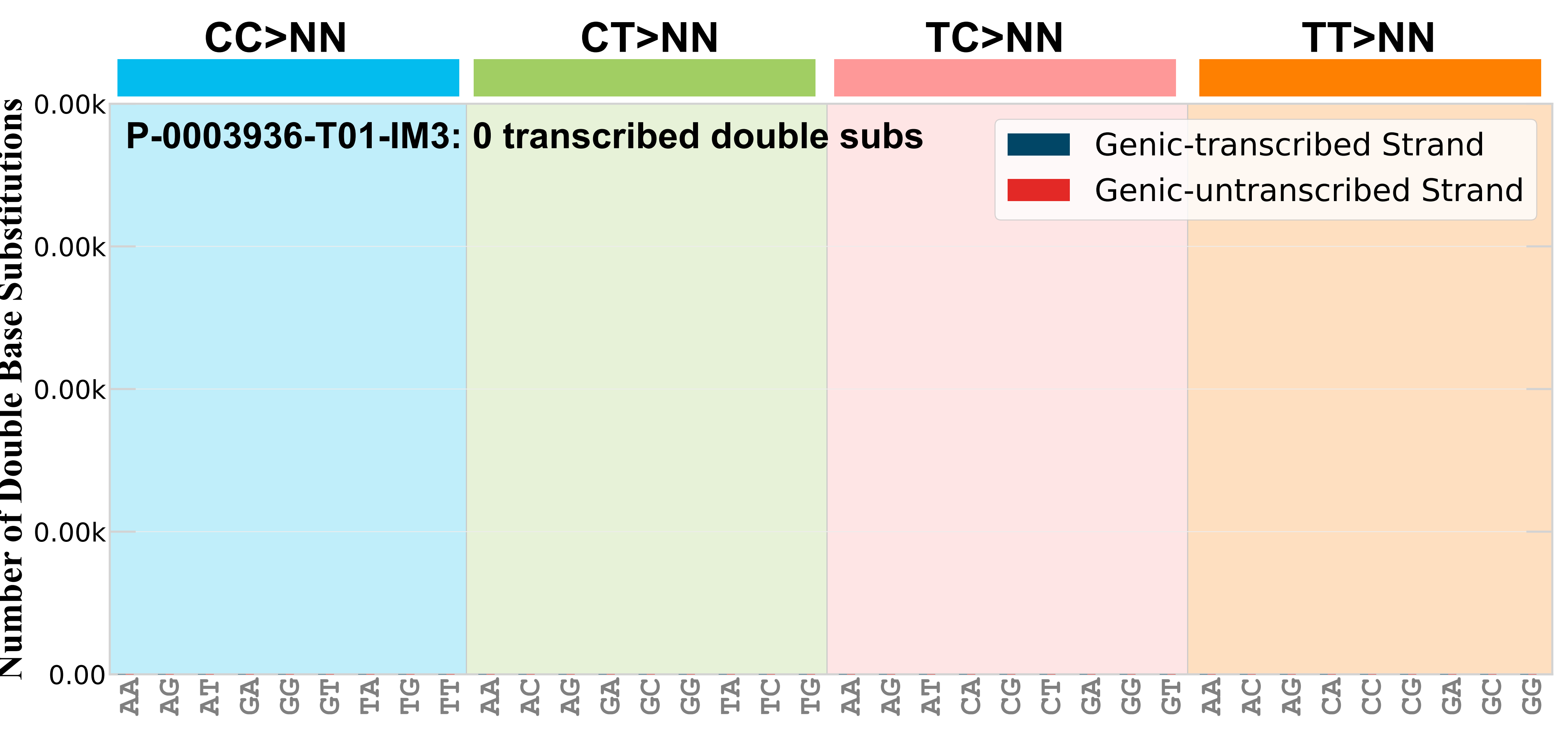


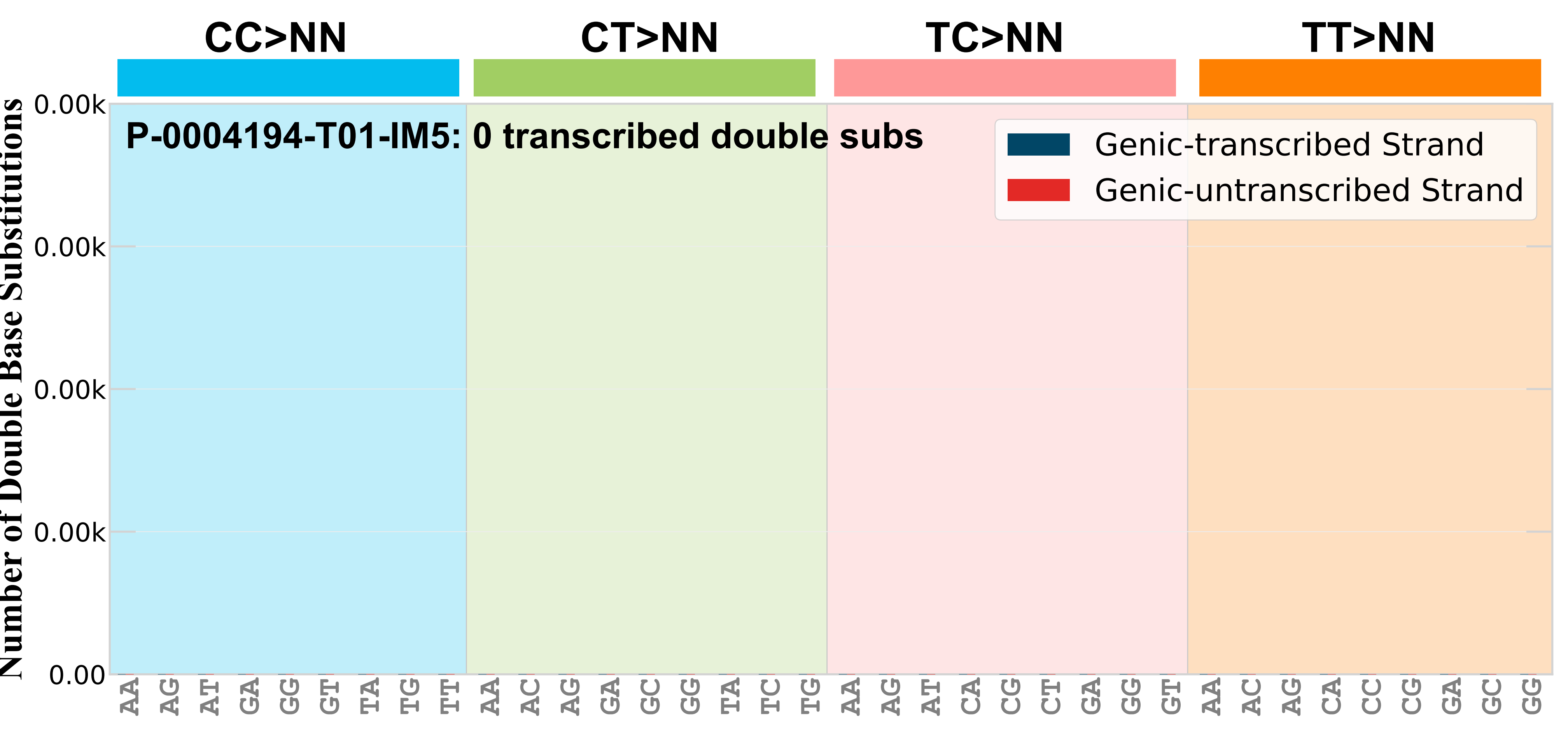




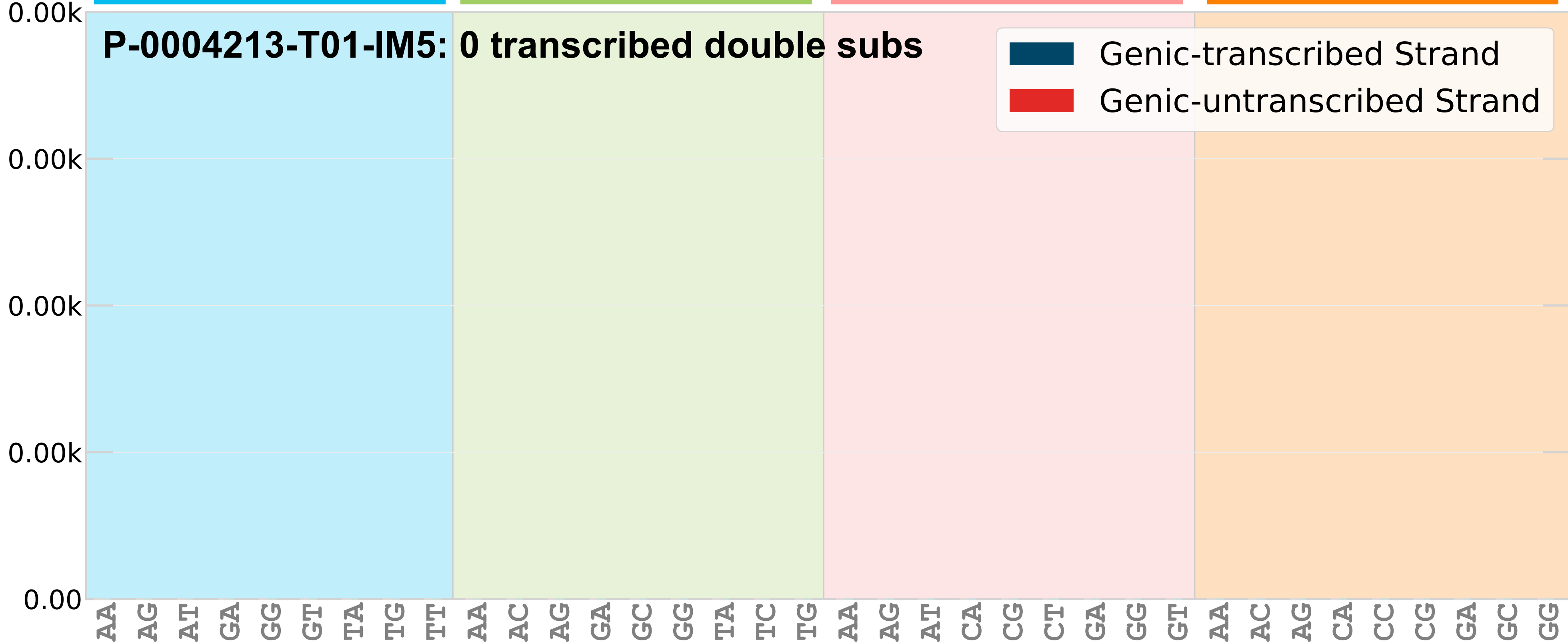


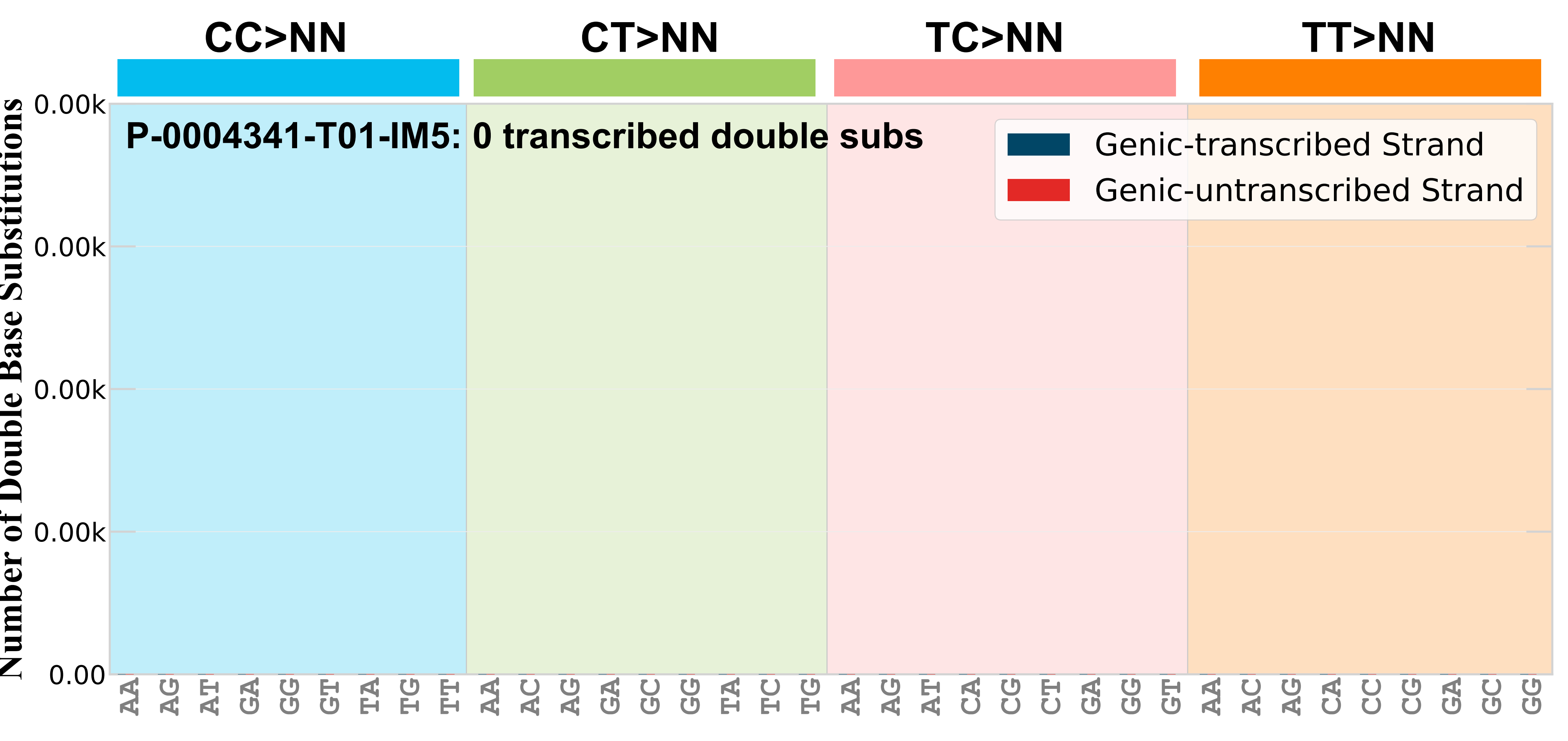


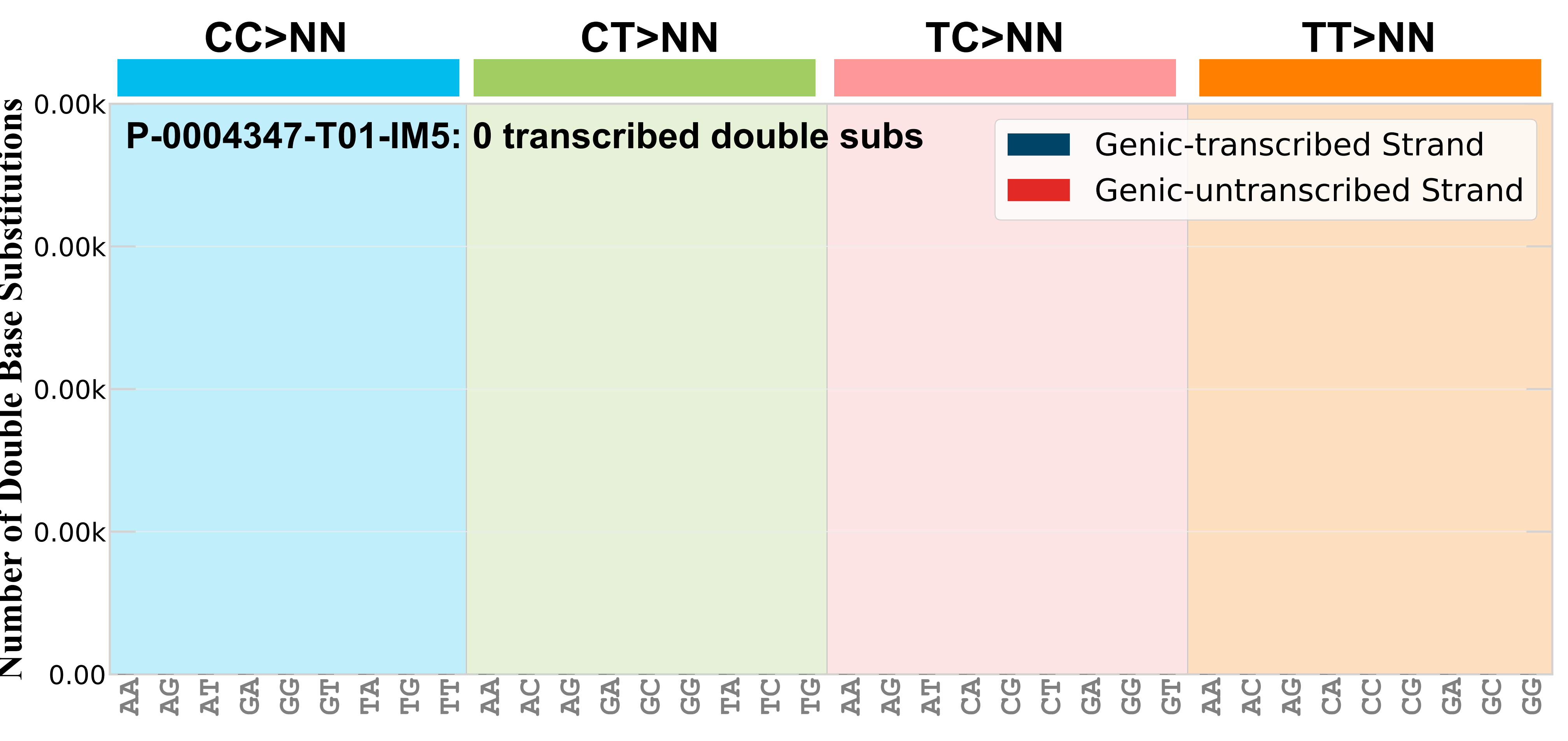




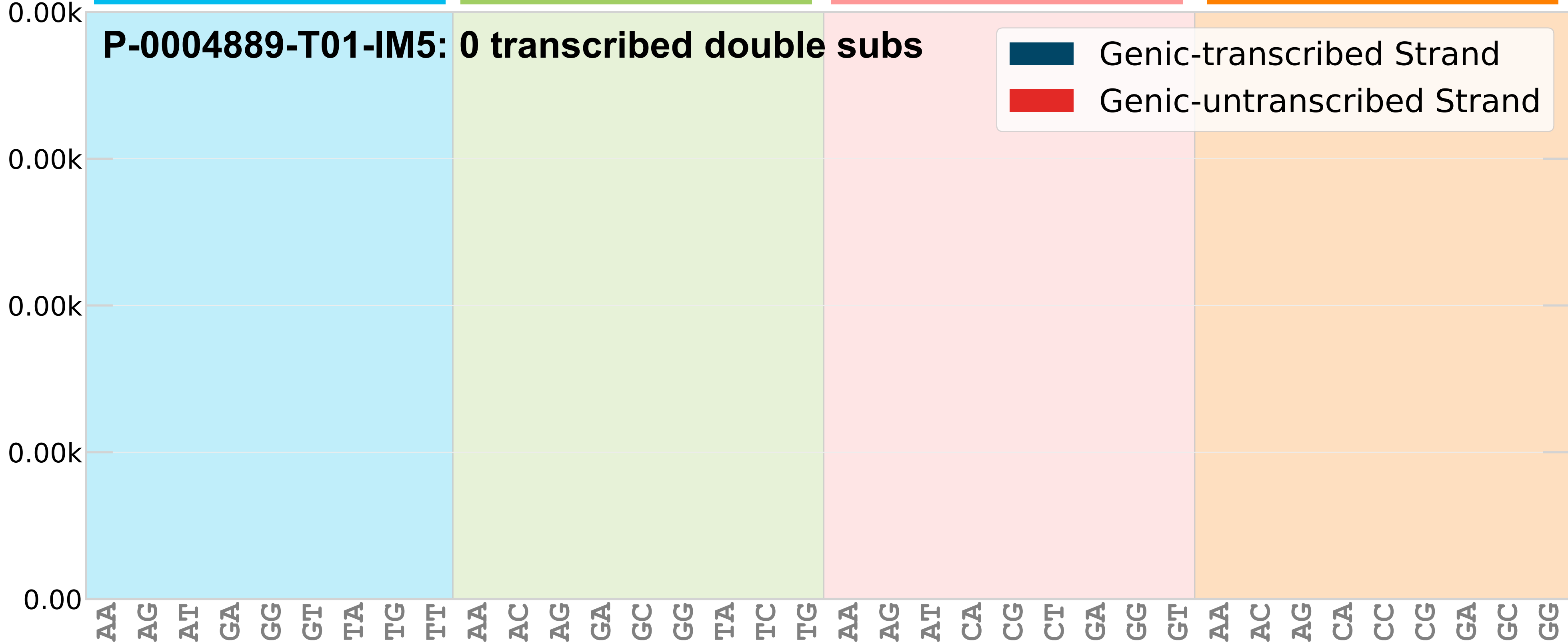
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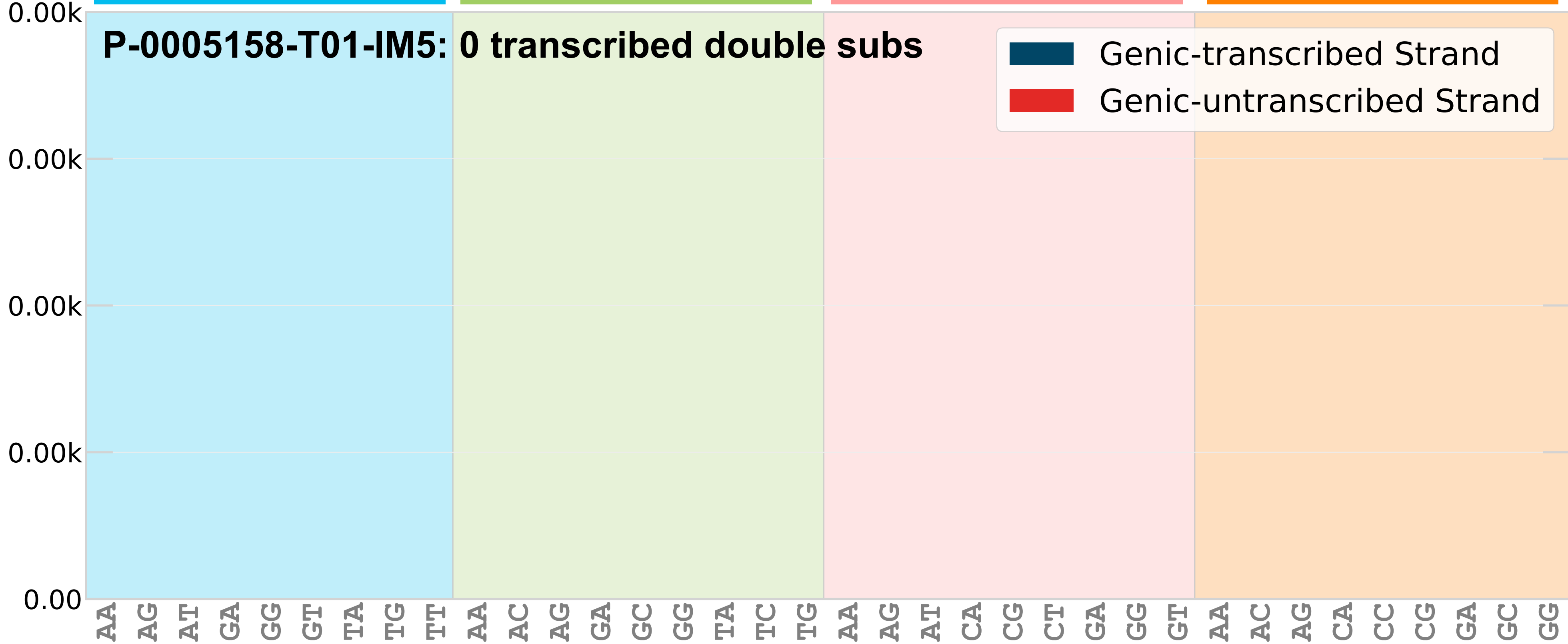




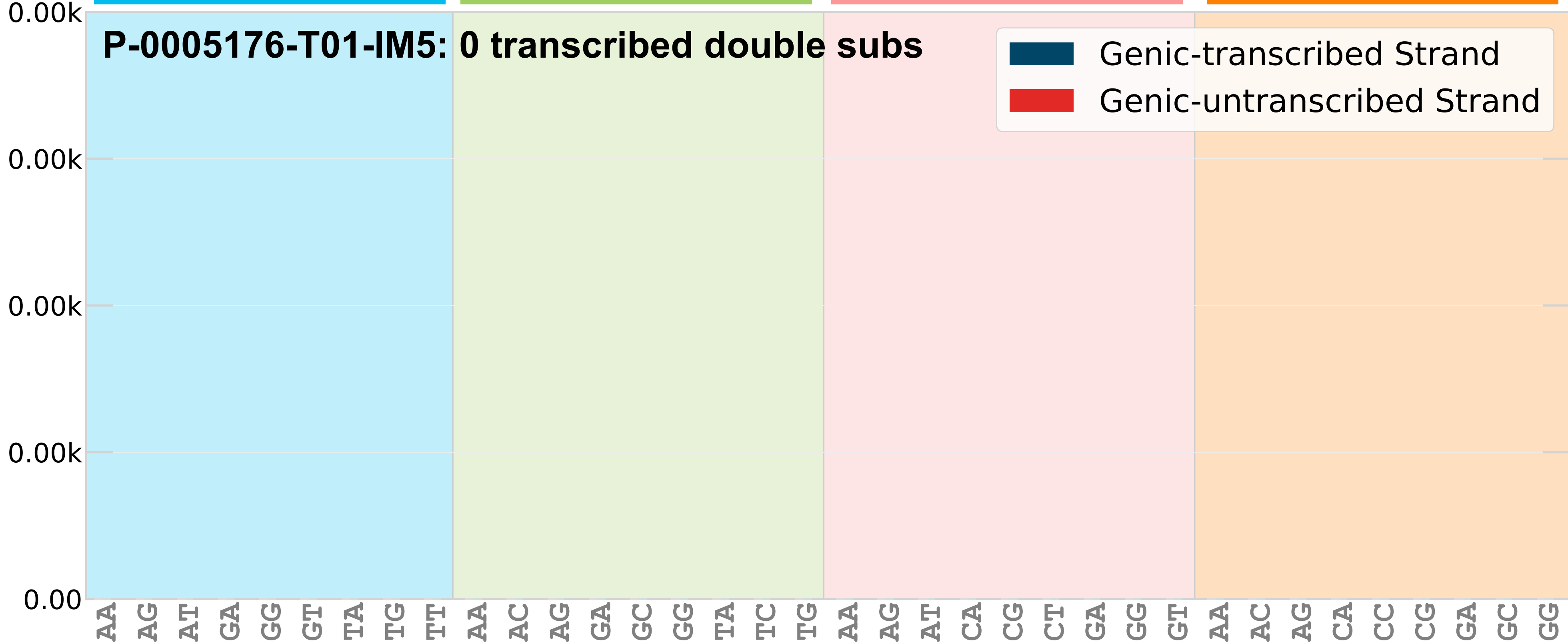
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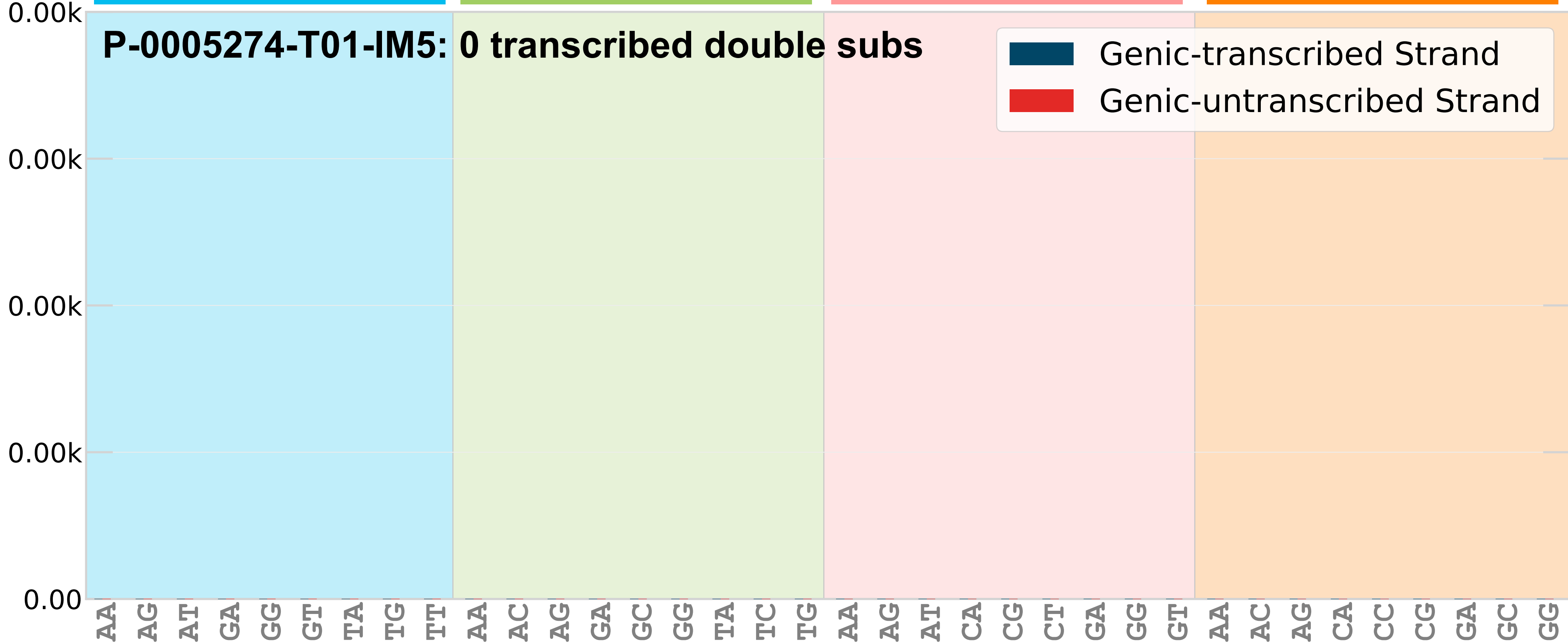
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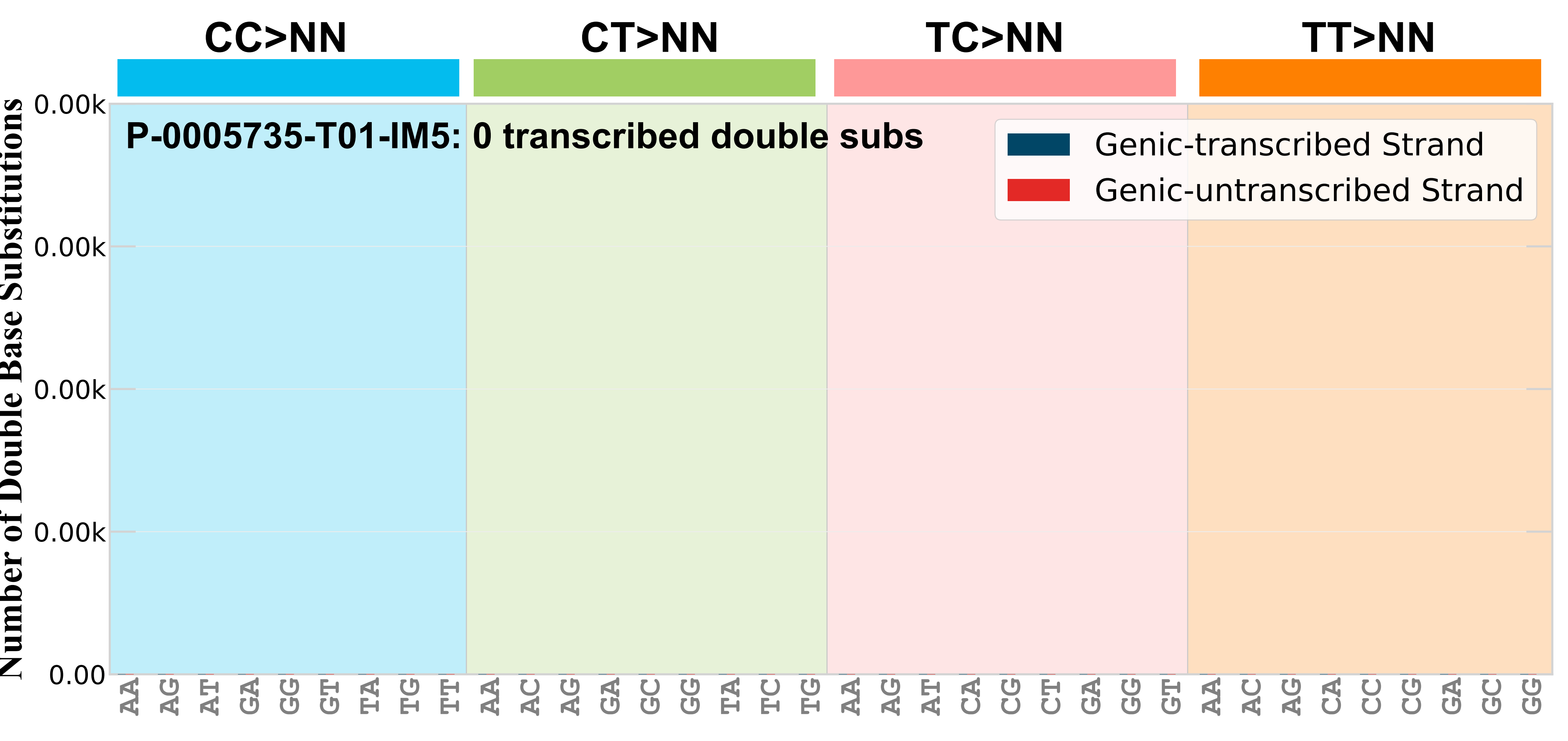


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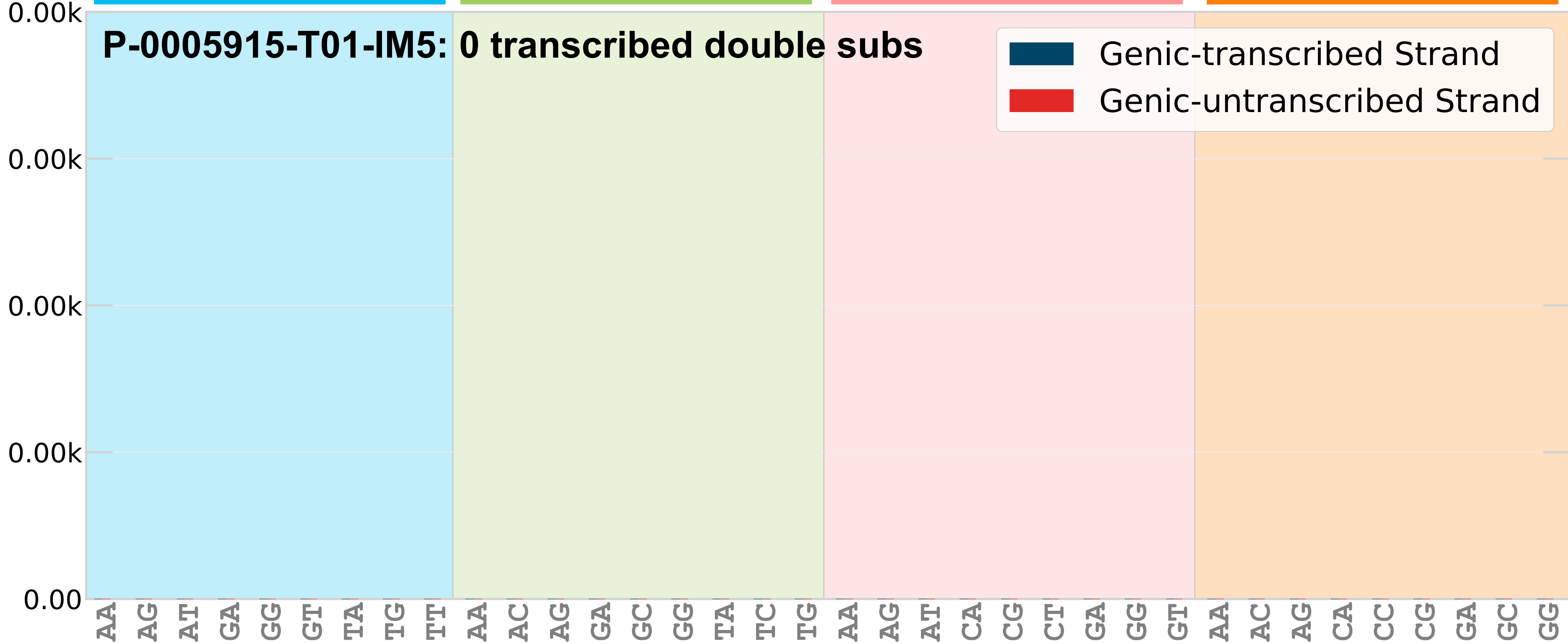


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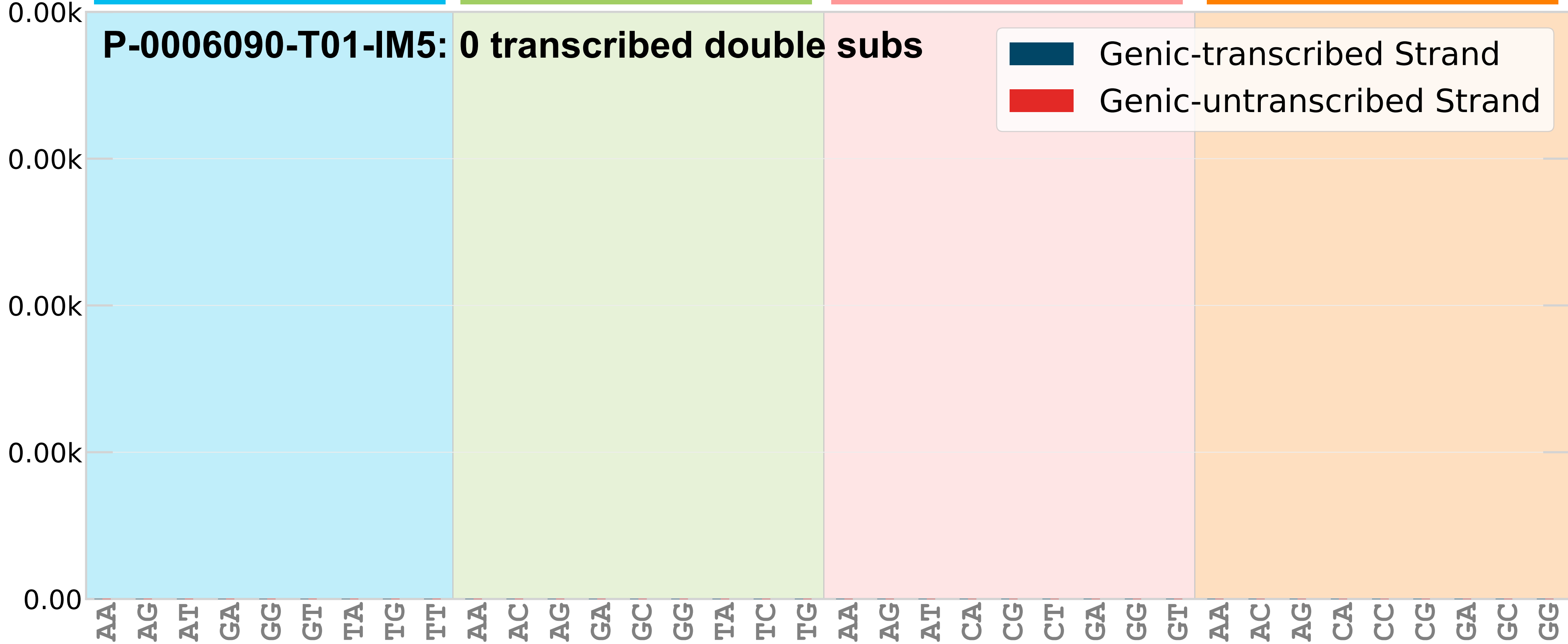


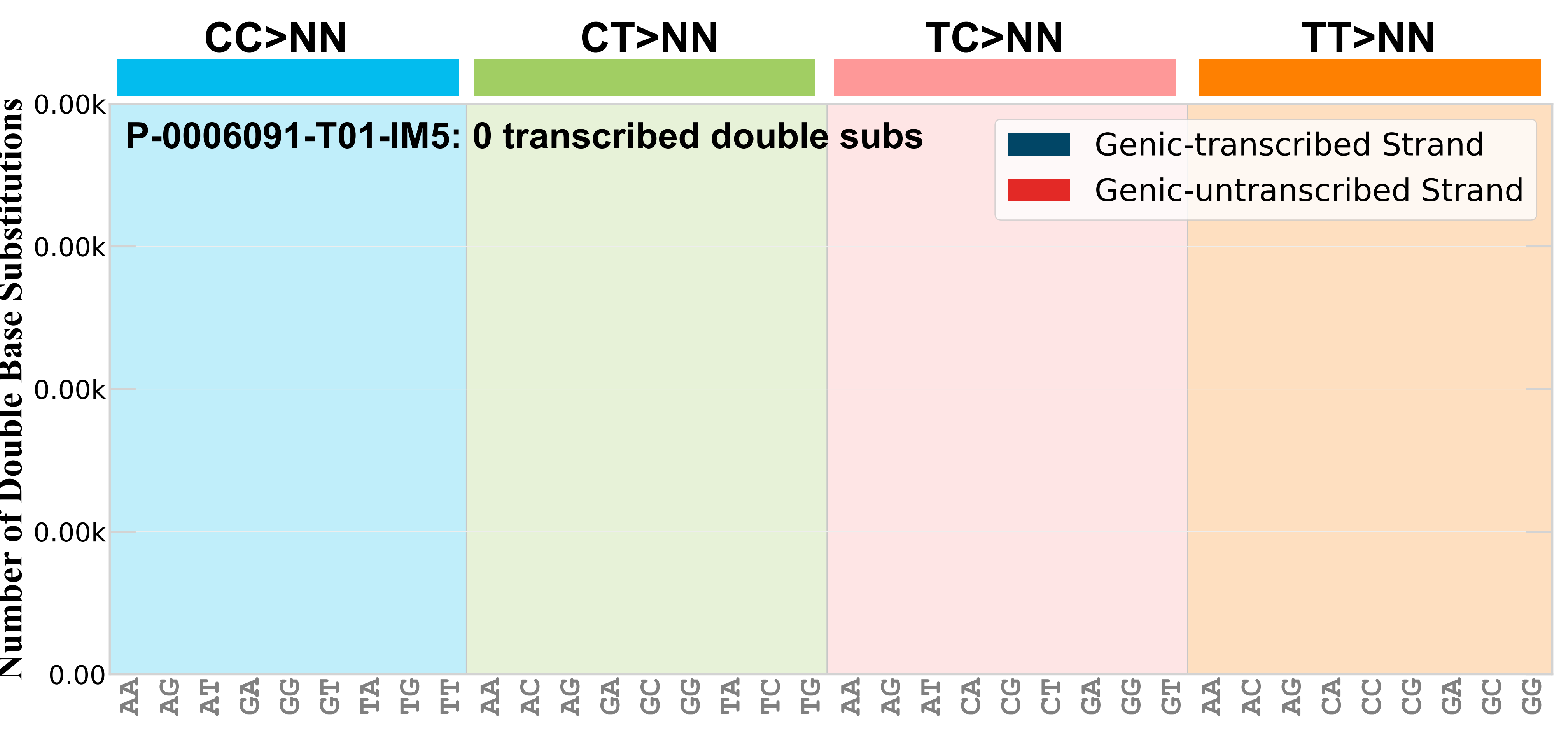


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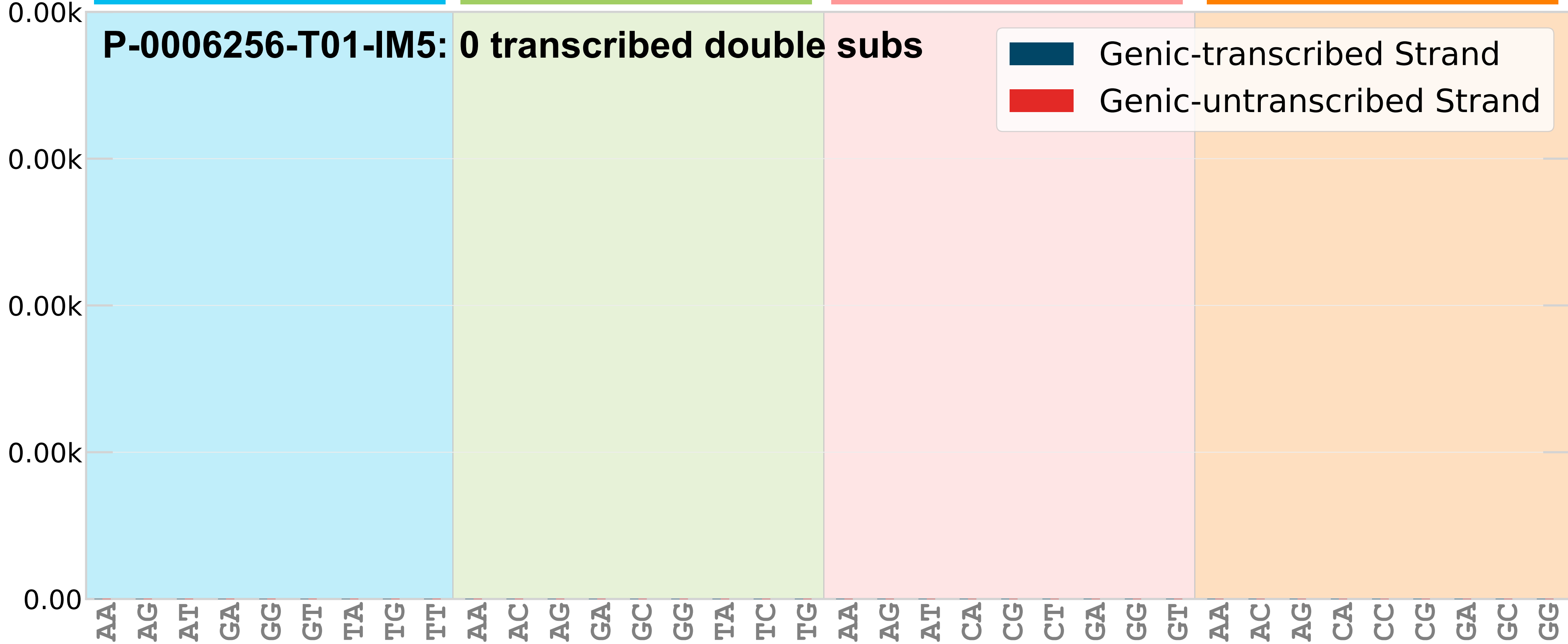


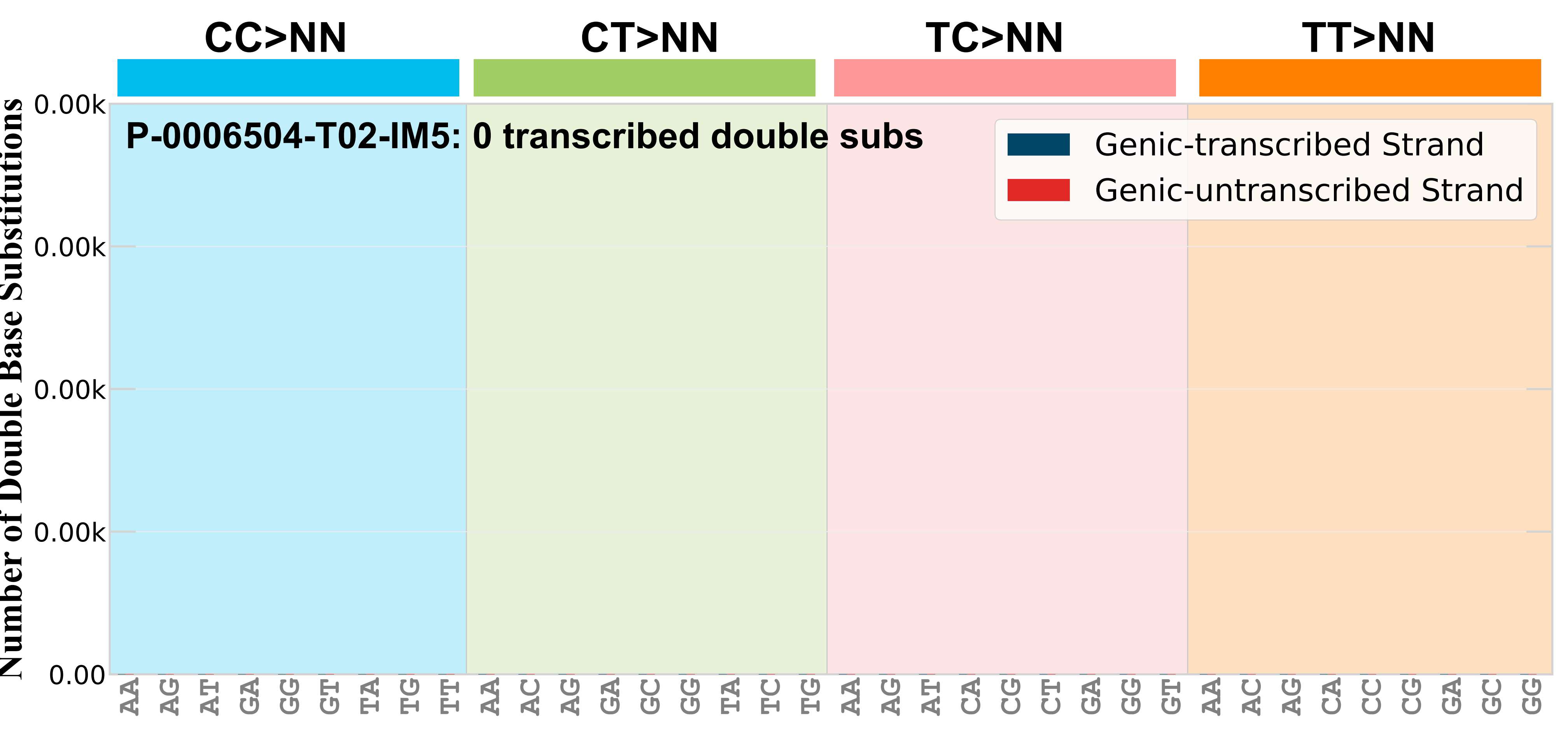
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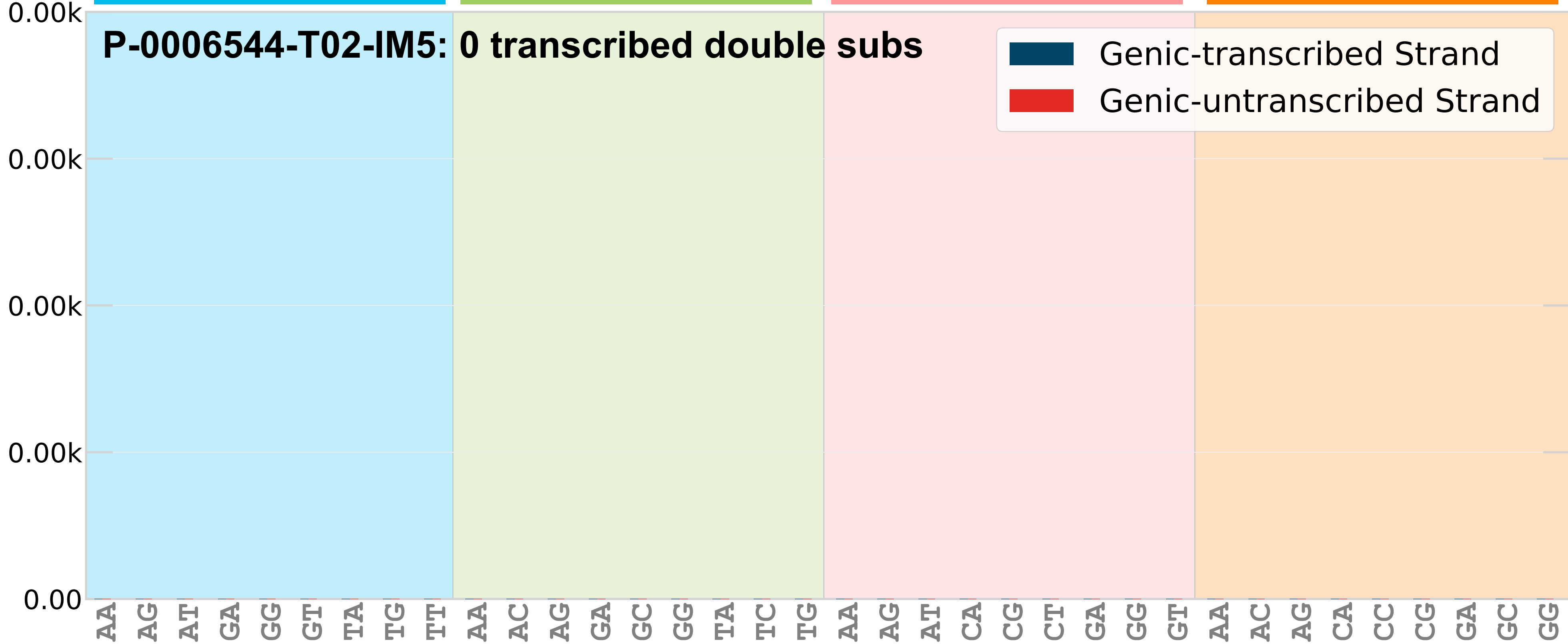


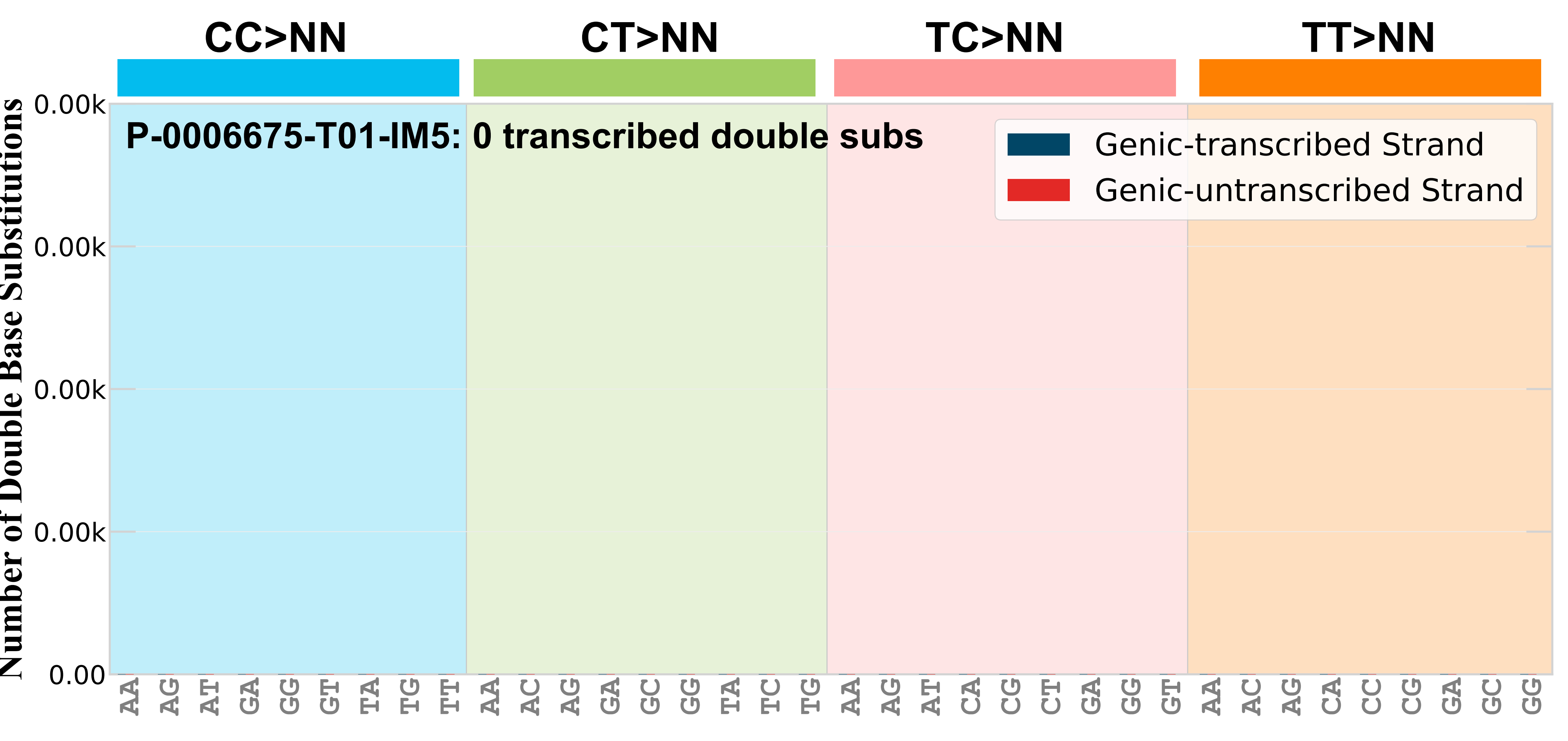
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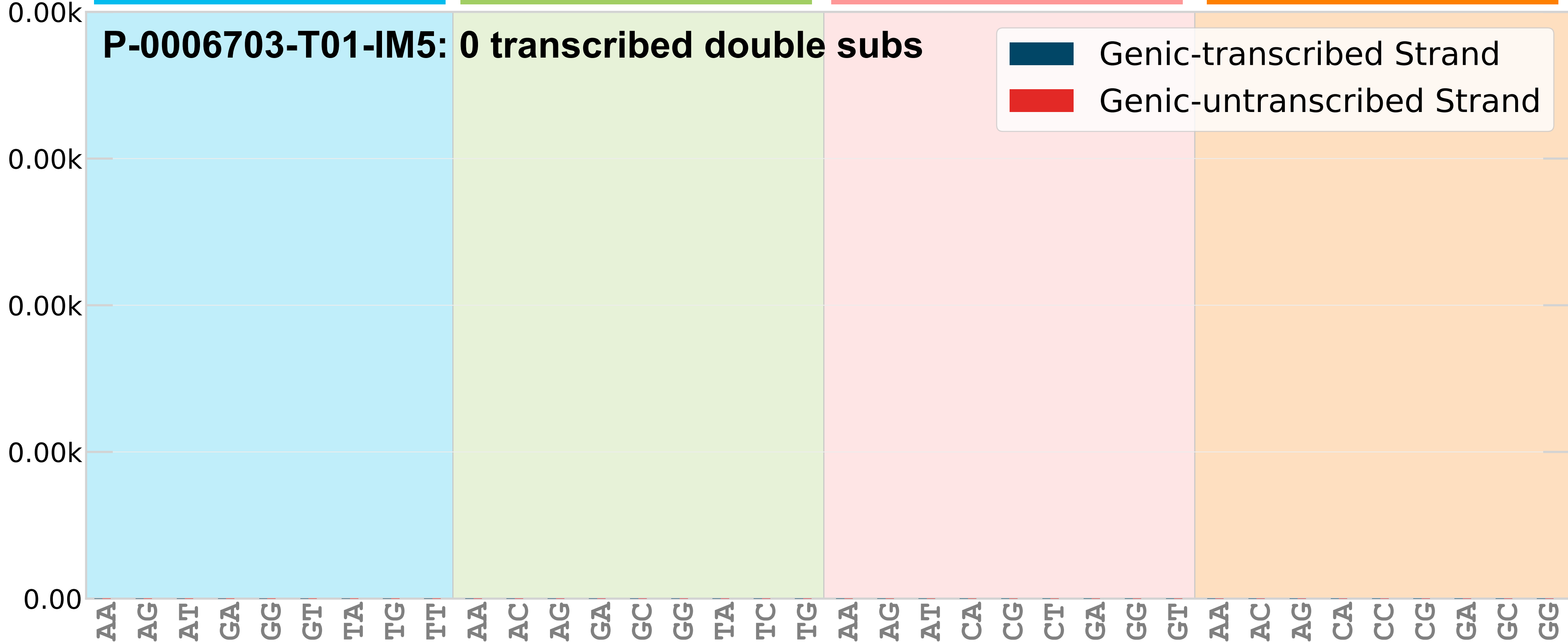


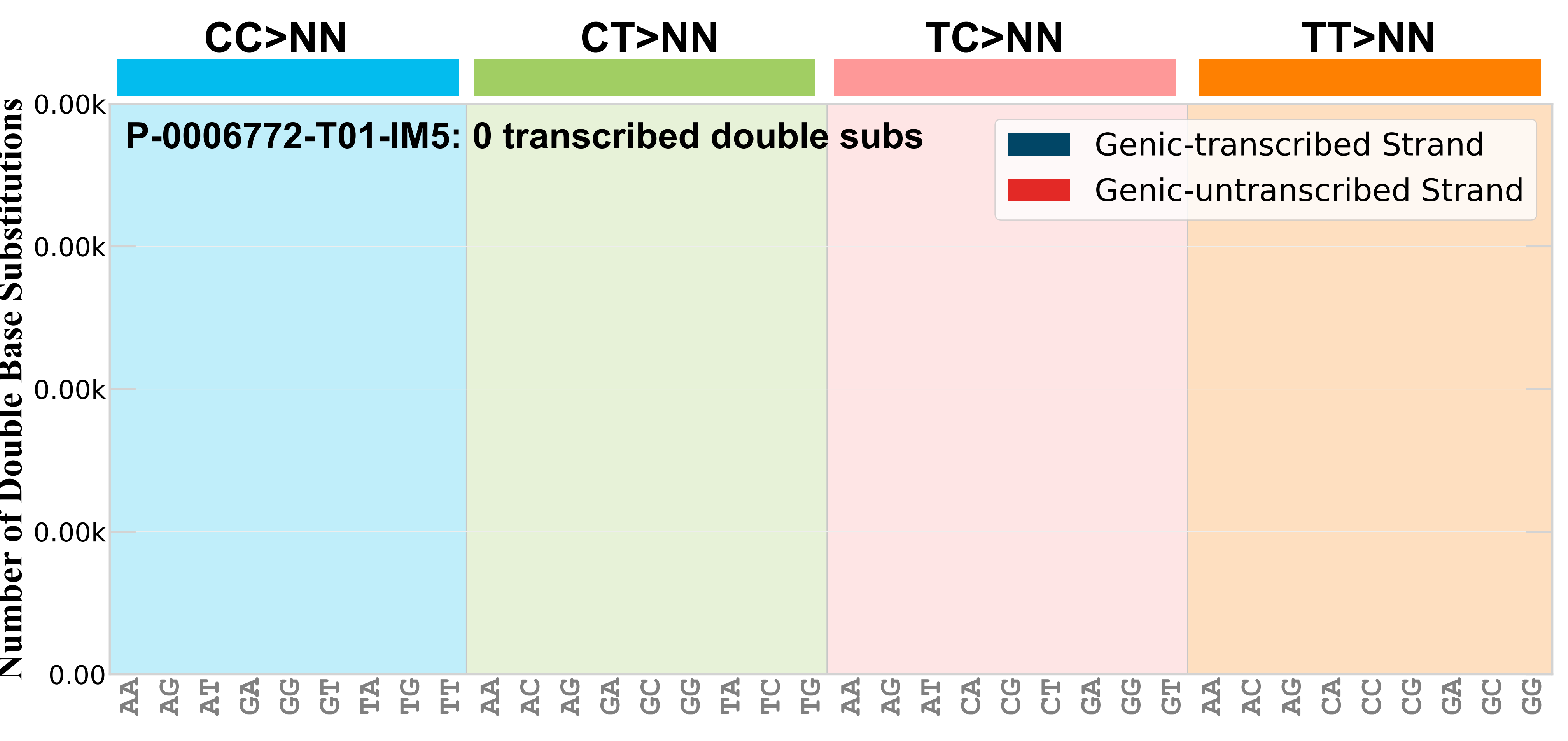
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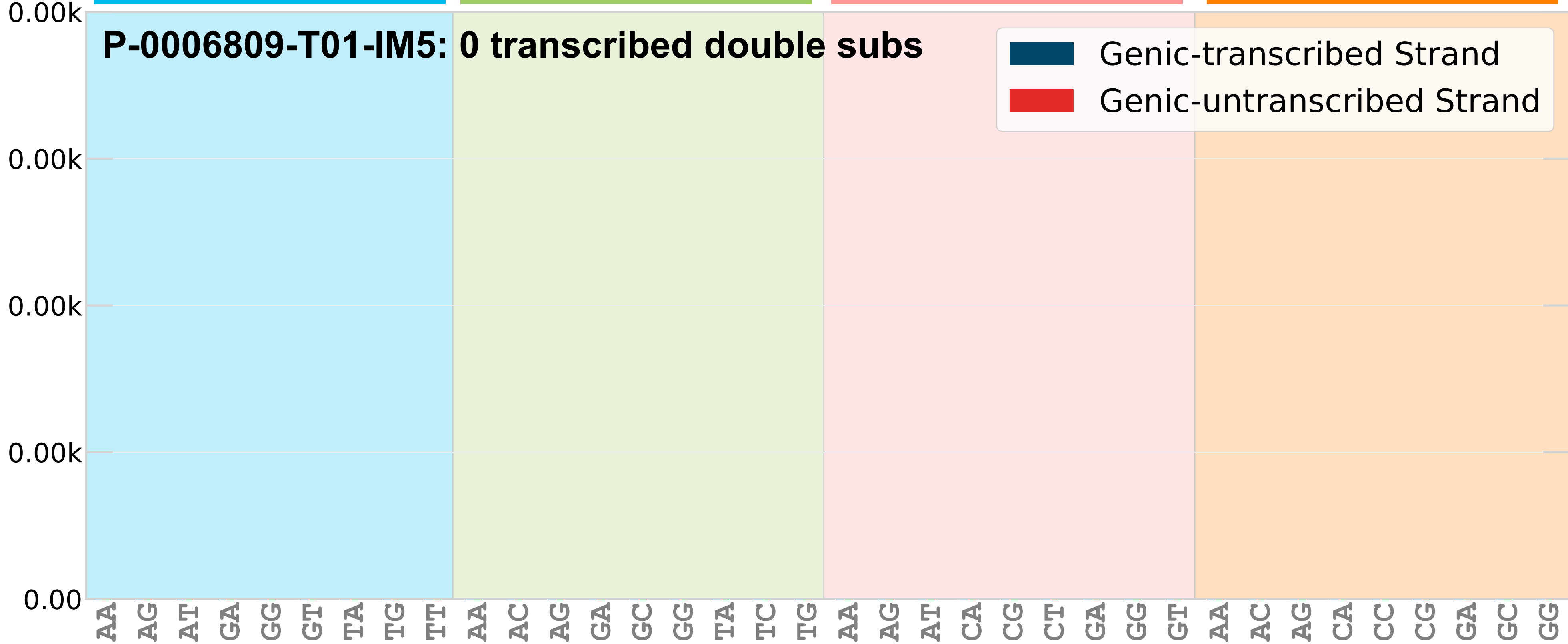


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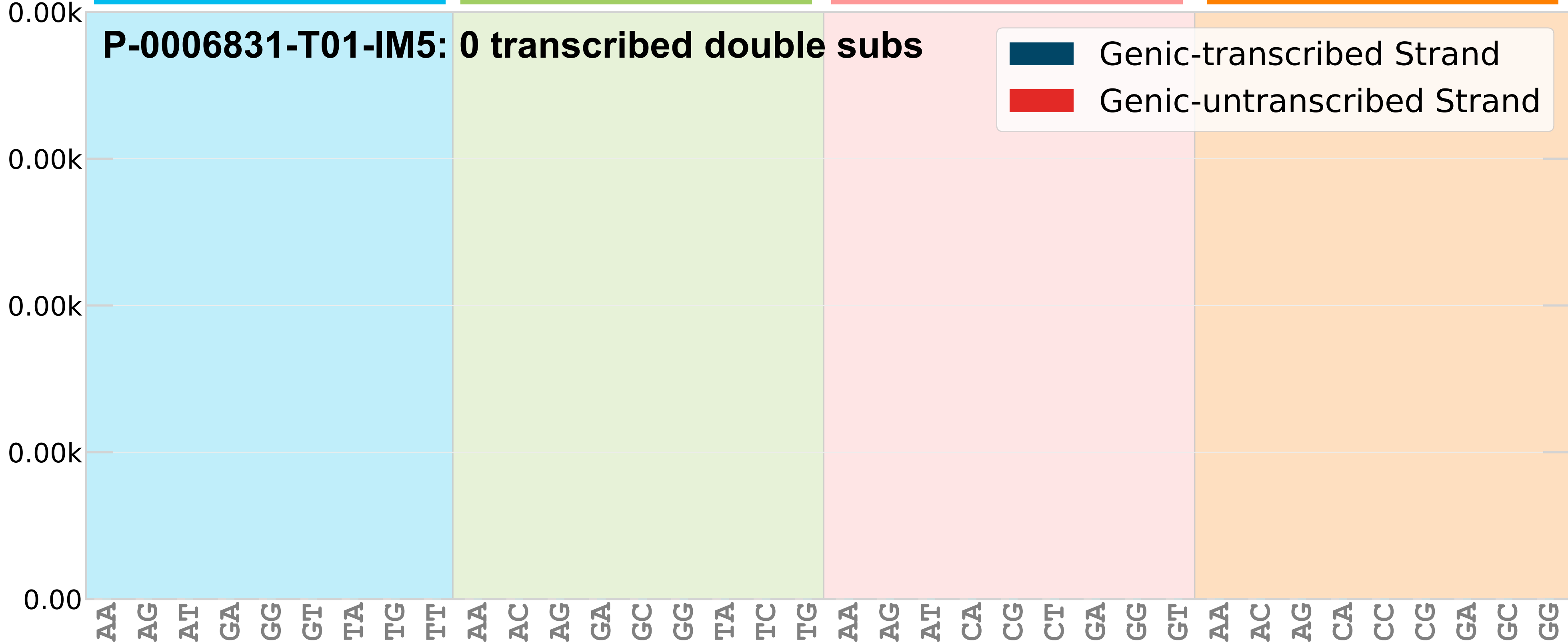


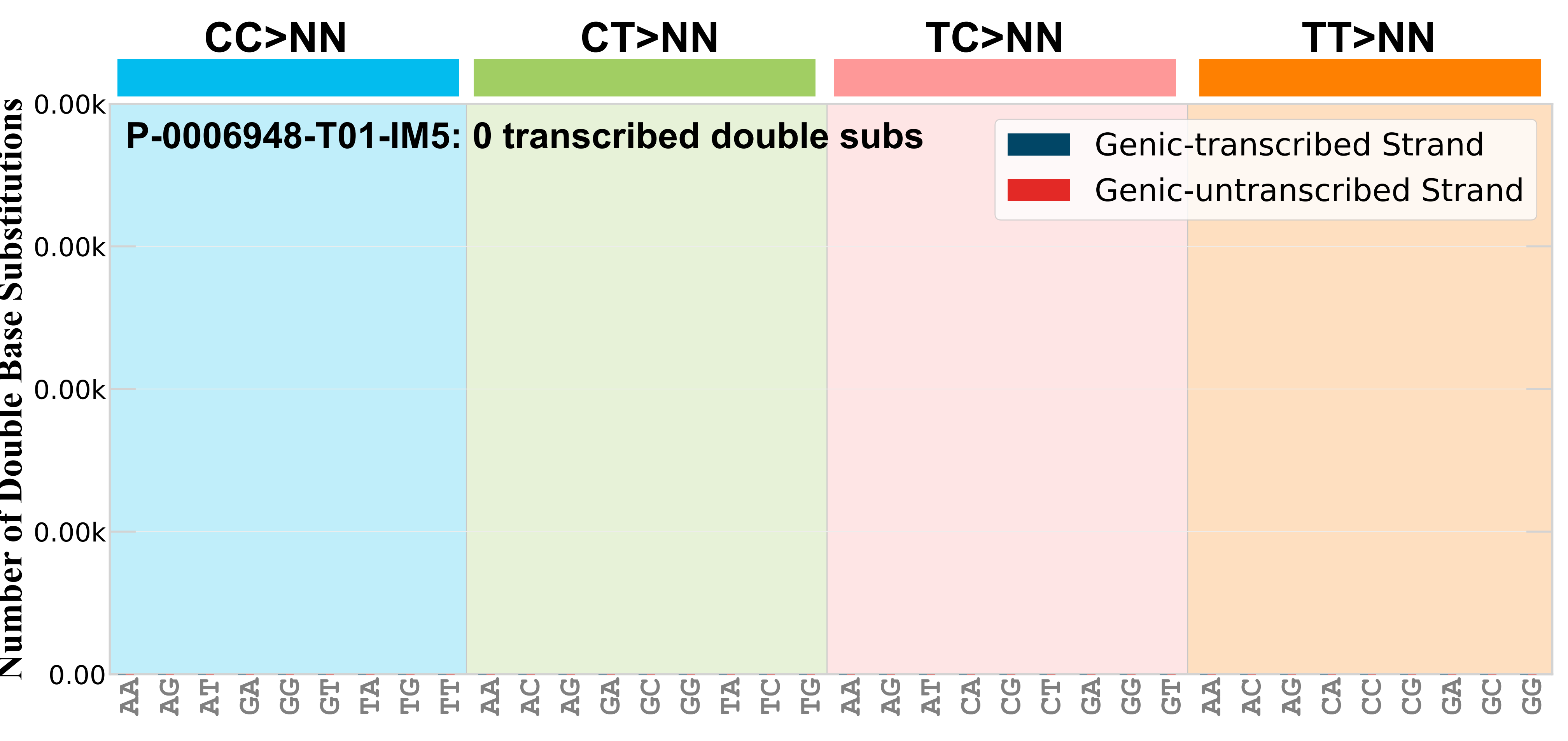


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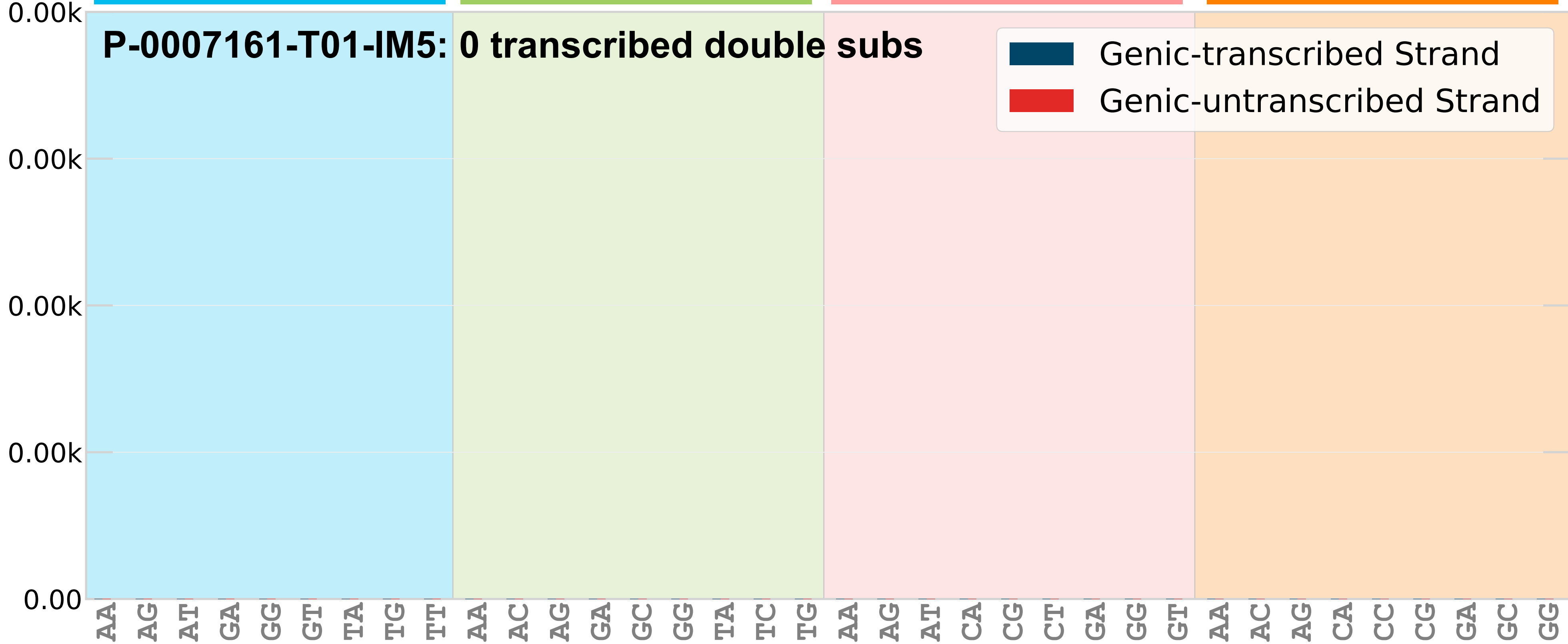


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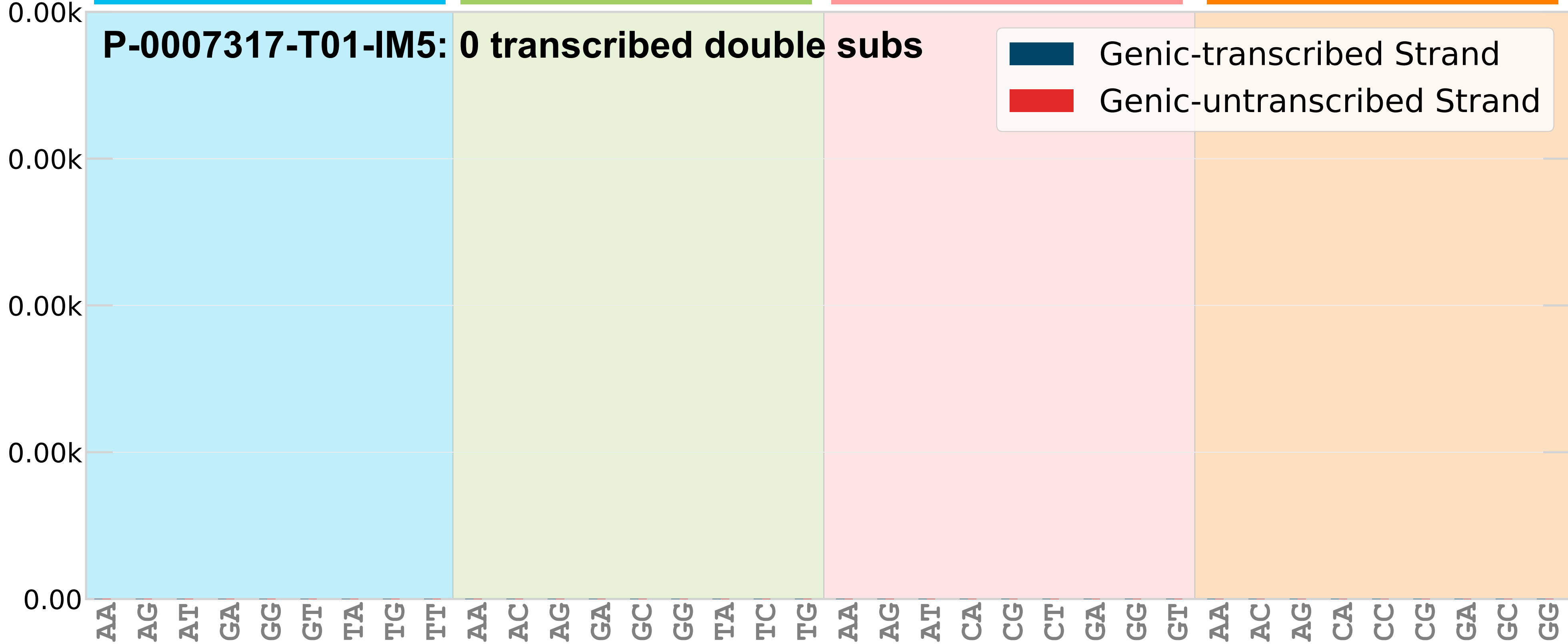




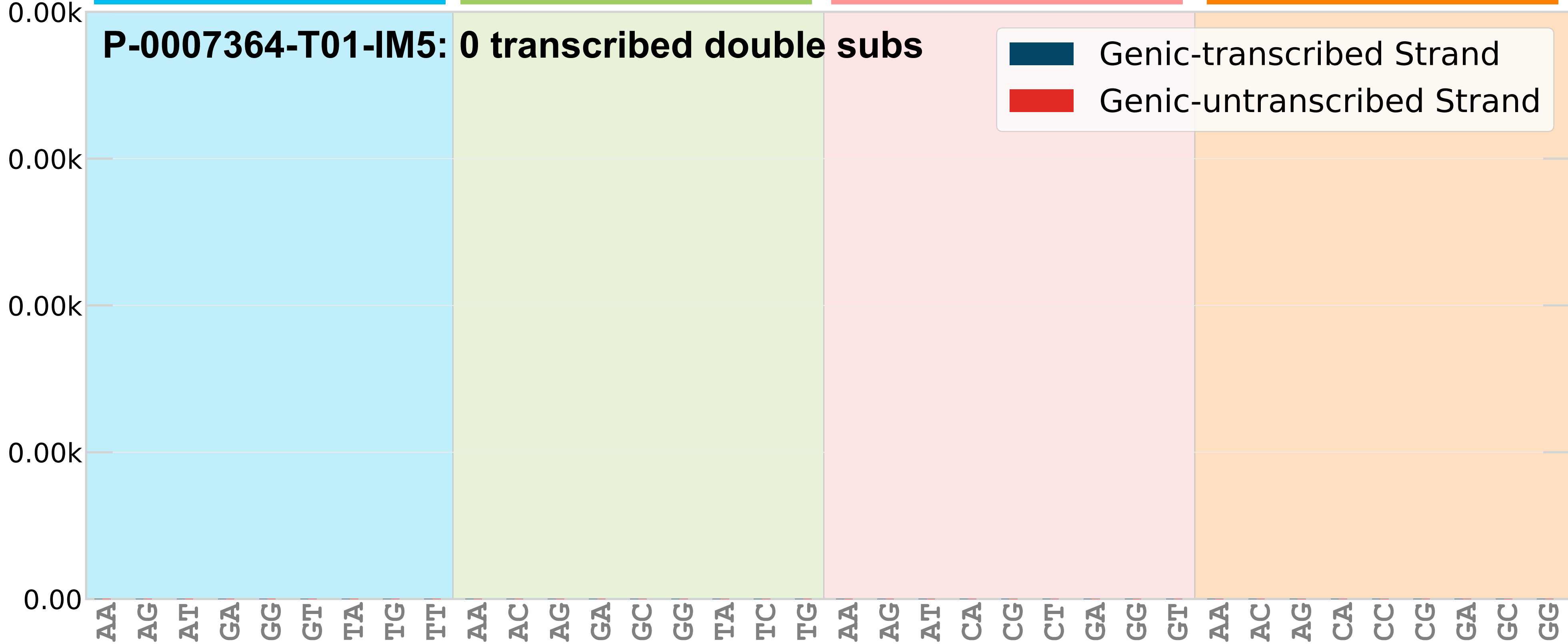
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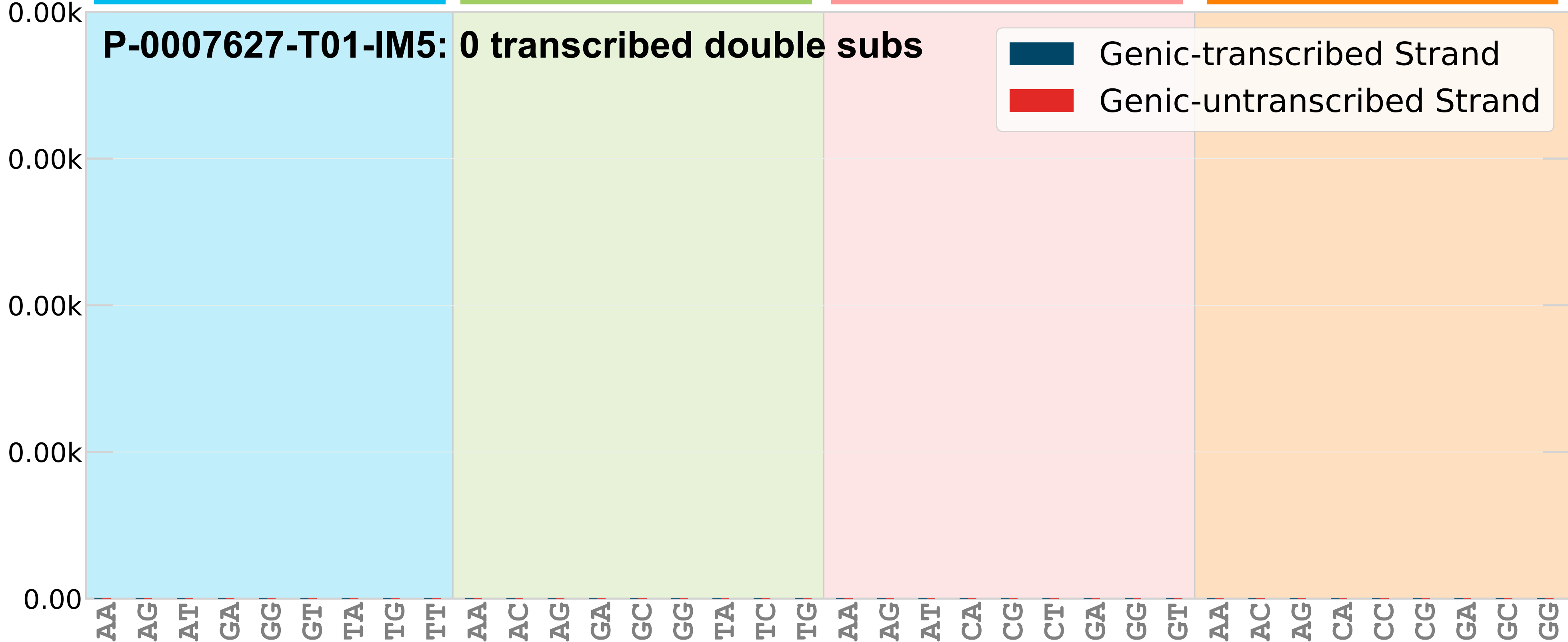
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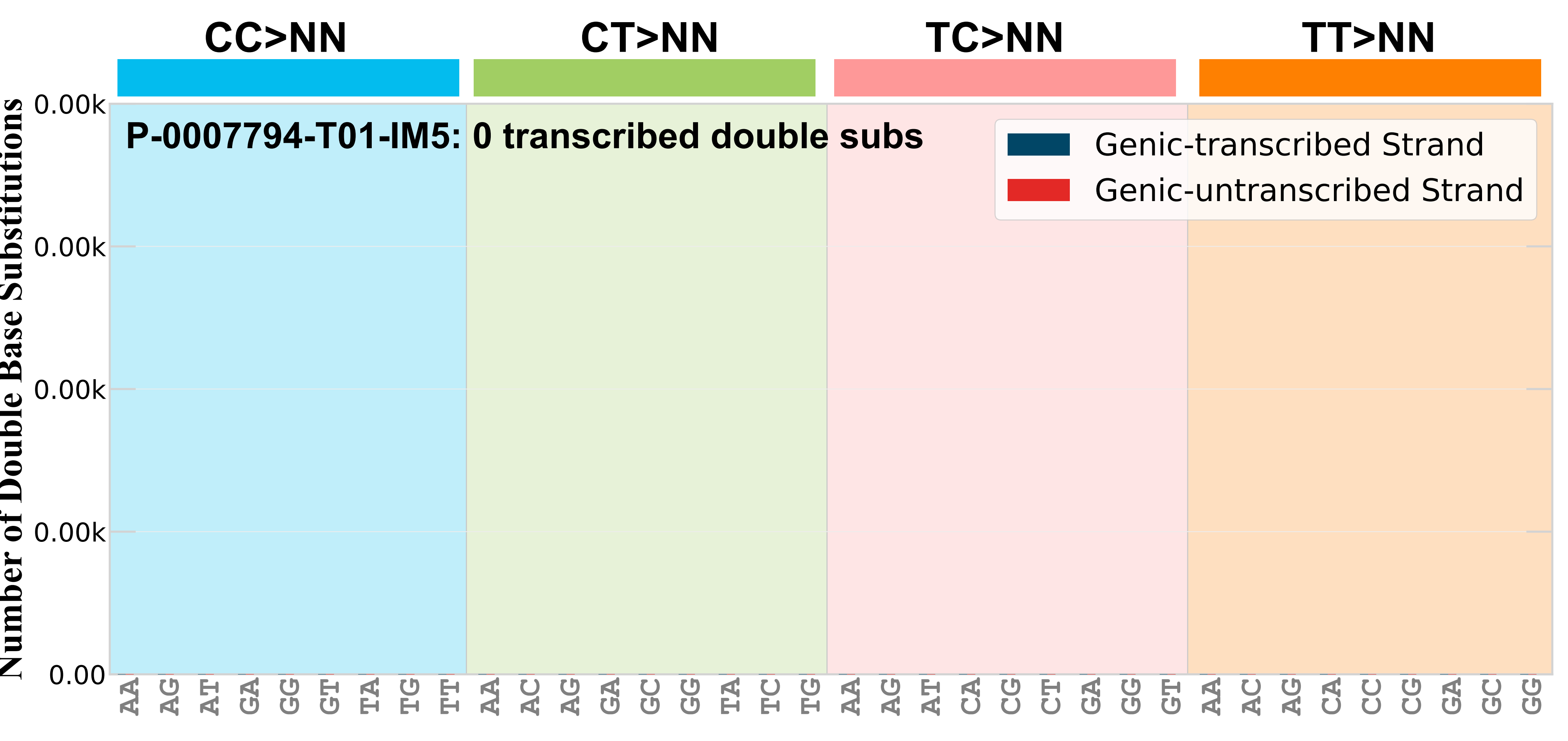


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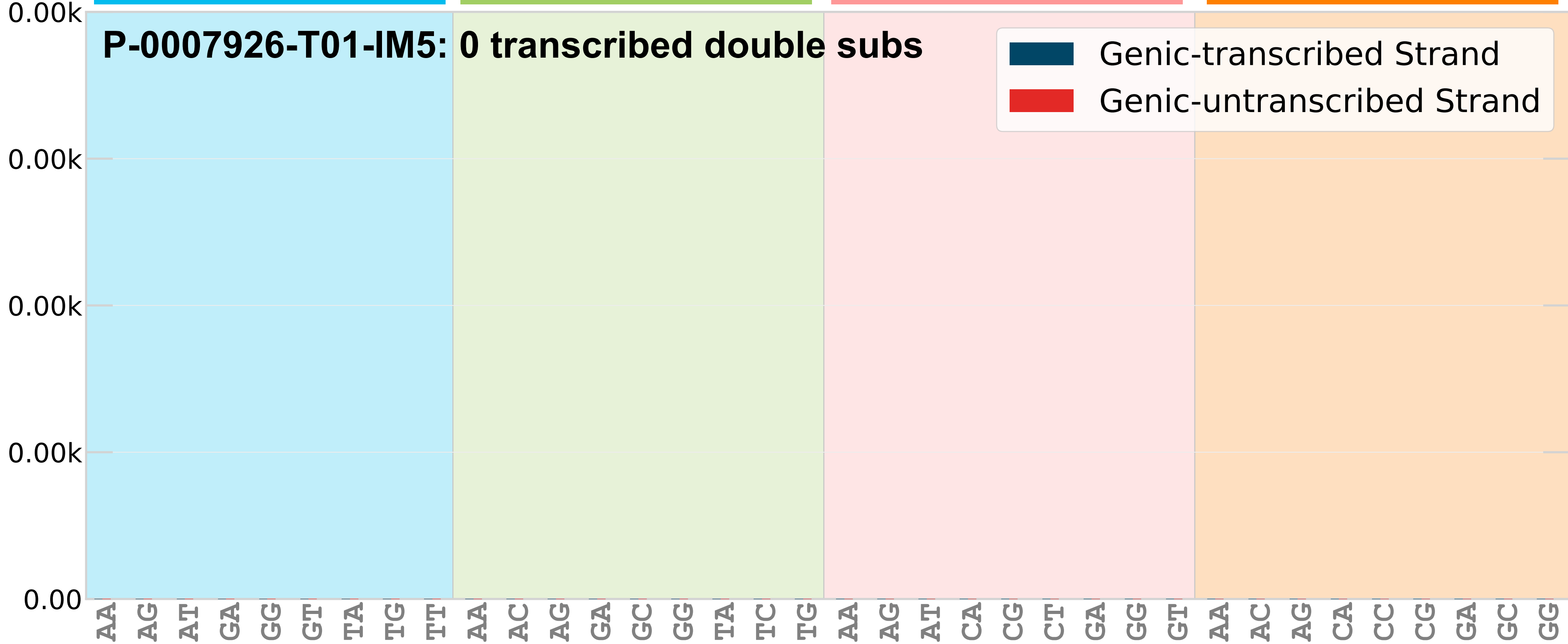


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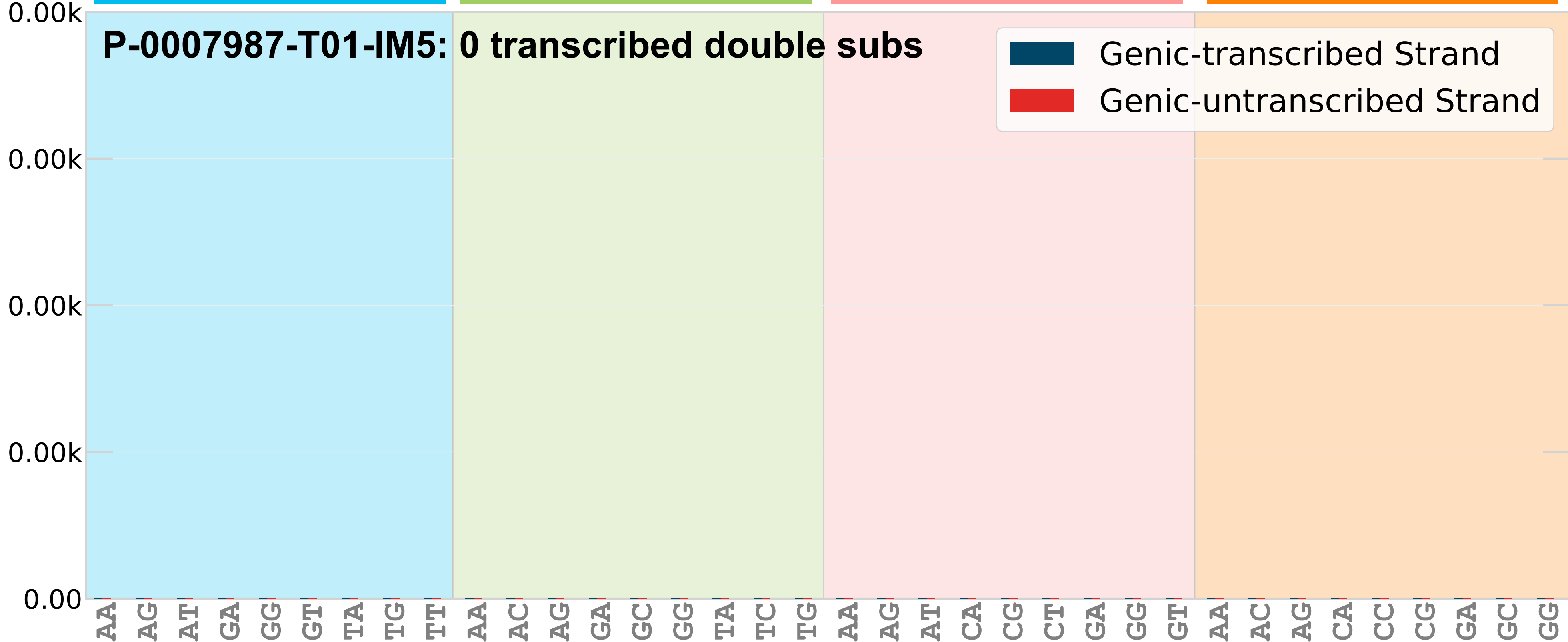




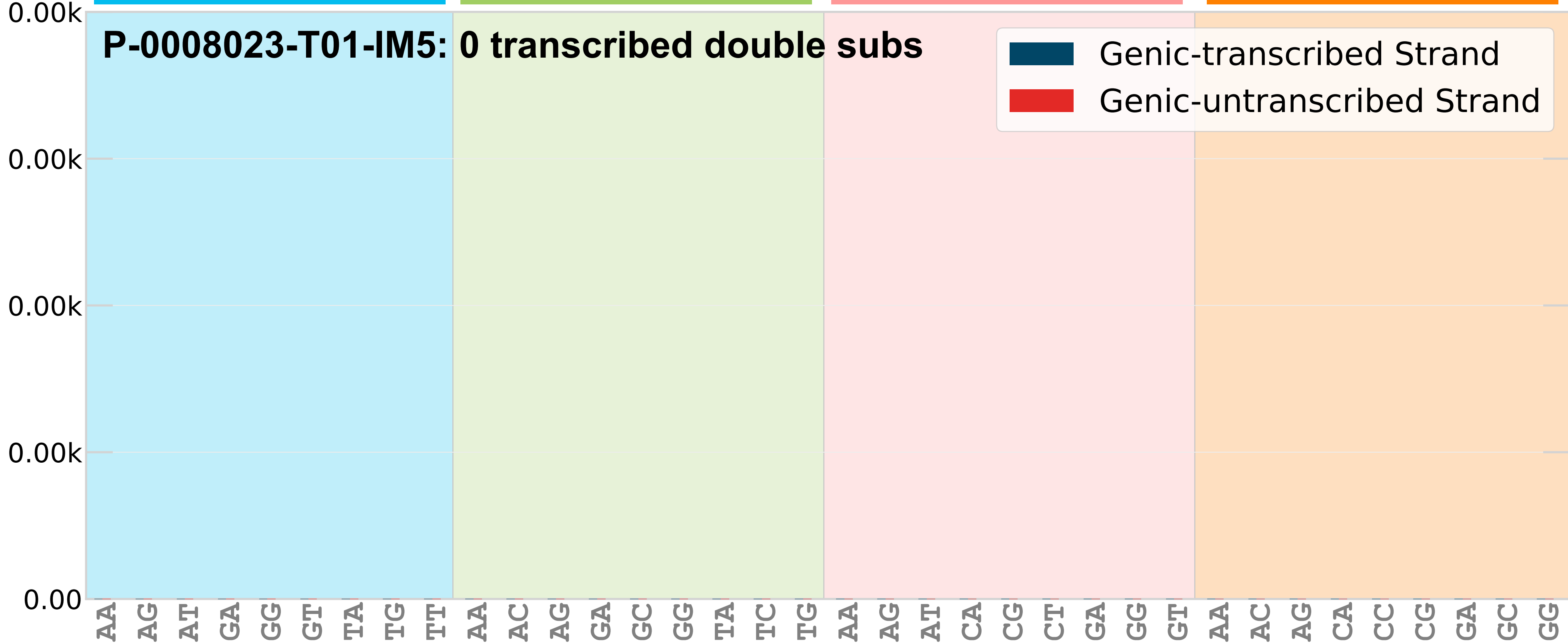
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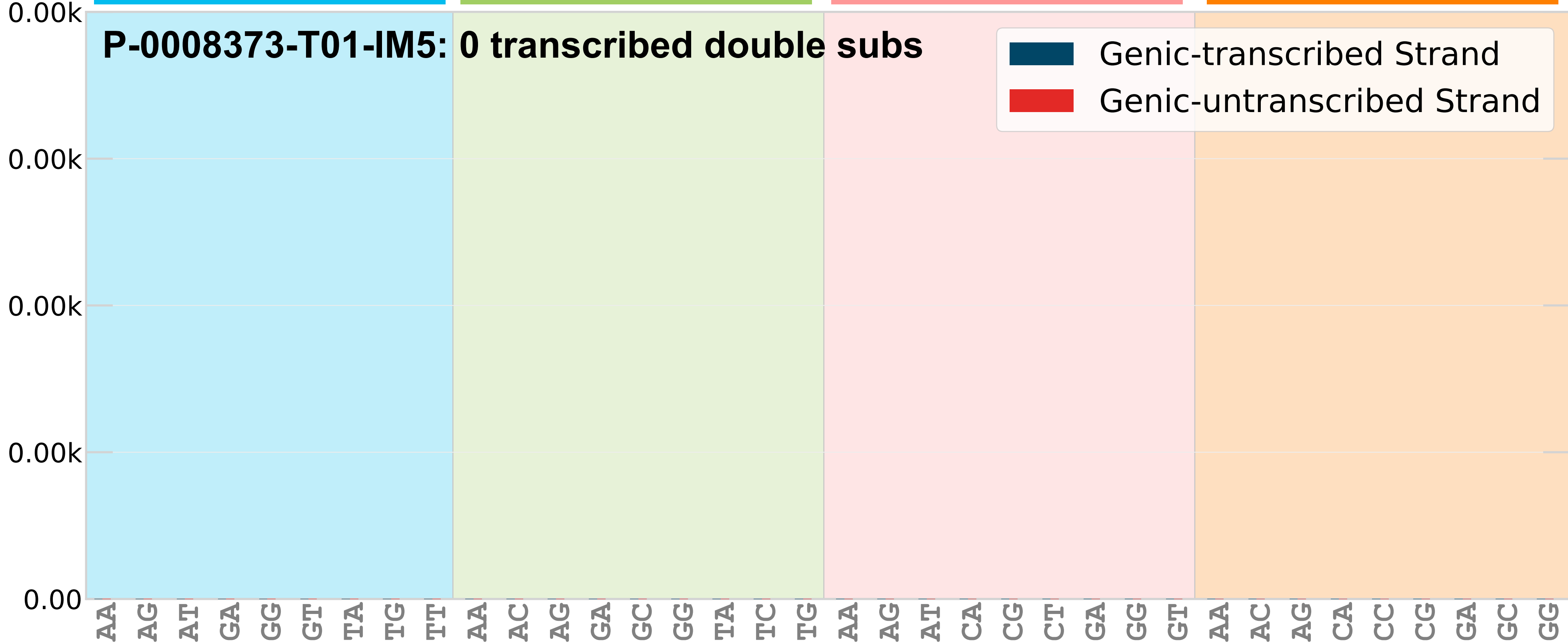
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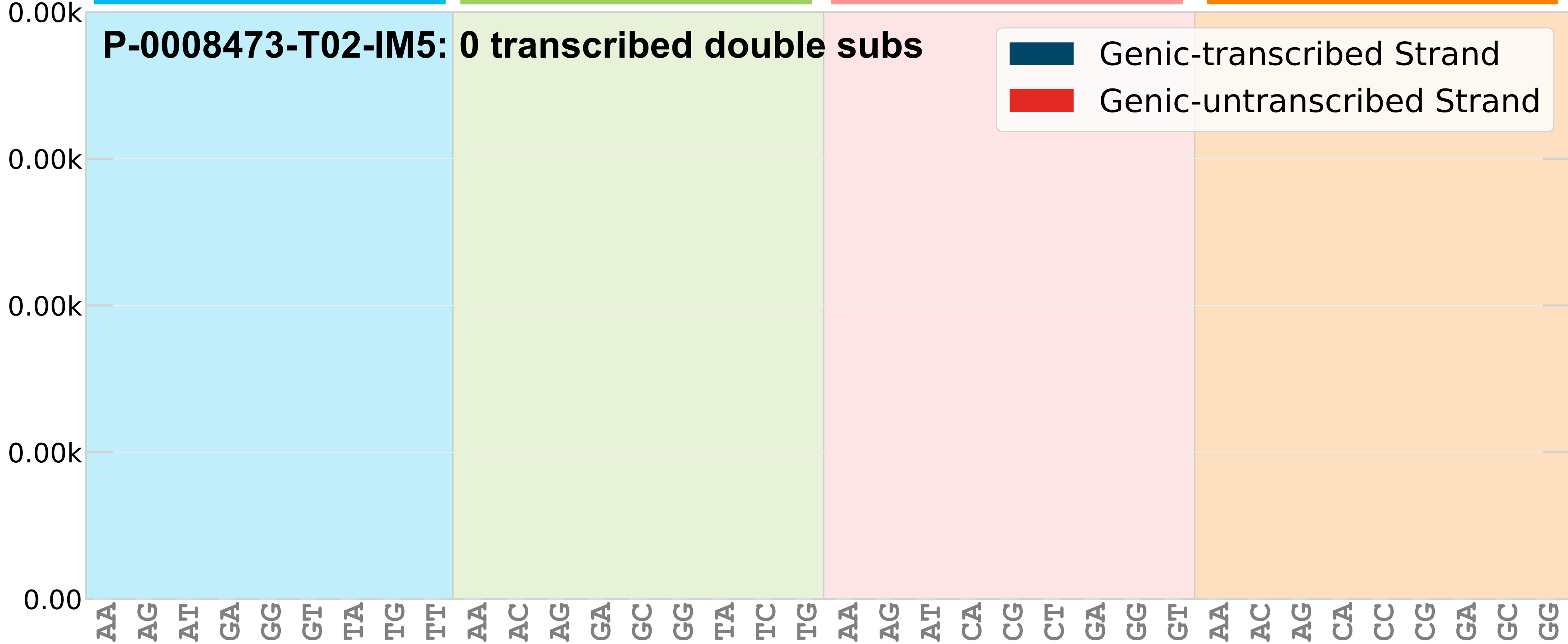
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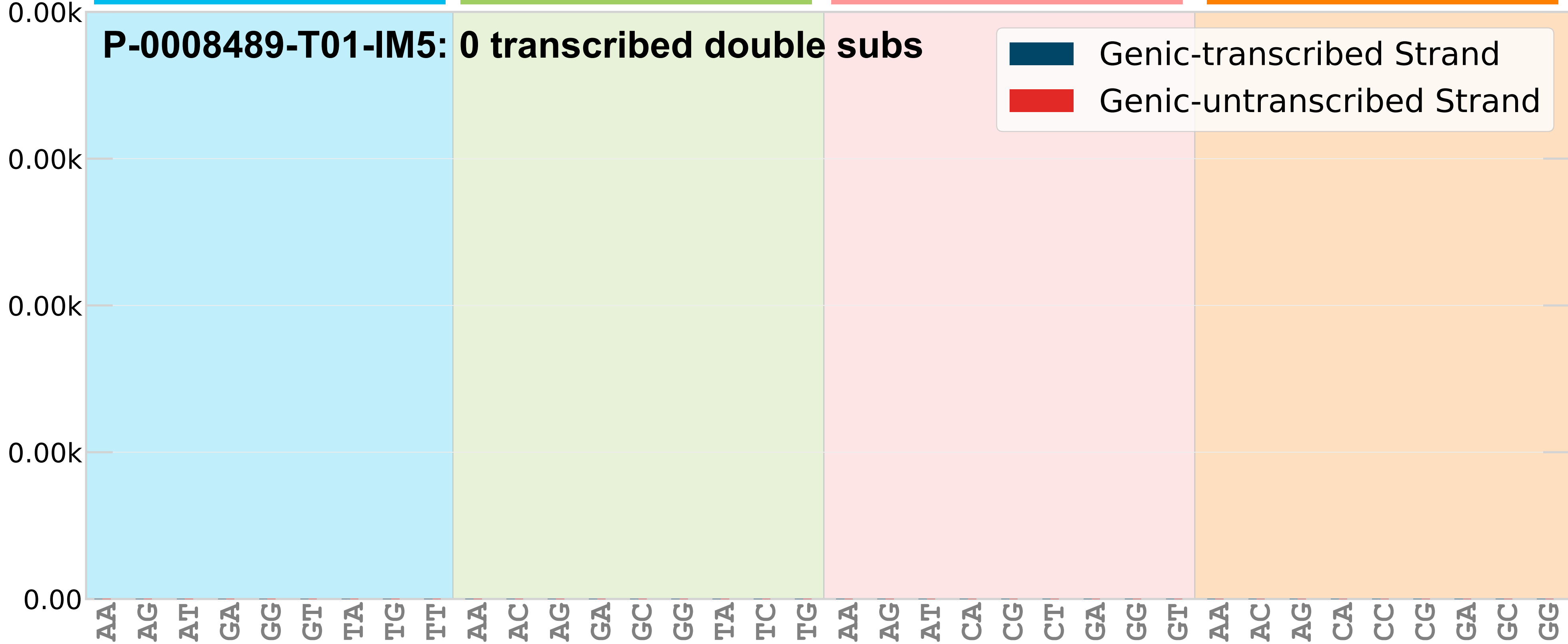
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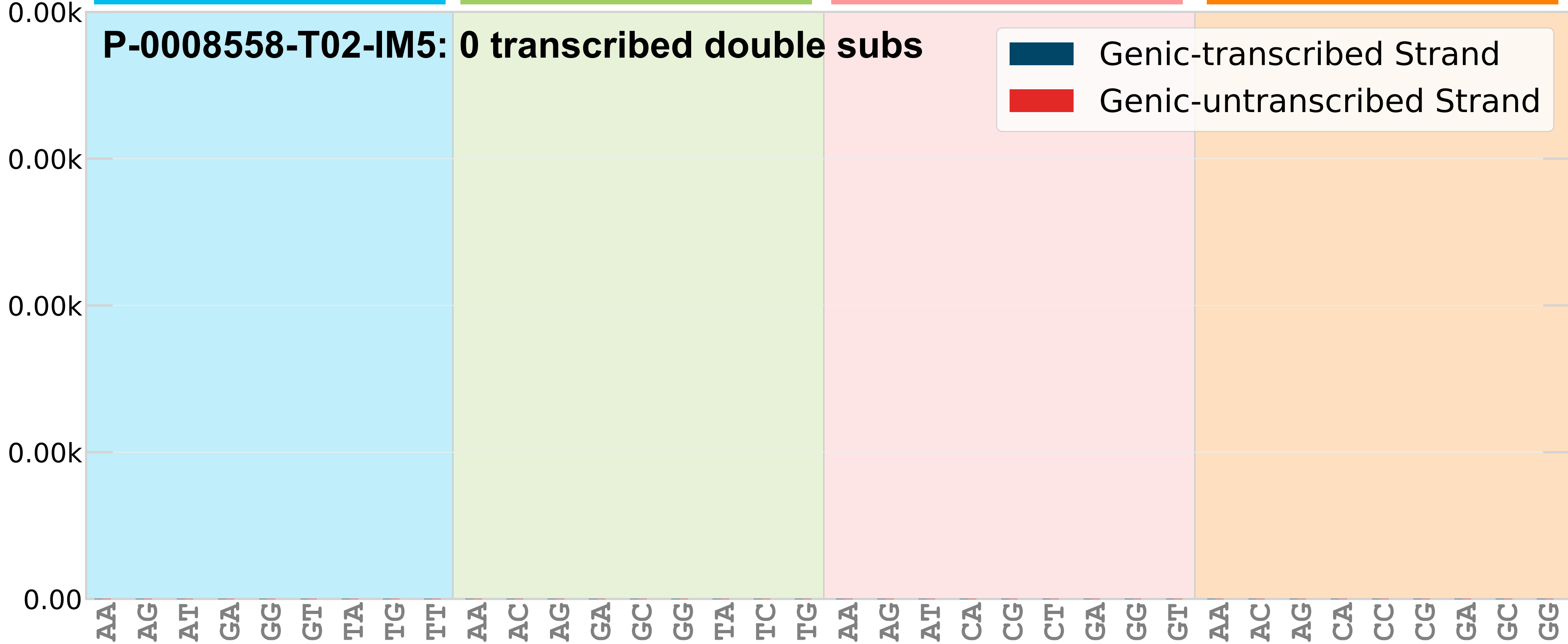
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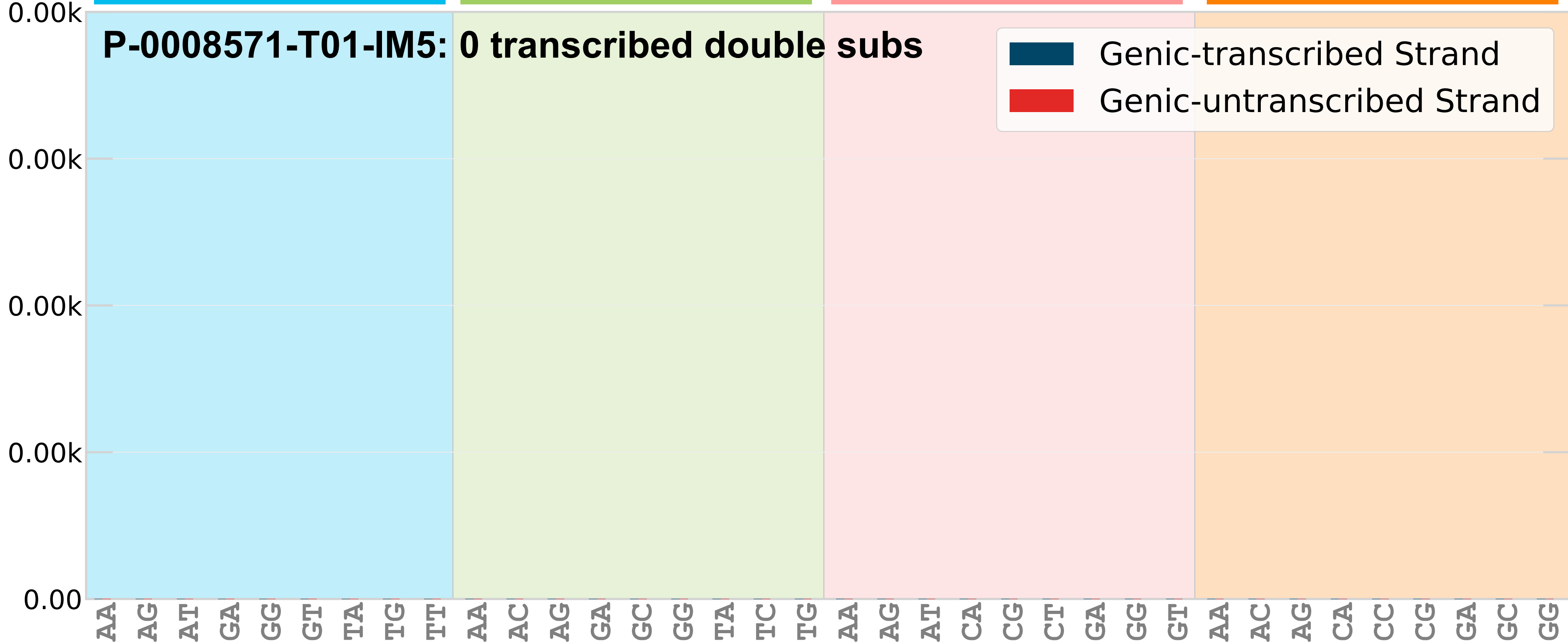
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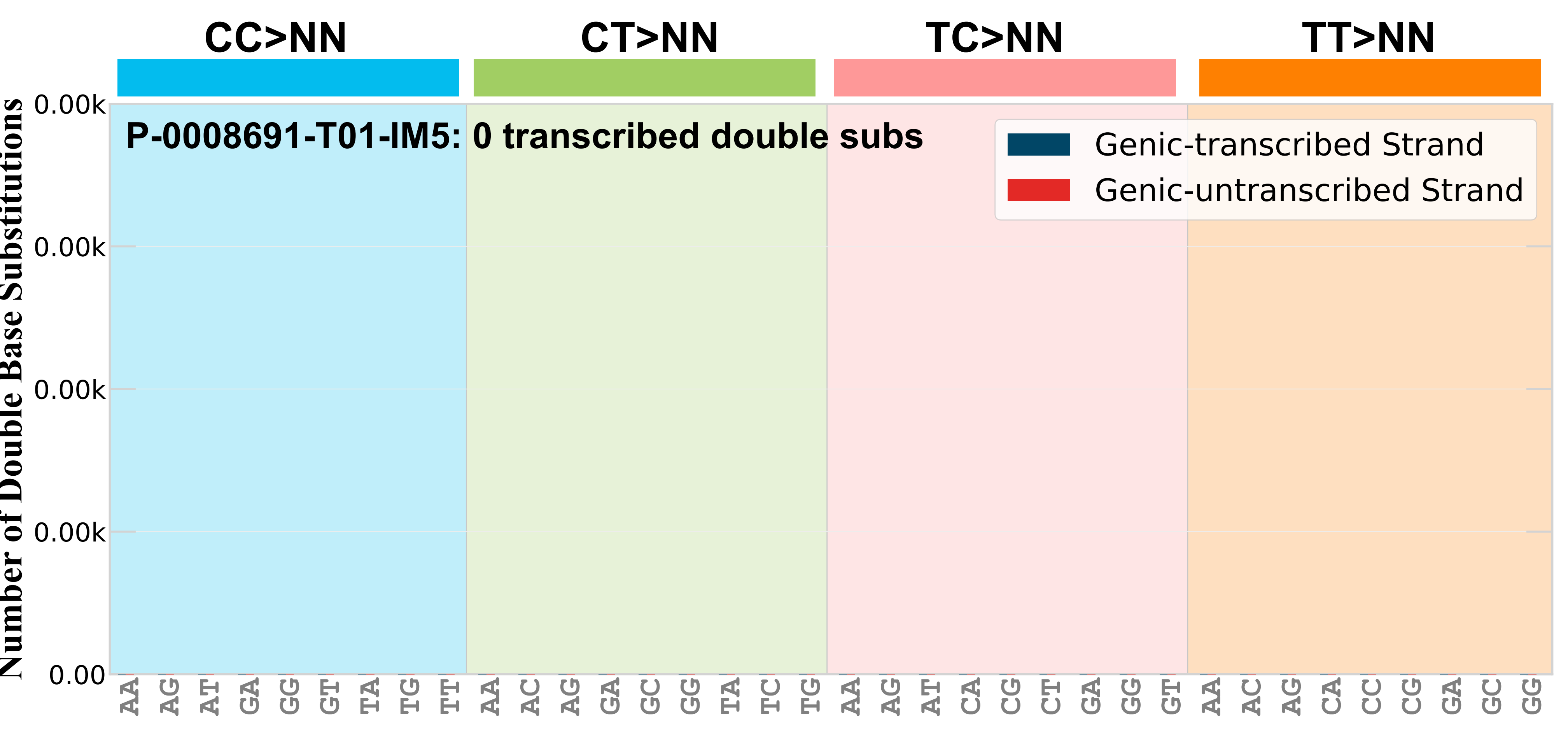


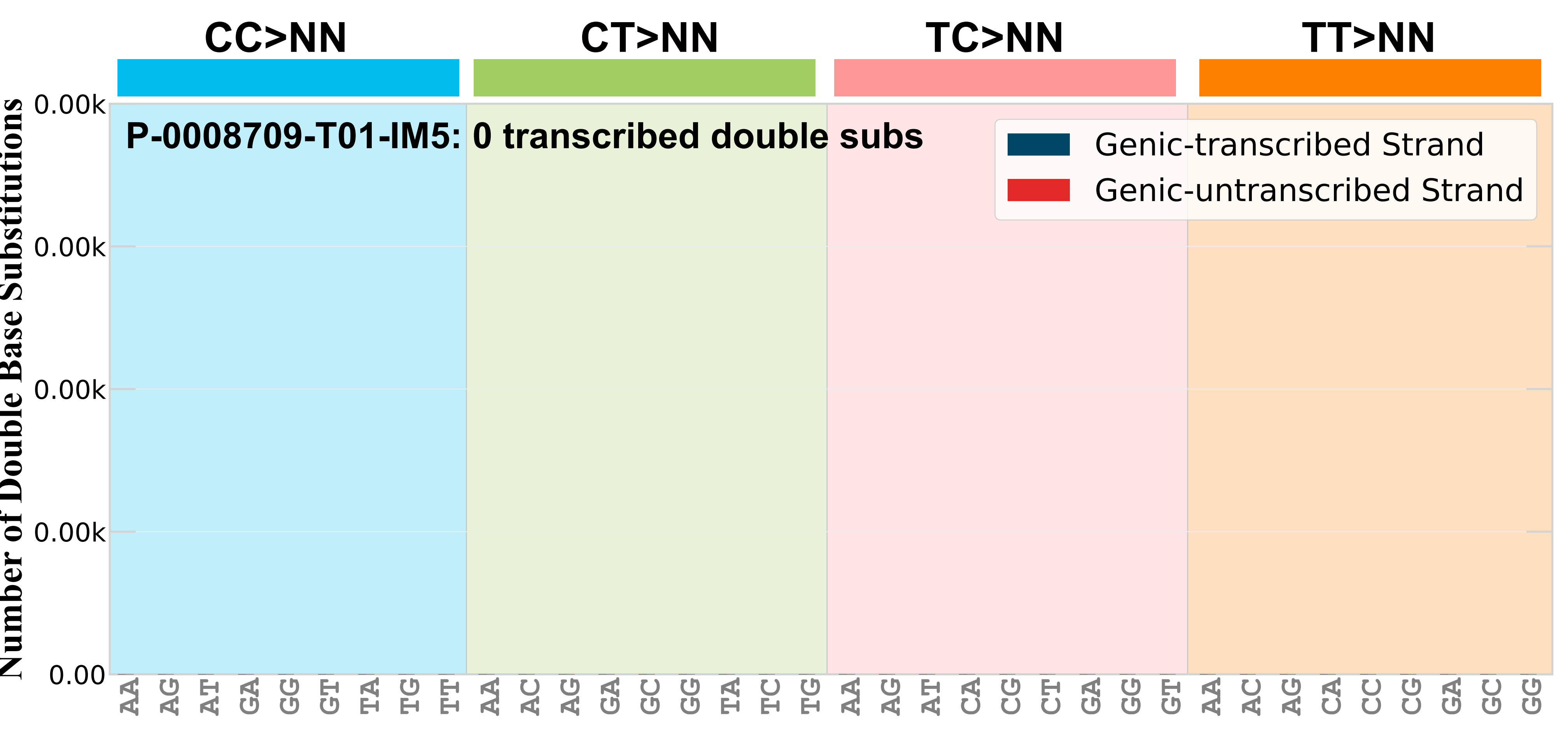
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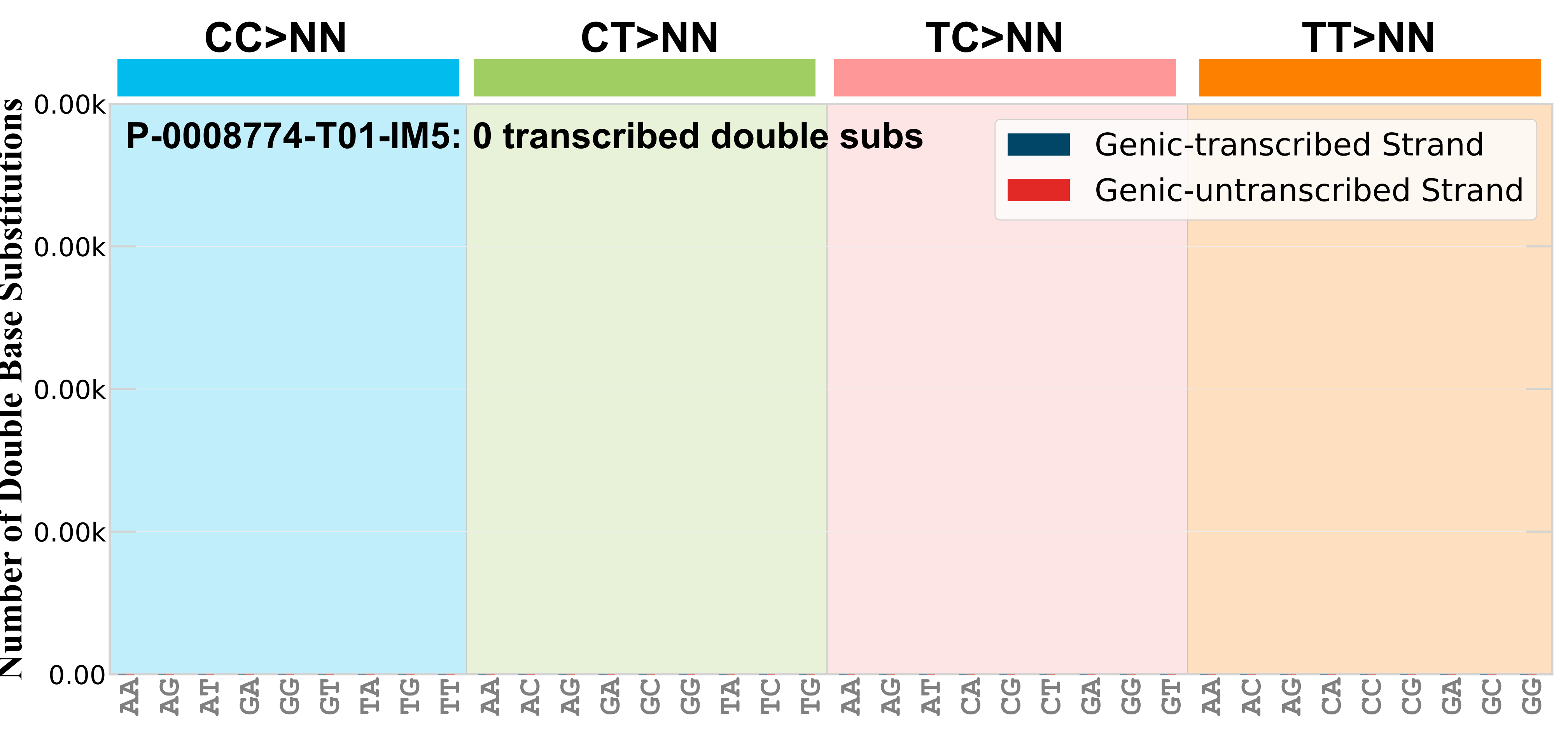


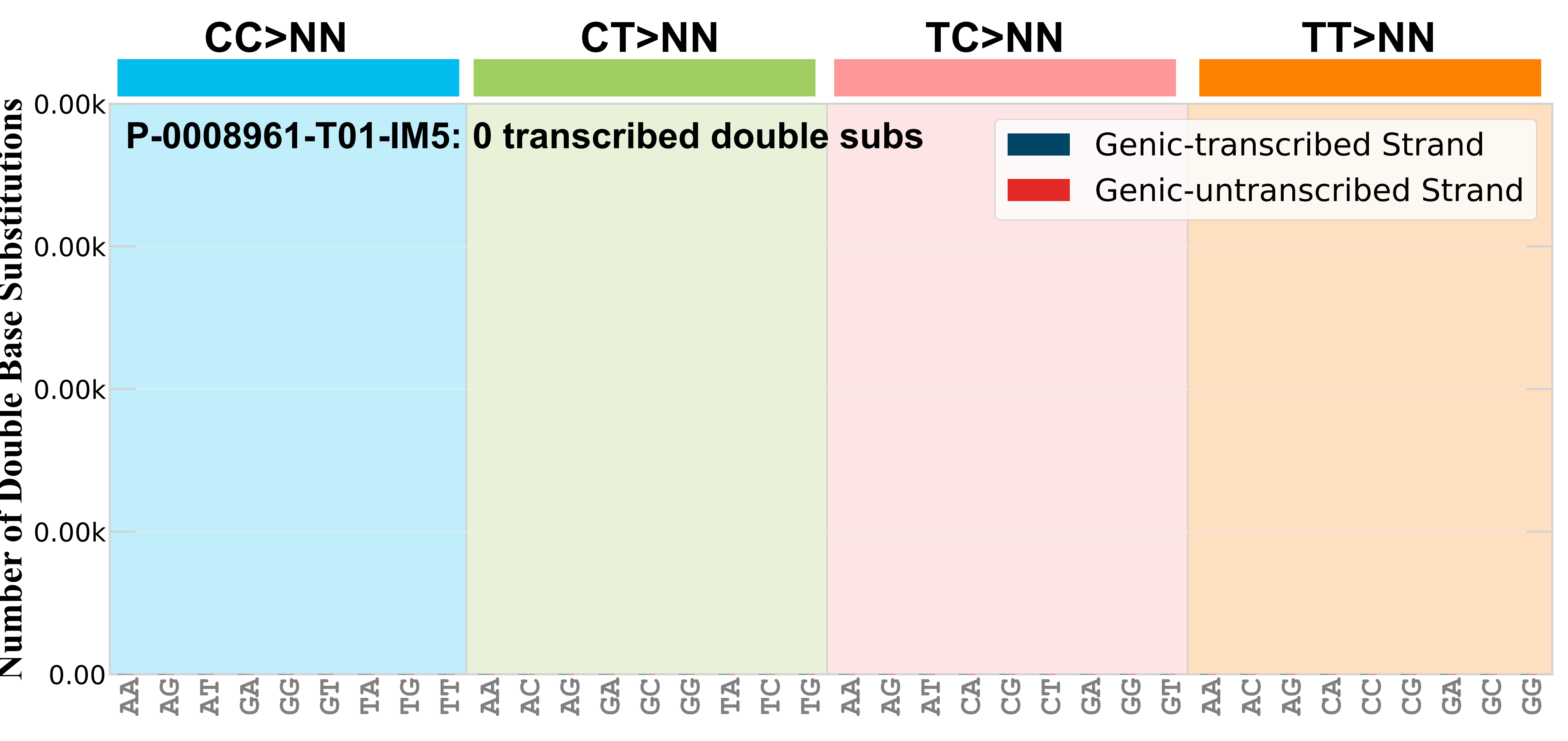
TT>NN











Number of Double Base Substitutions

CC>NN

CT>NN

TC>NN

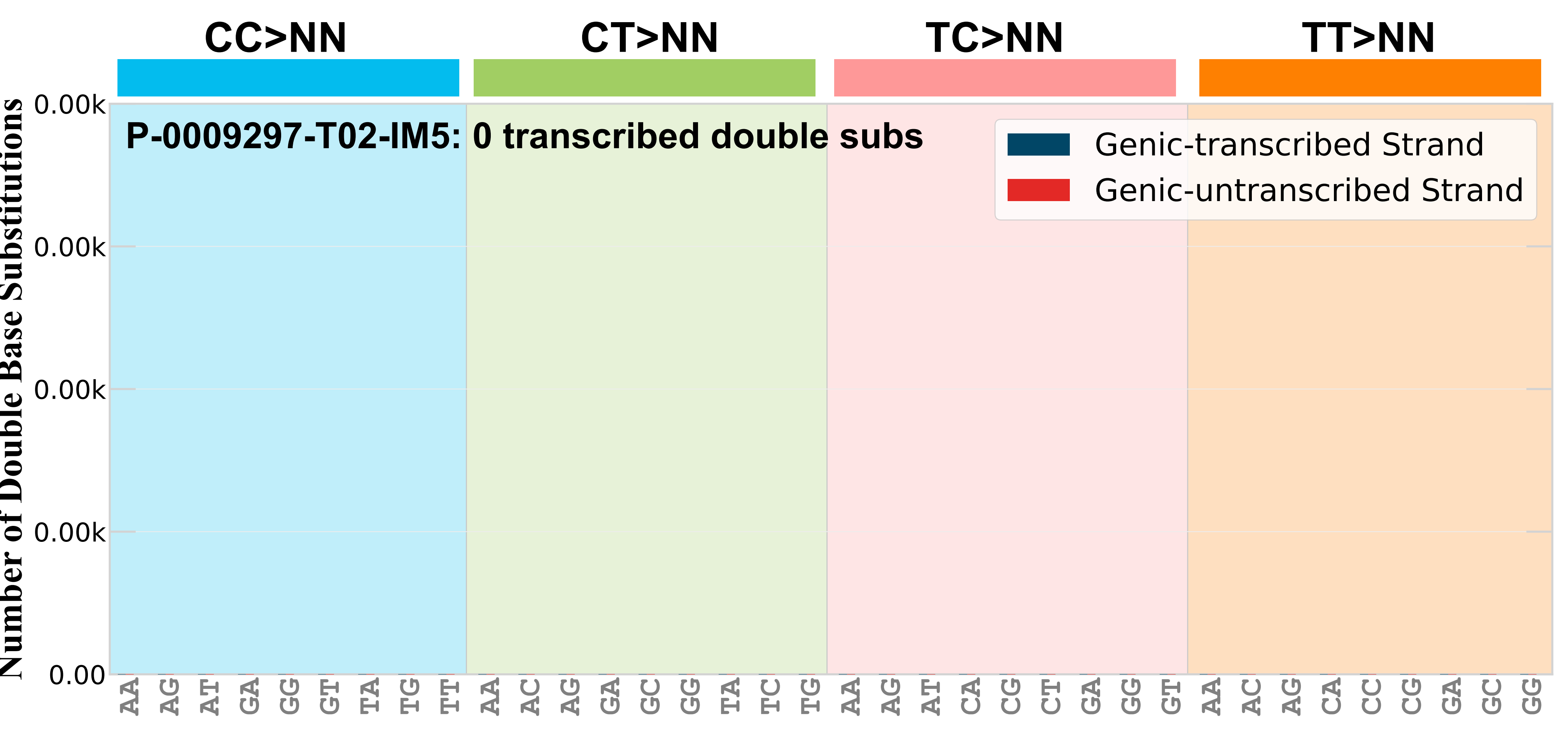
TT>NN

P-0009221-T01-IM5: 0 transcribed double subs

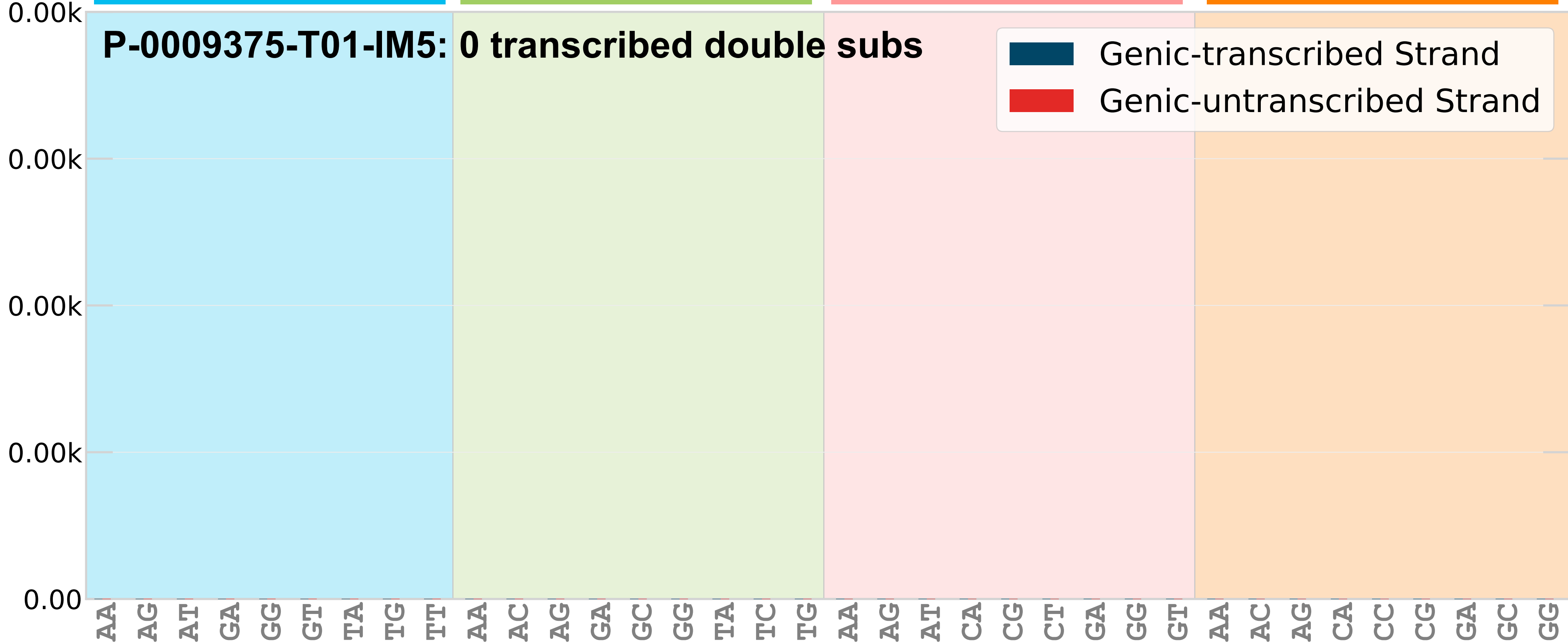
Genic-transcribed Strand

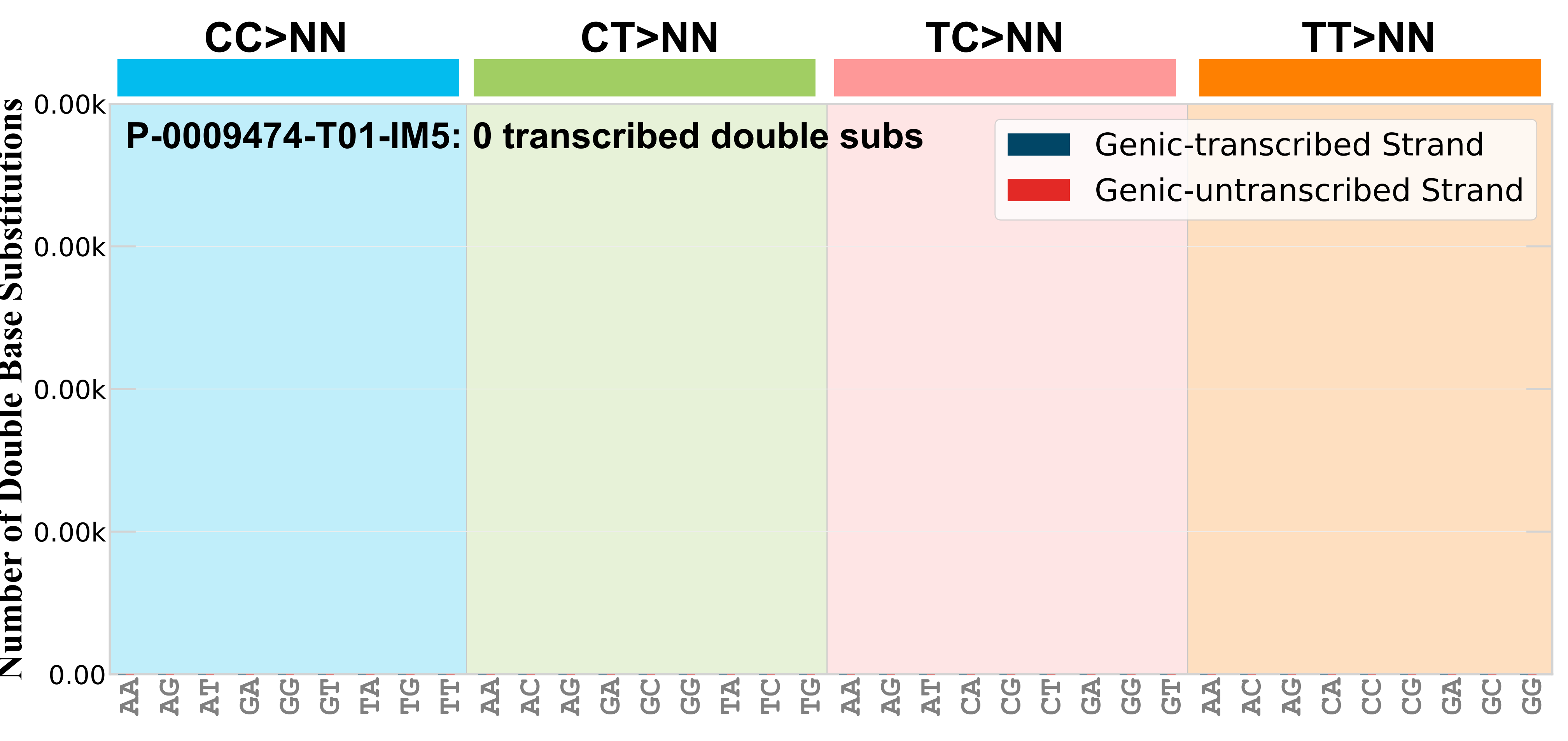
Genic-untranscribed Strand

AA AG AT GA GG GT TA TG TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG CT GA GG GT AA AC AG CA CC CG GA GC GG

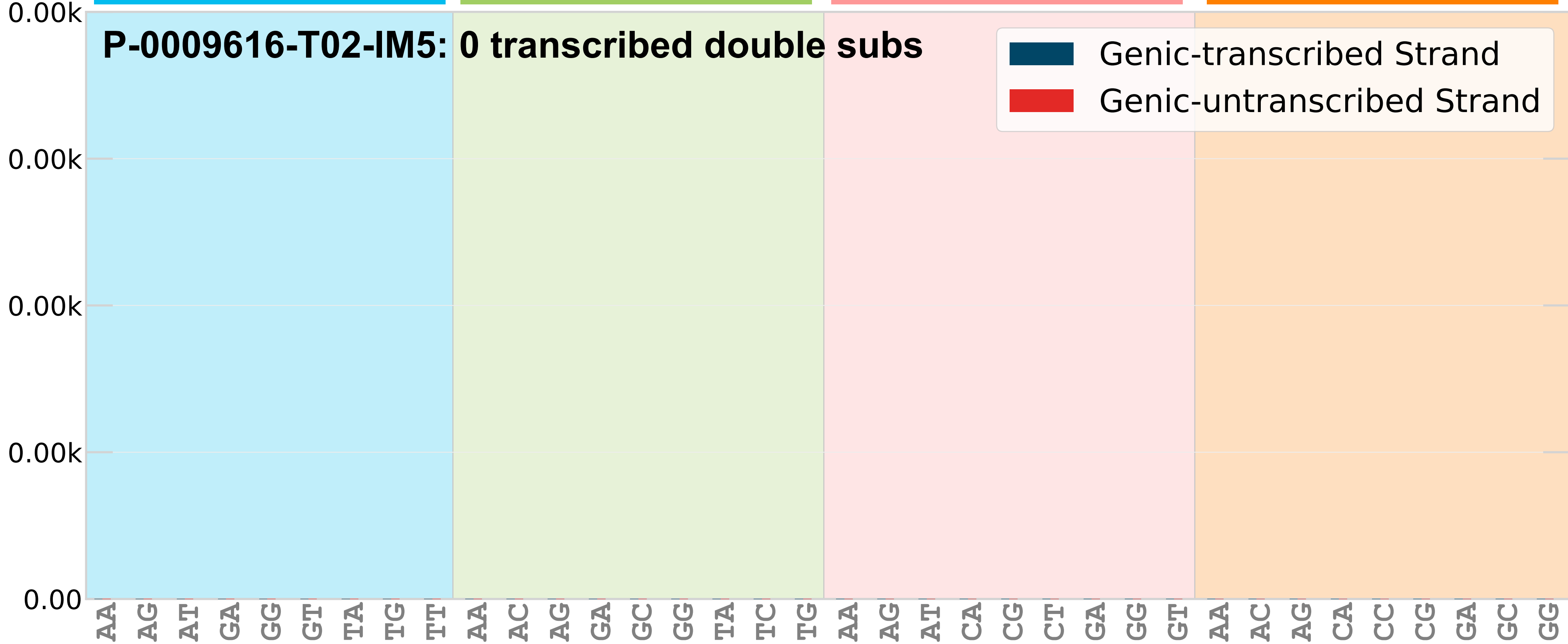


TT>NN

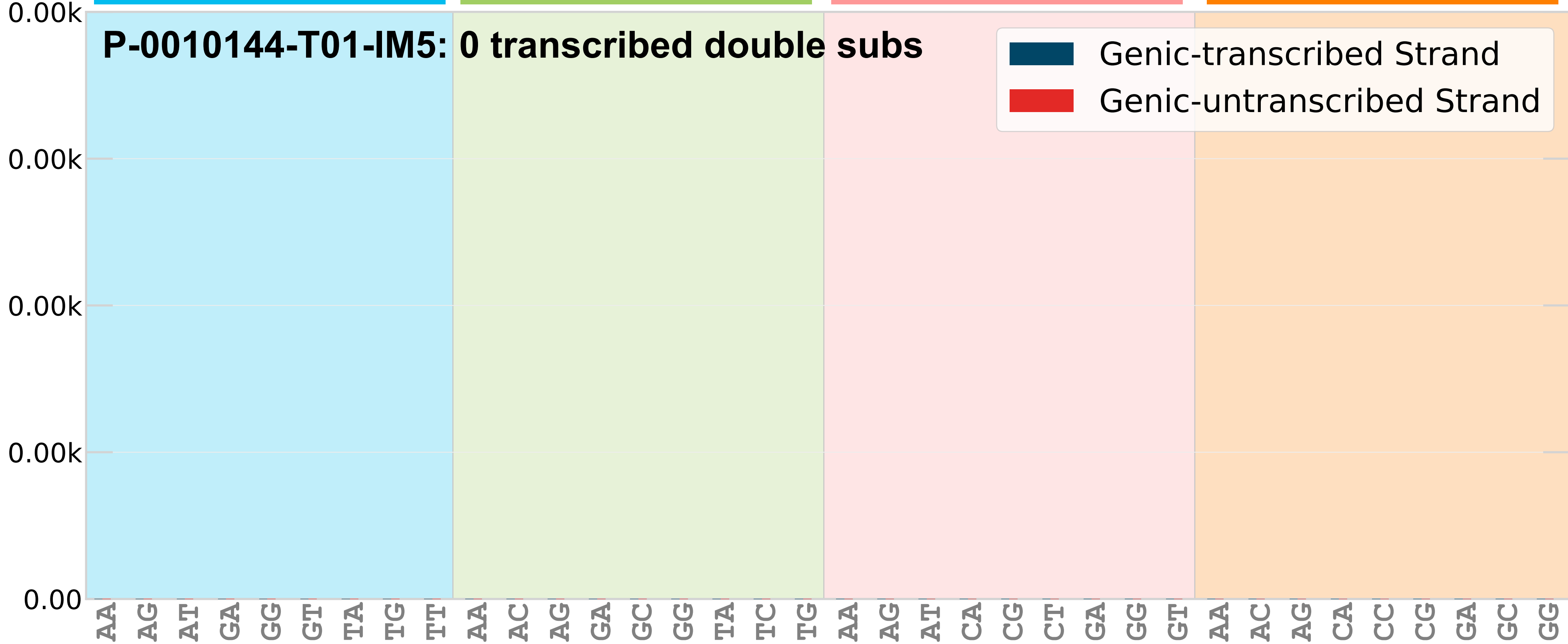




TT>NN



TT>NN



Number of Double Base Substitutions

CC>NN

CT>NN

TC>NN

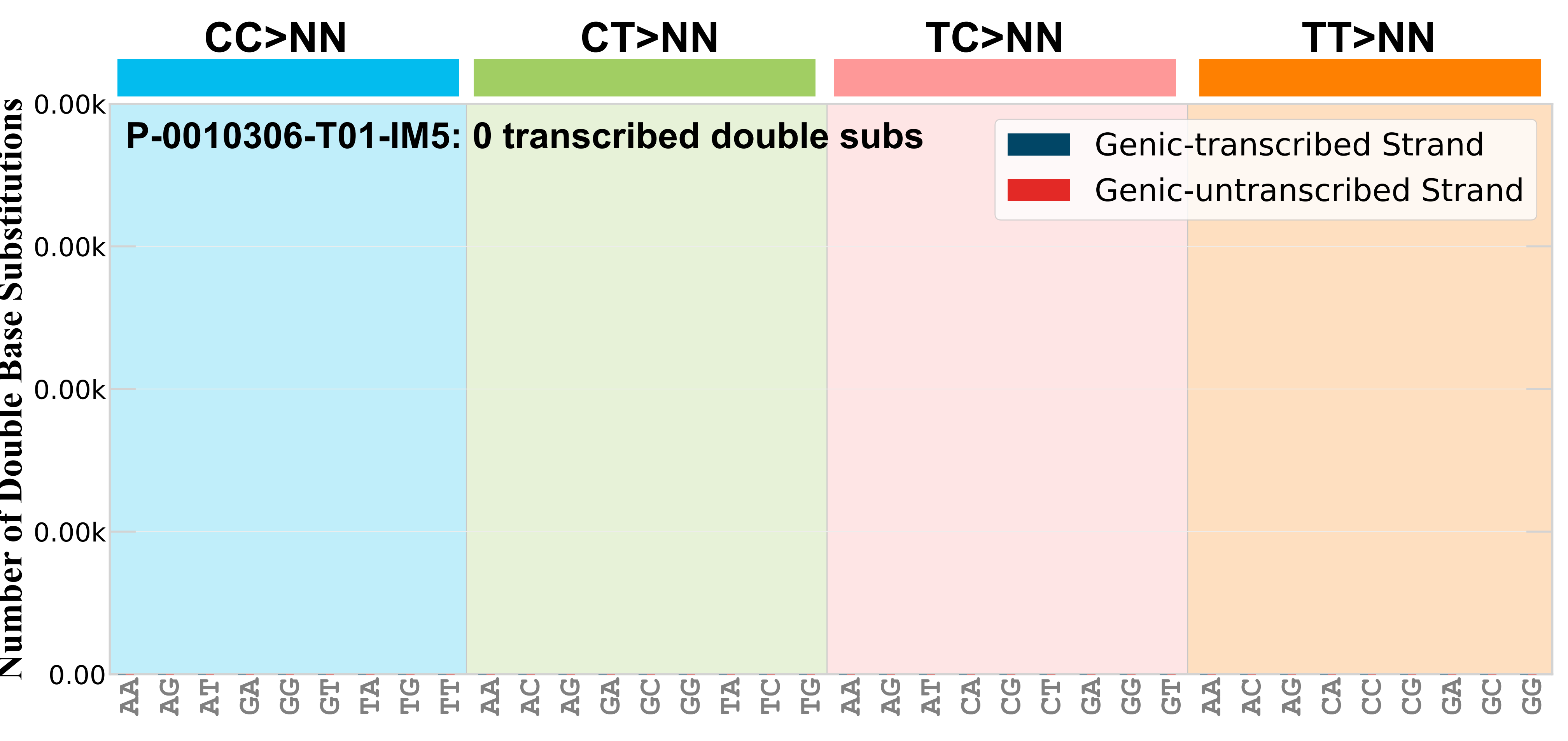
TT>NN

P-0010209-T01-IM5: 0 transcribed double subs

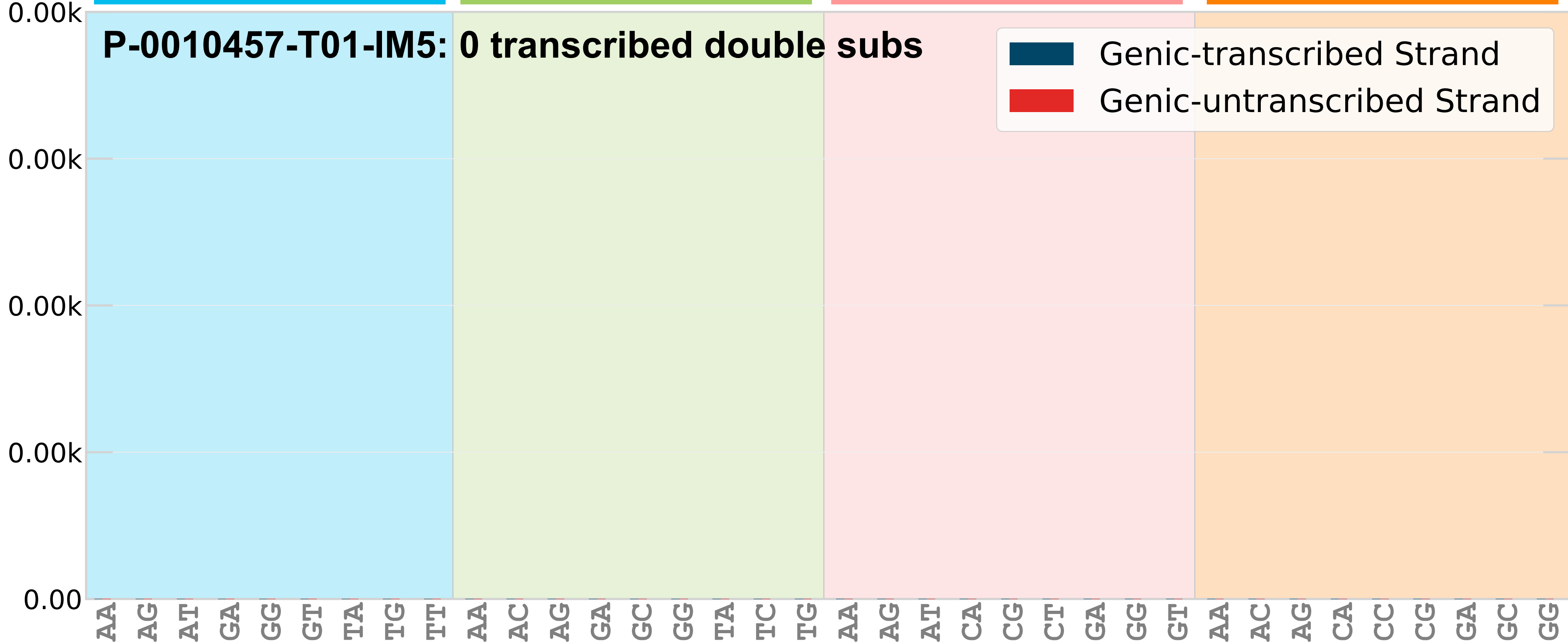
Genic-transcribed Strand

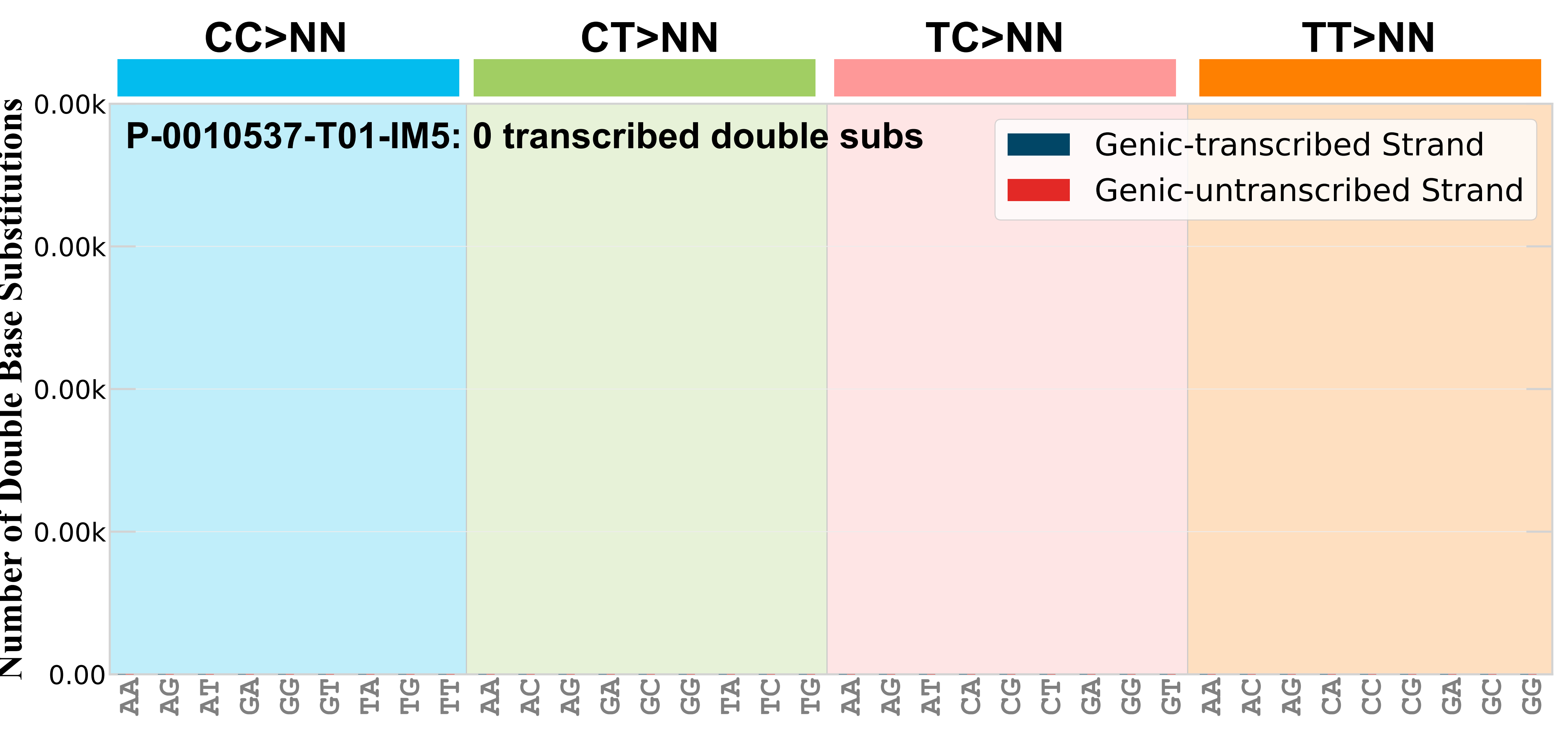
Genic-untranscribed Strand

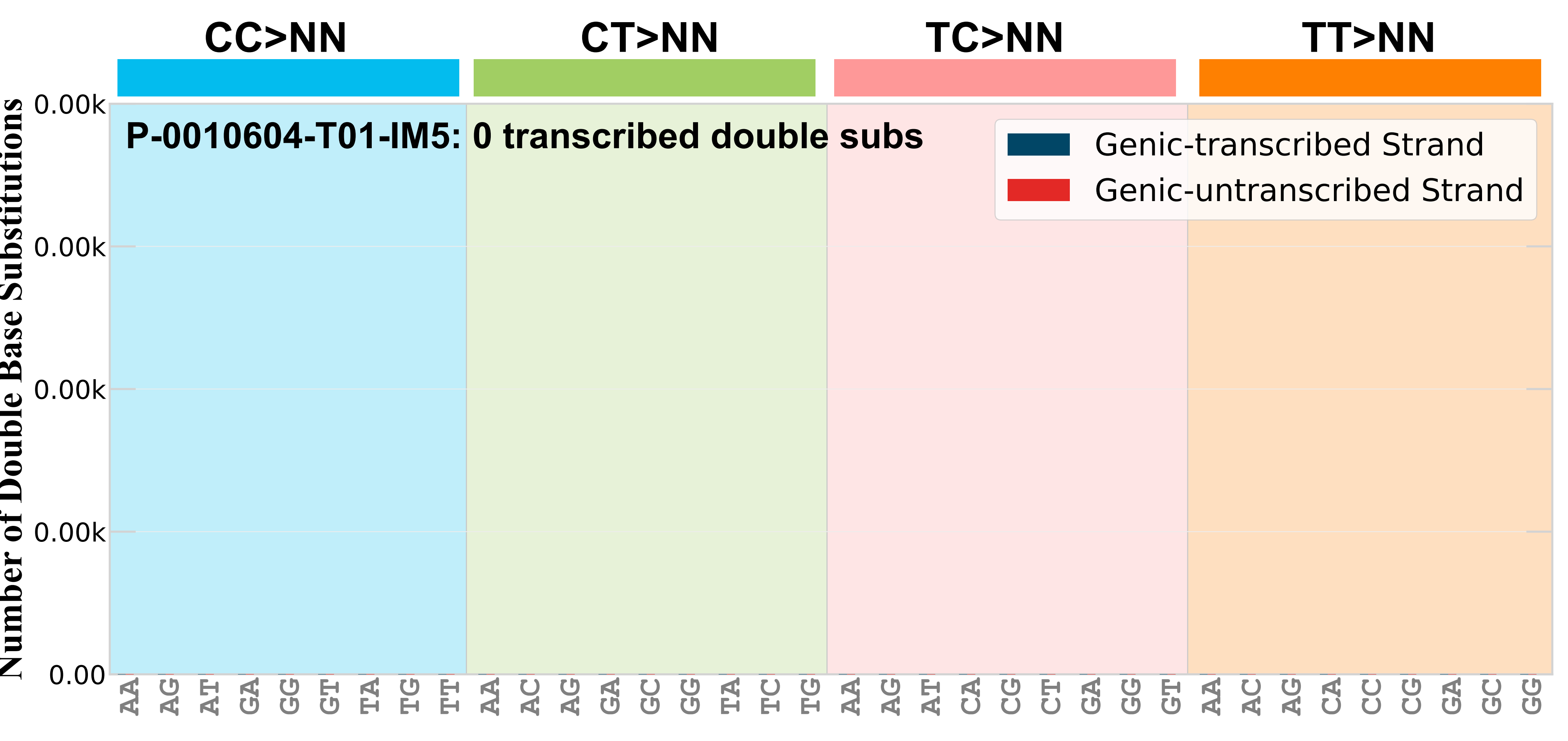
AA AG AT GA GG GT TA TG TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG CT GA GG GT AA AC AG CA CC CG GA GC GG



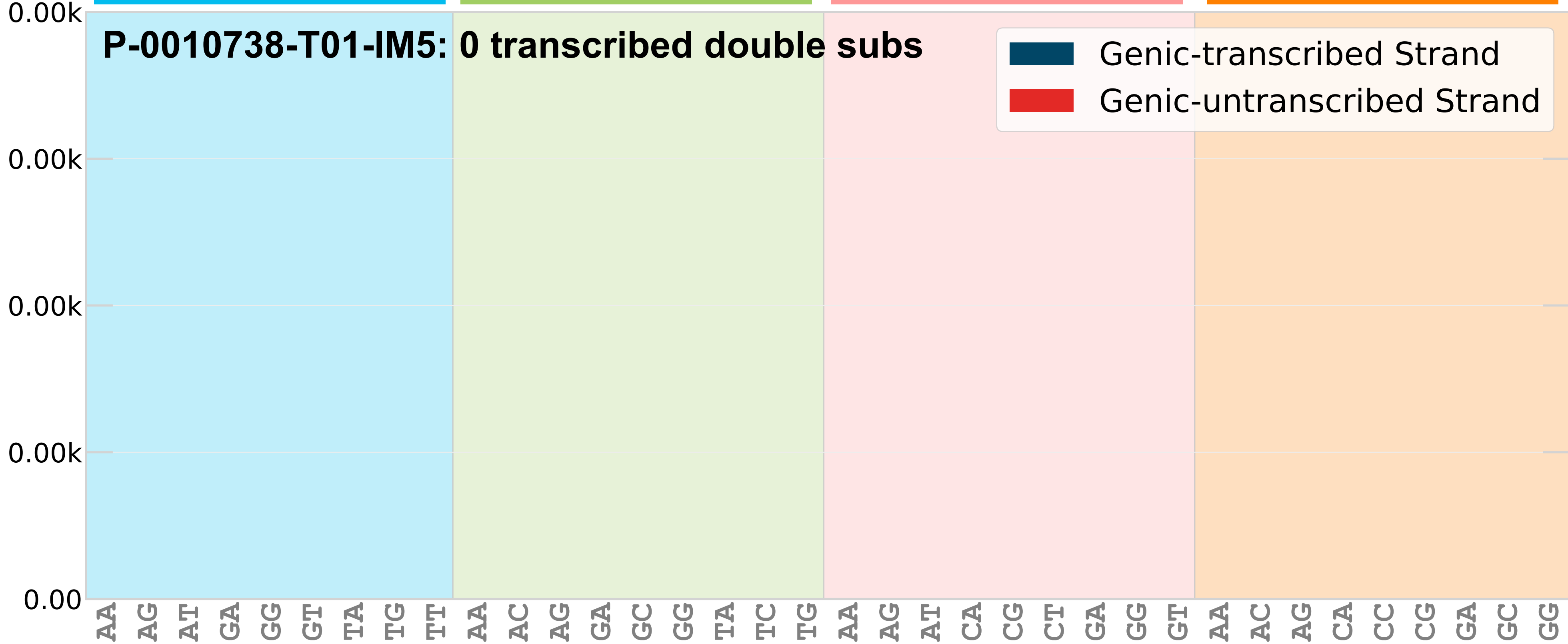
TT>NN



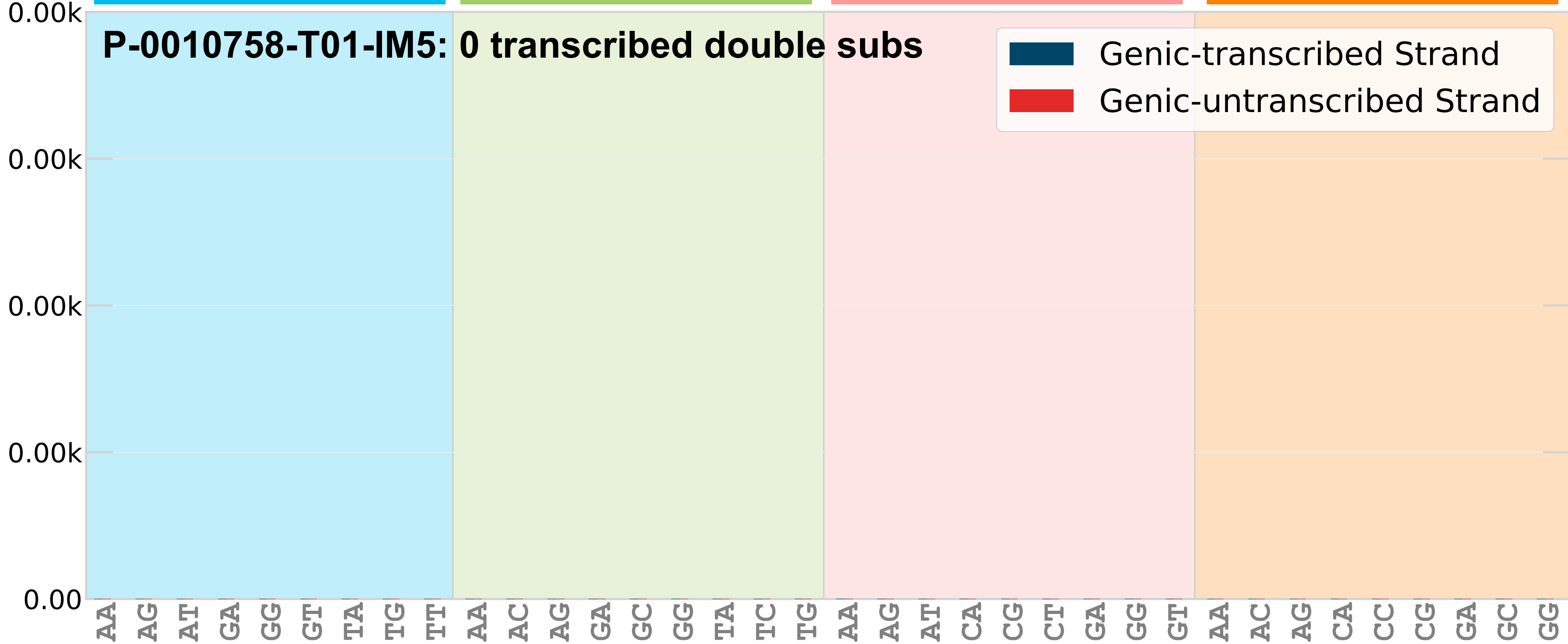


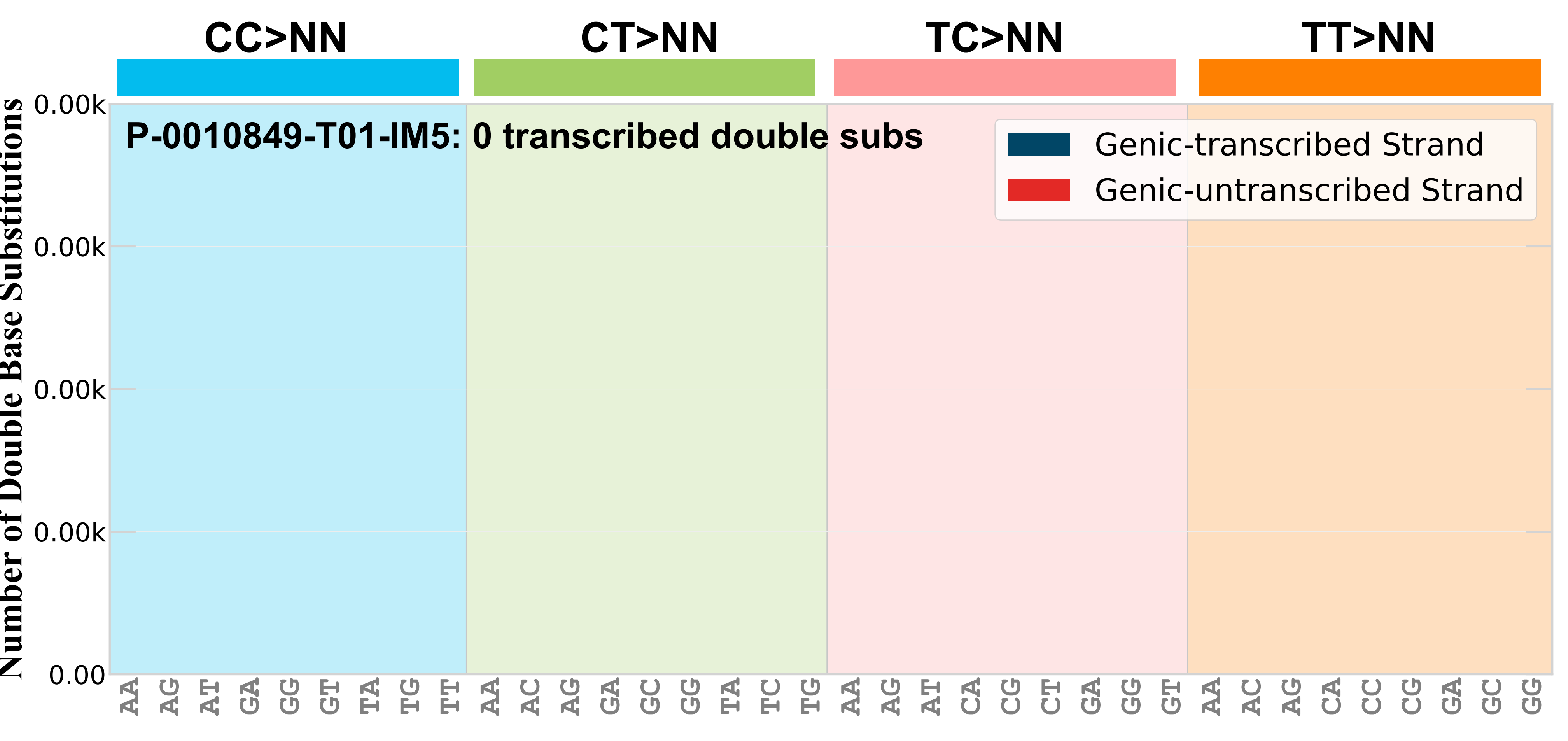


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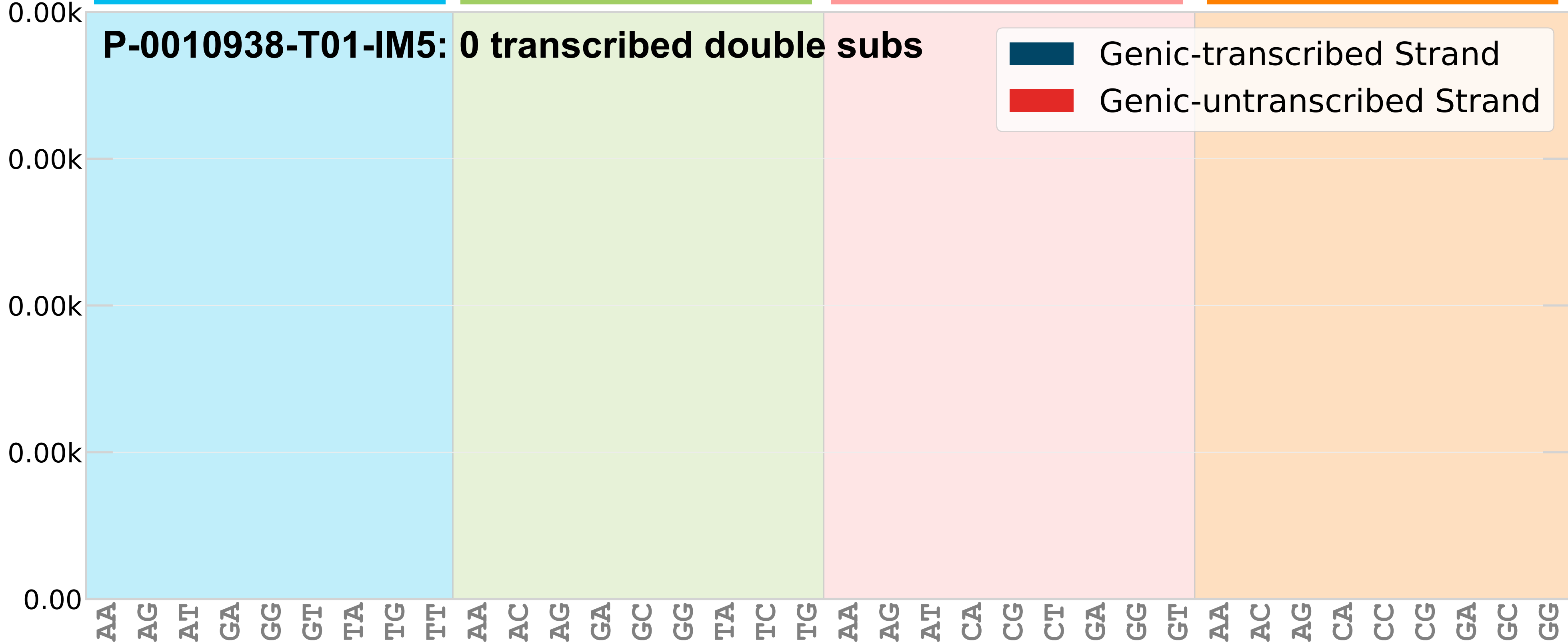


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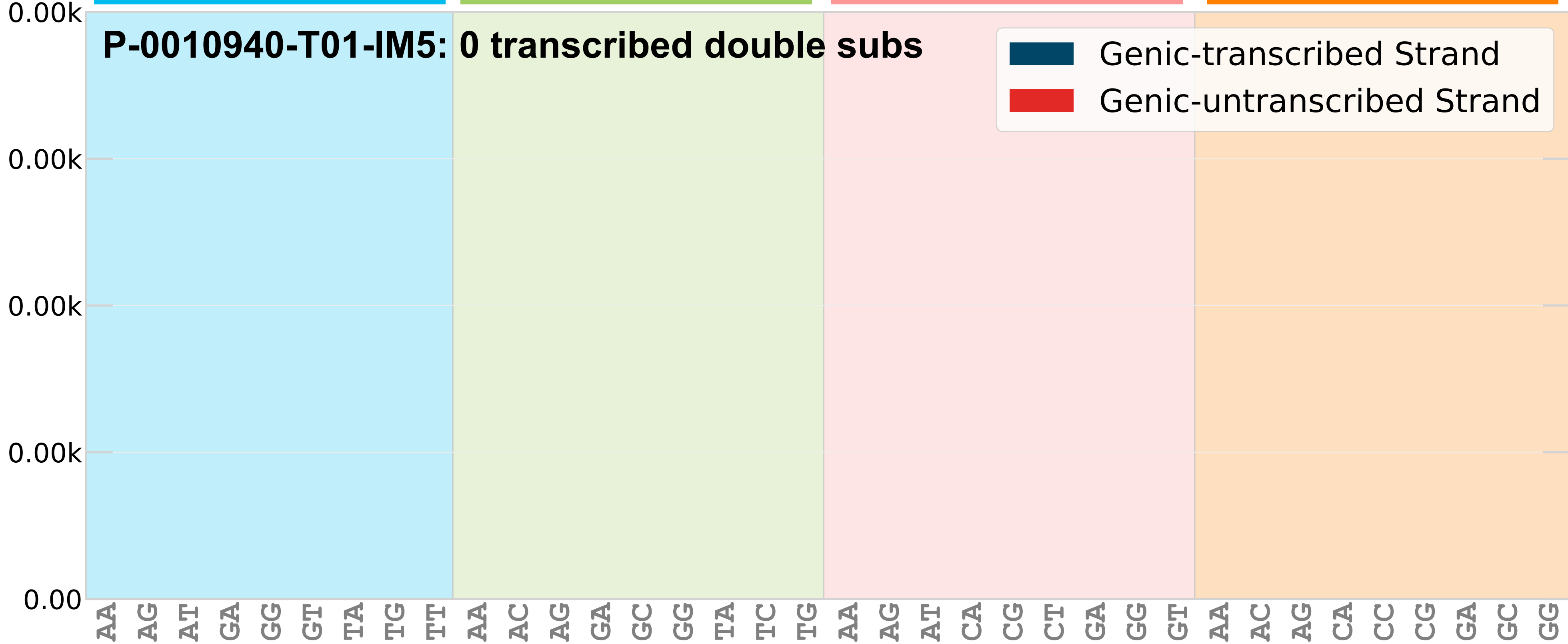


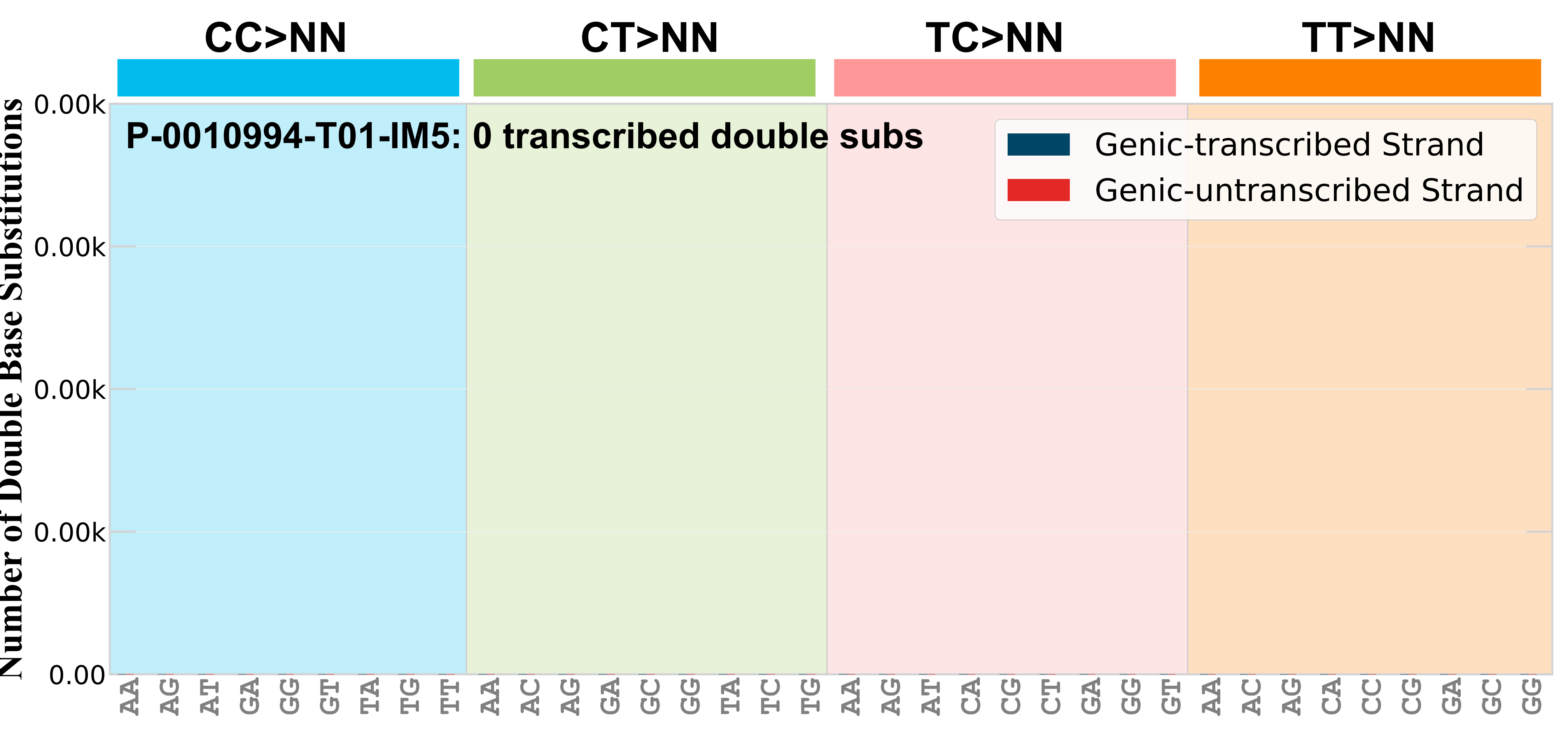


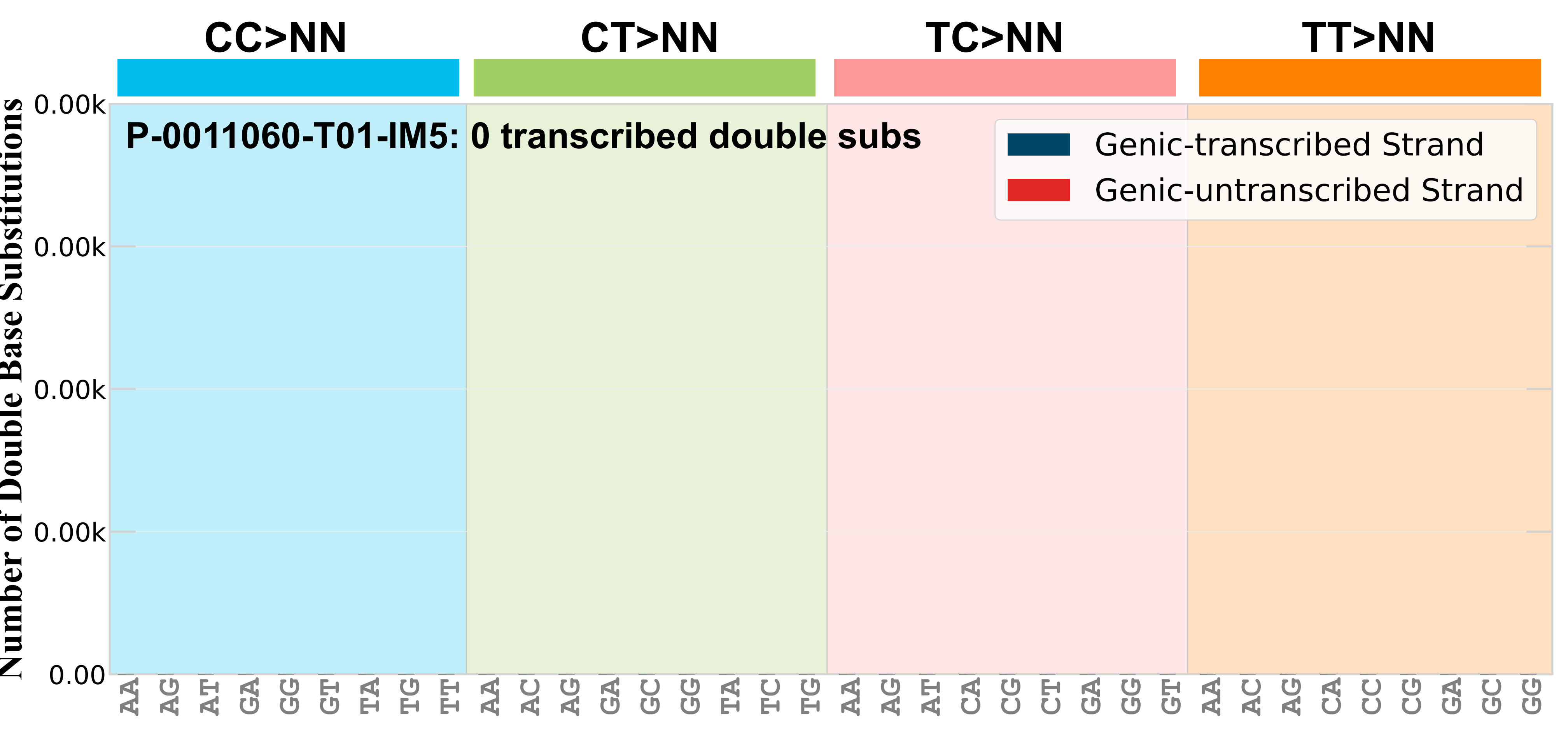
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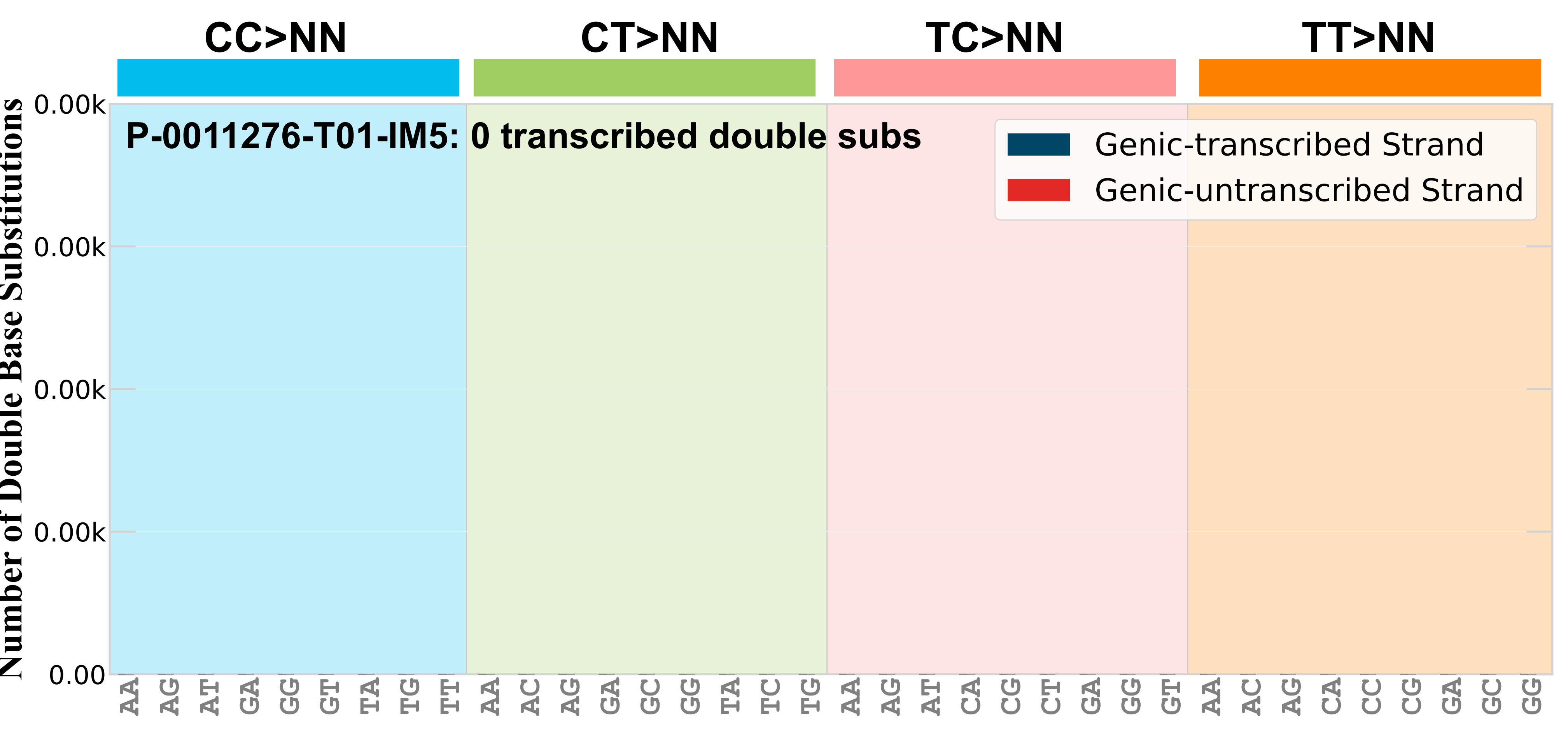


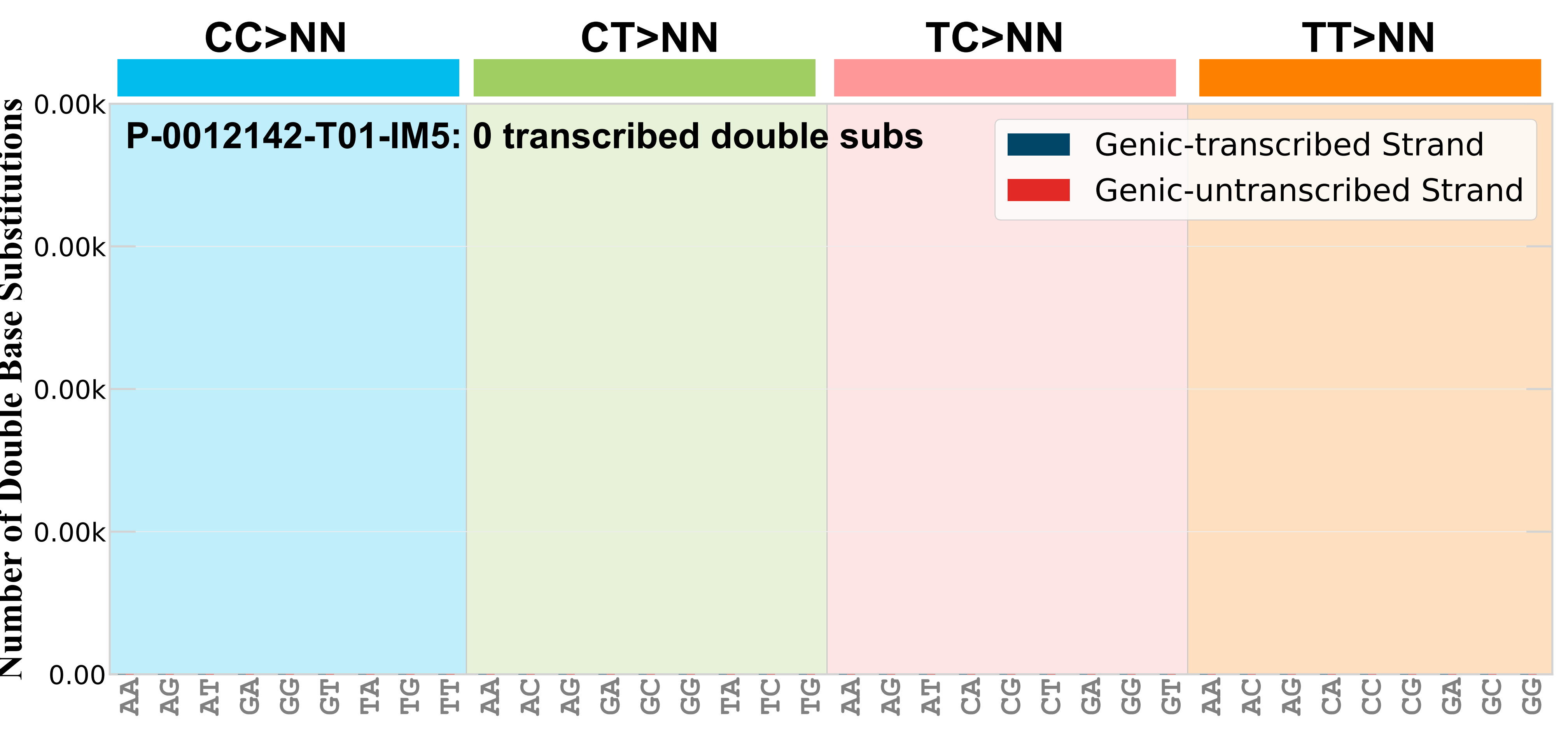
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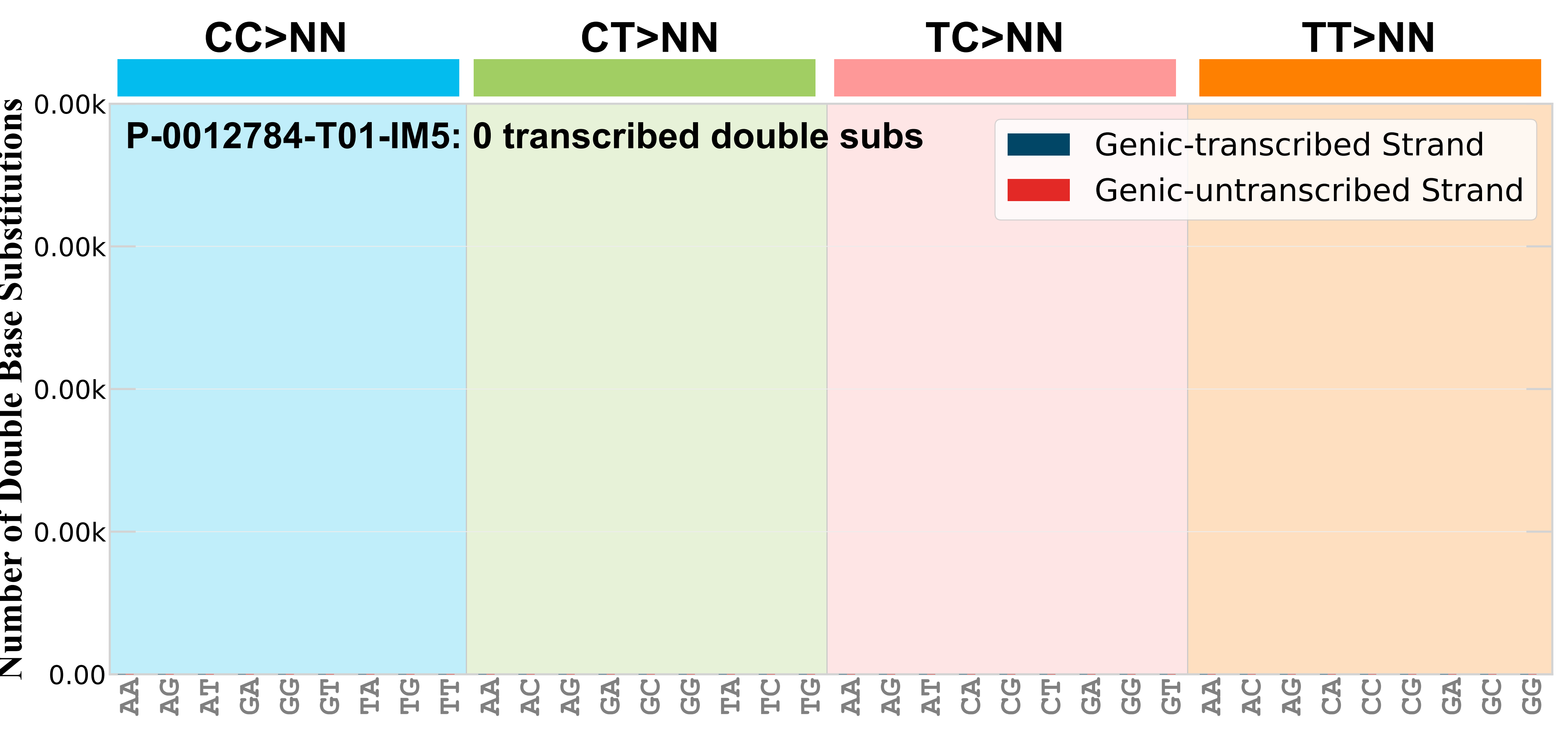




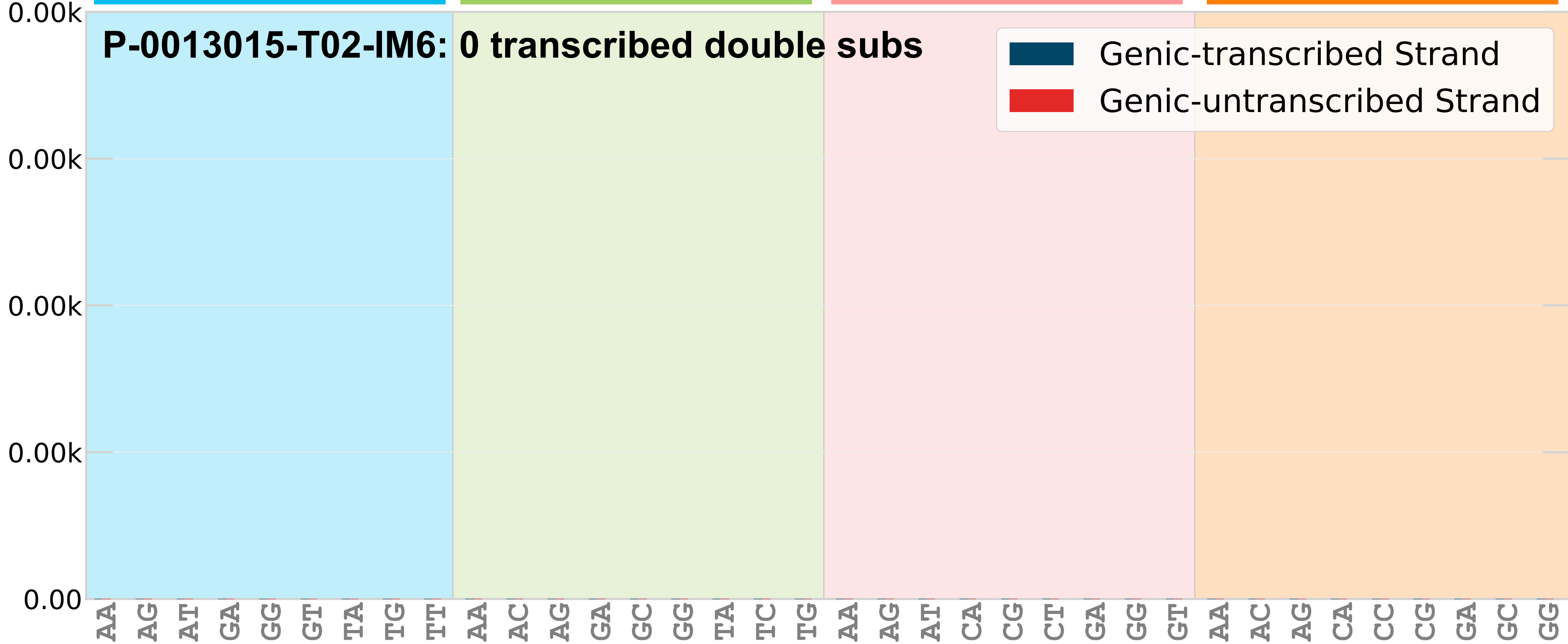




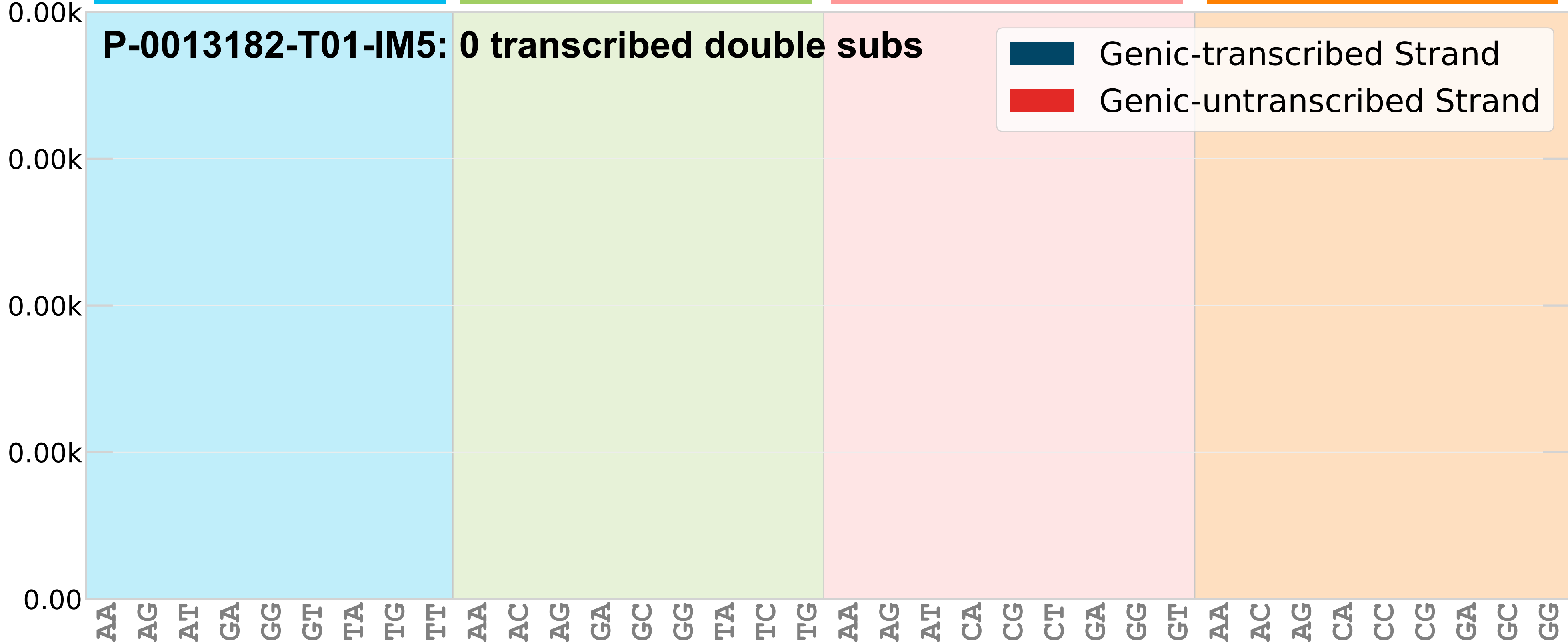




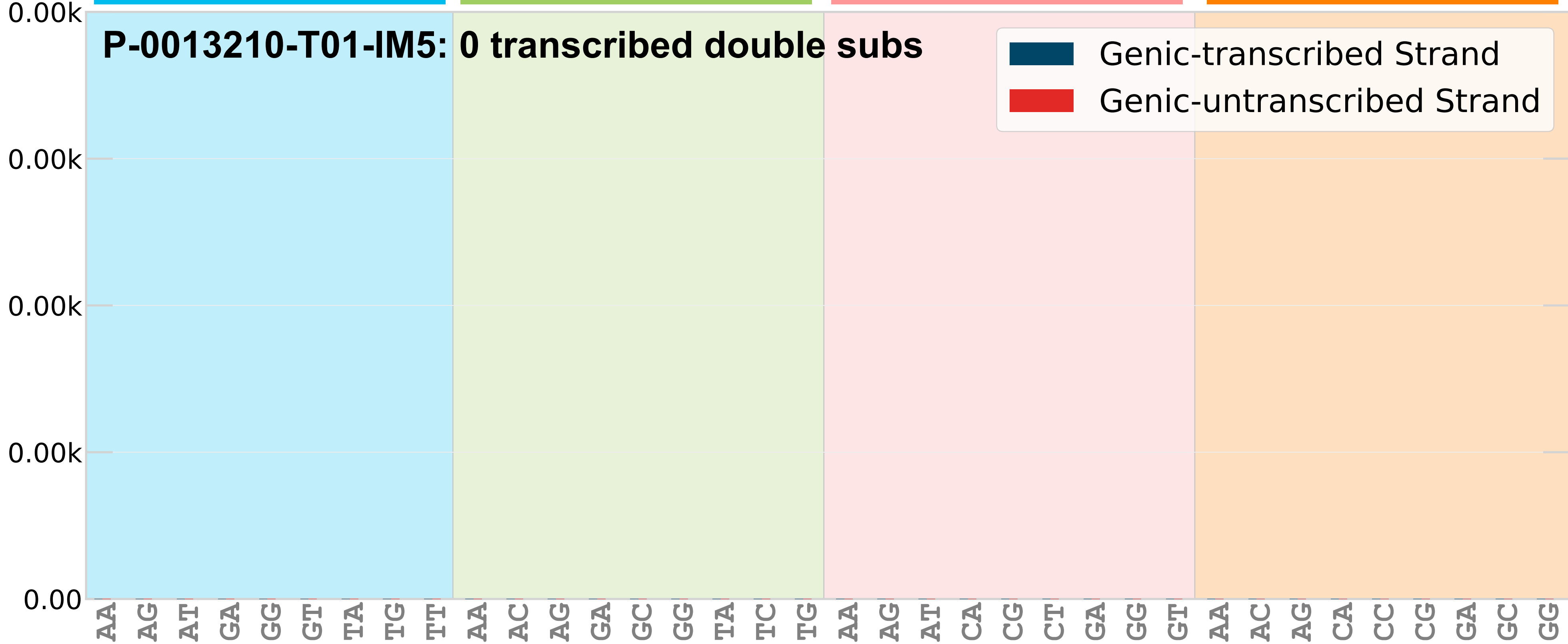
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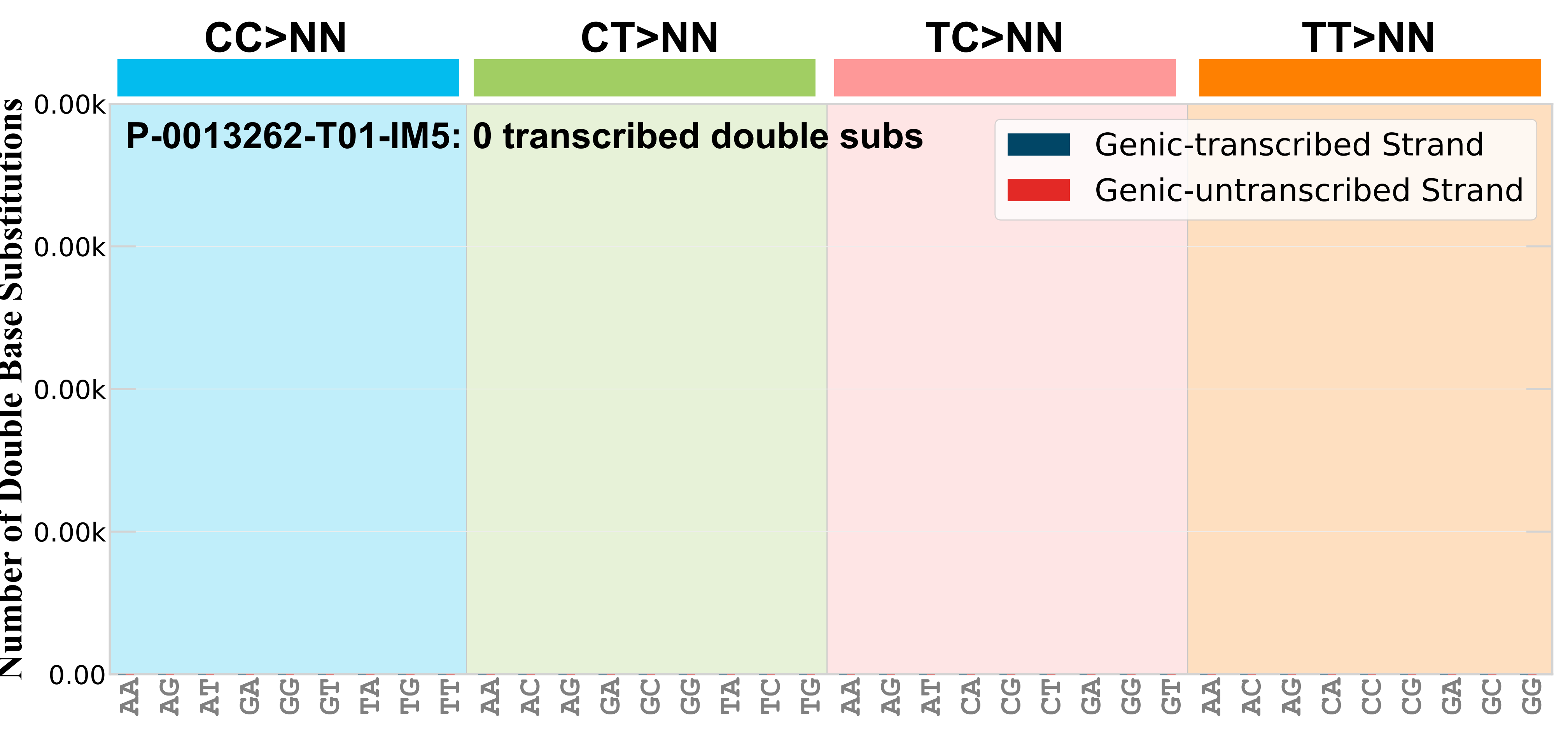


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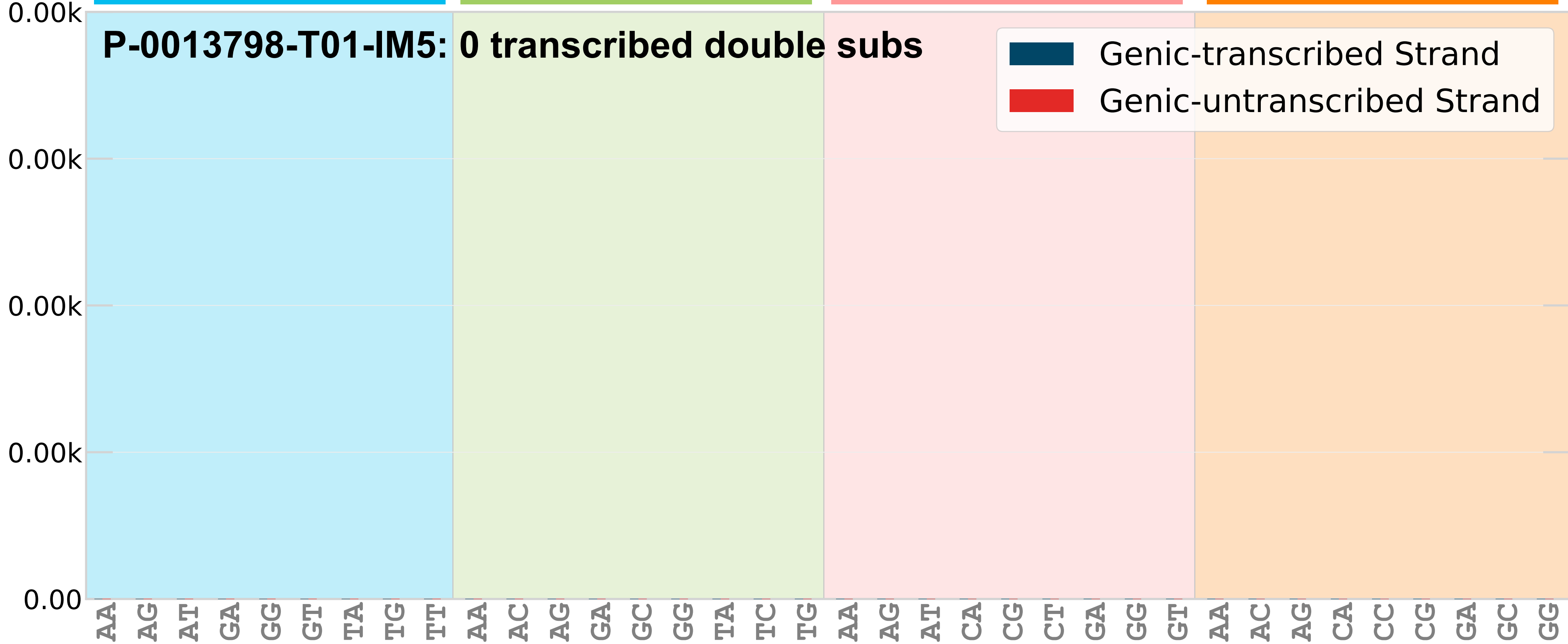


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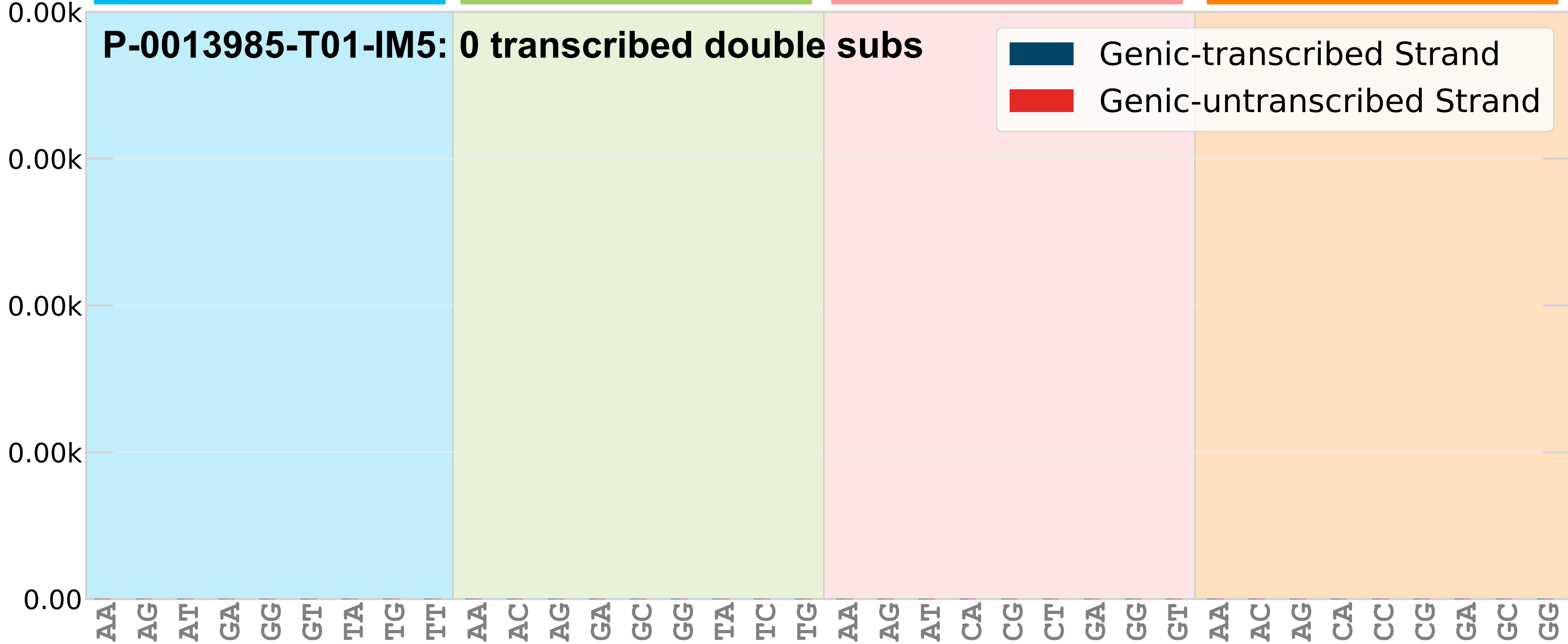




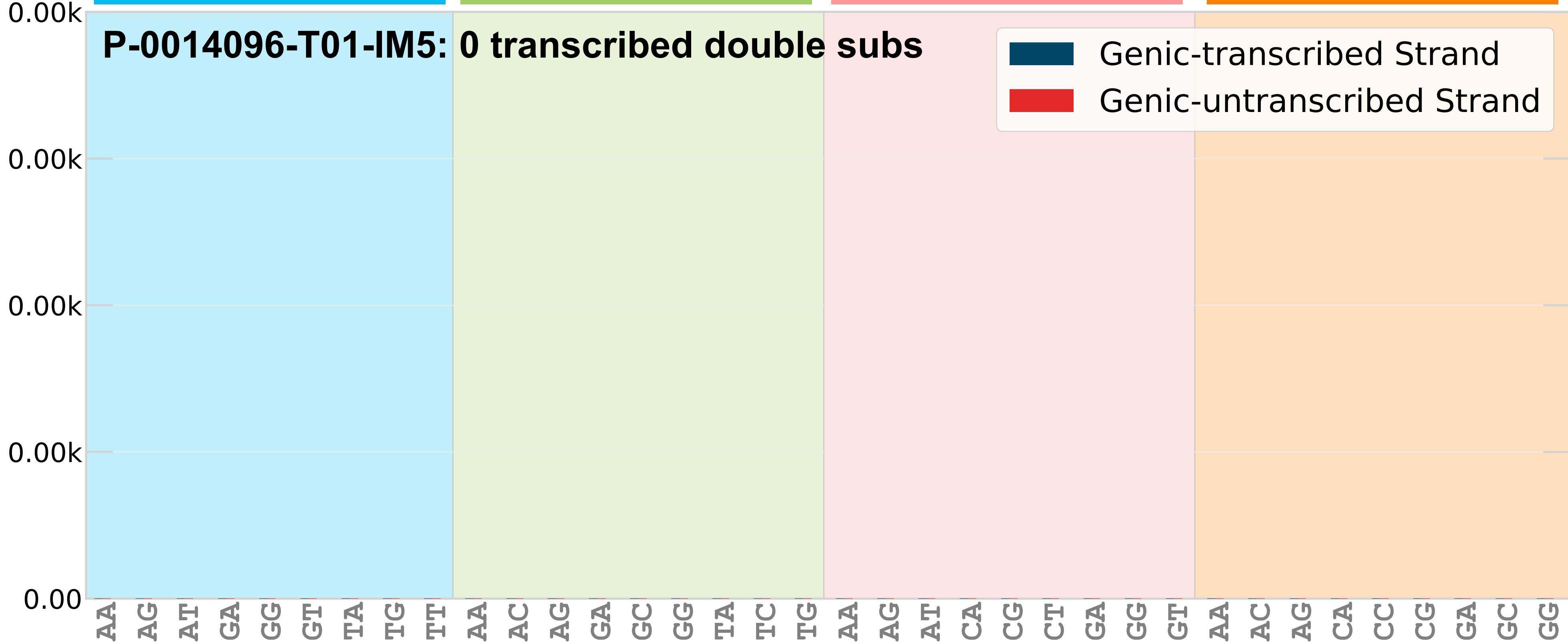
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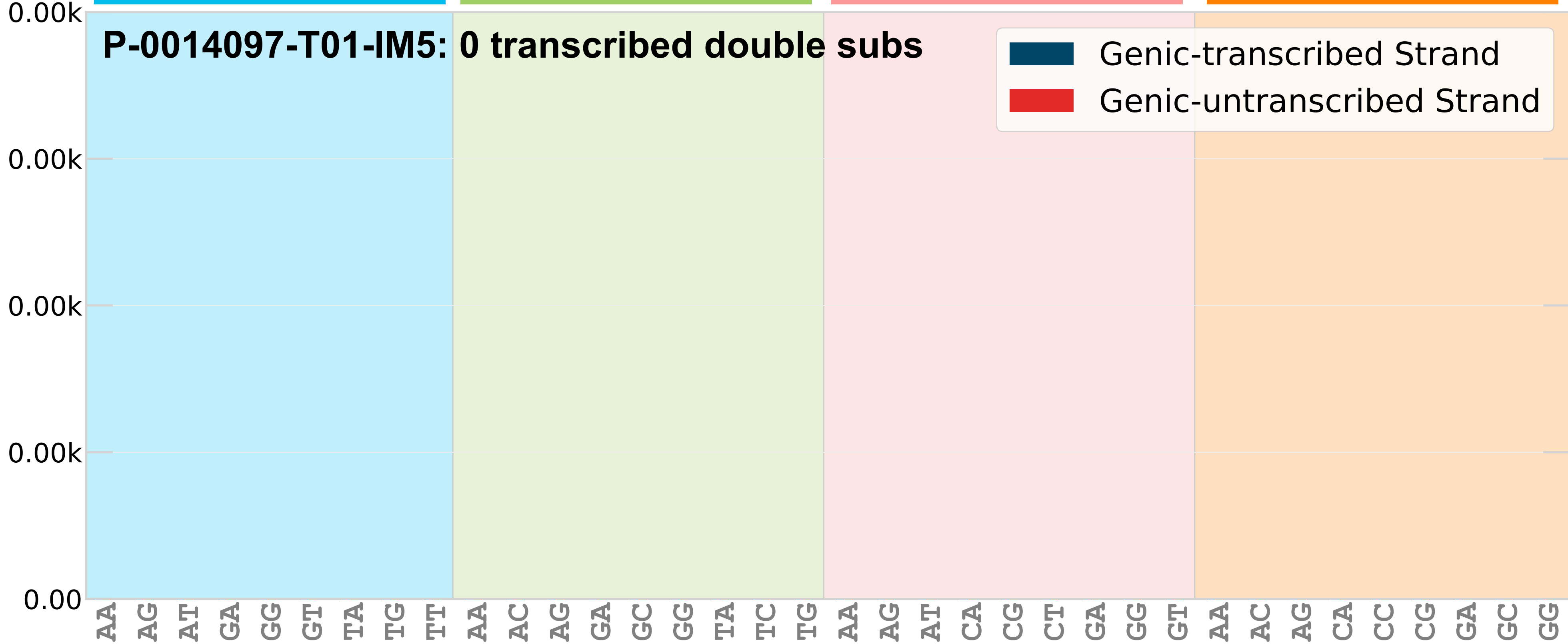
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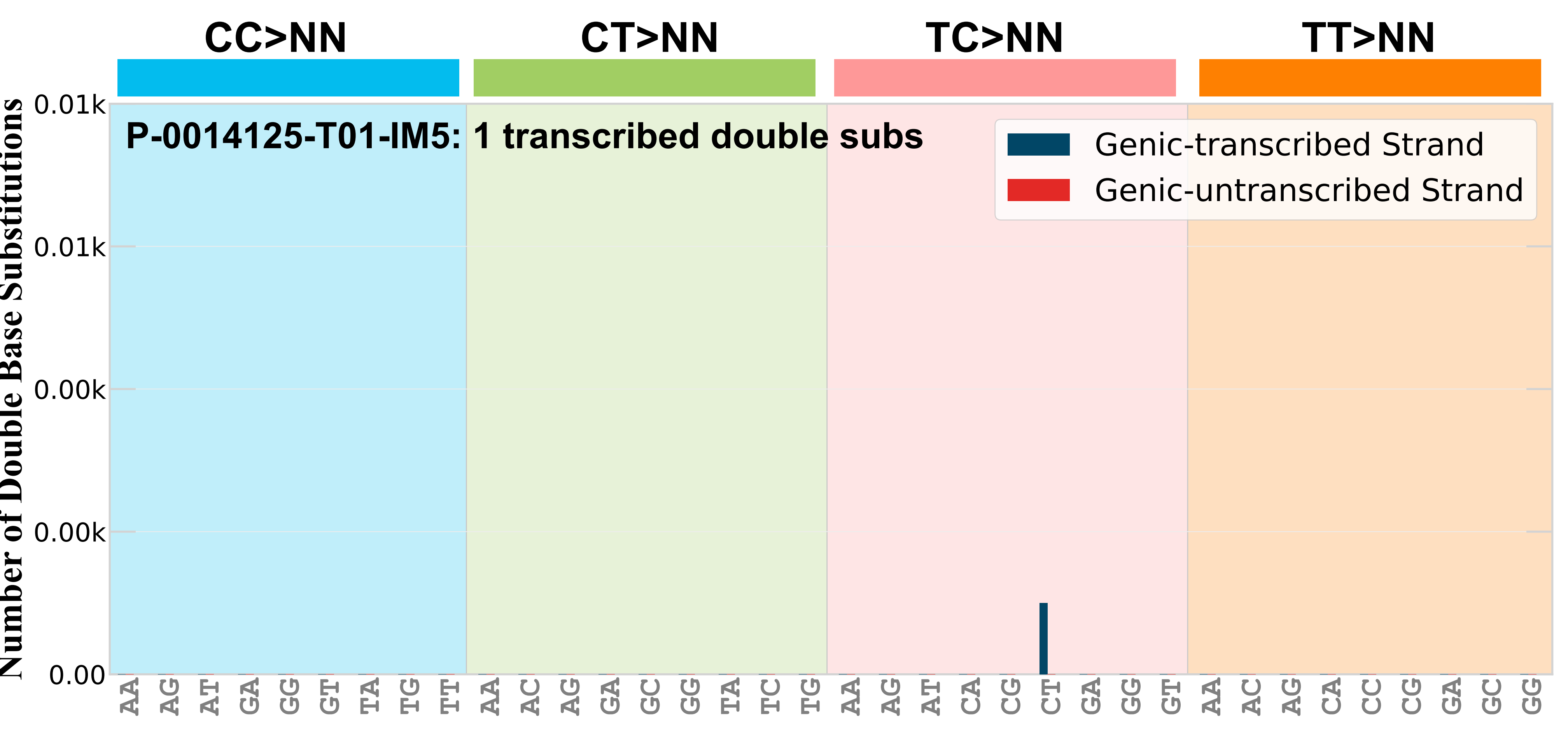


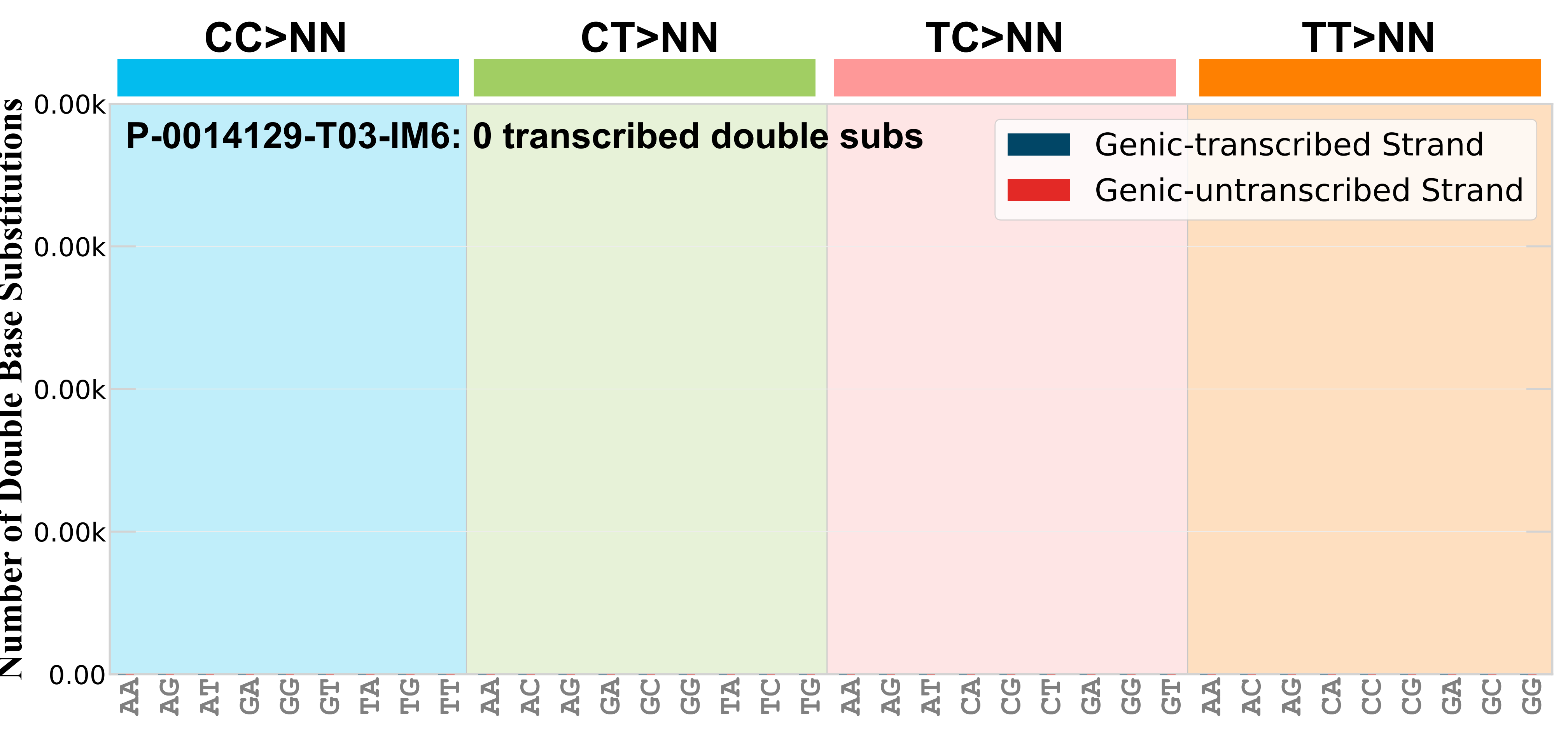
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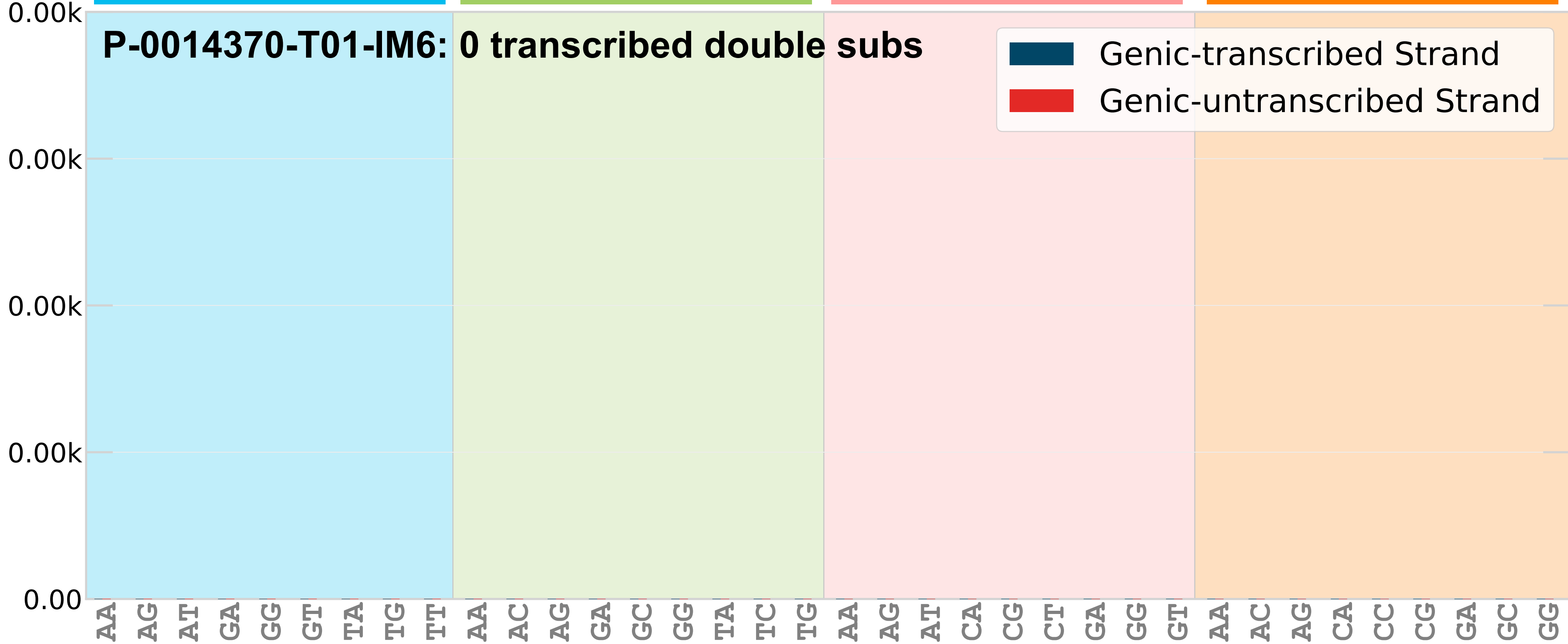
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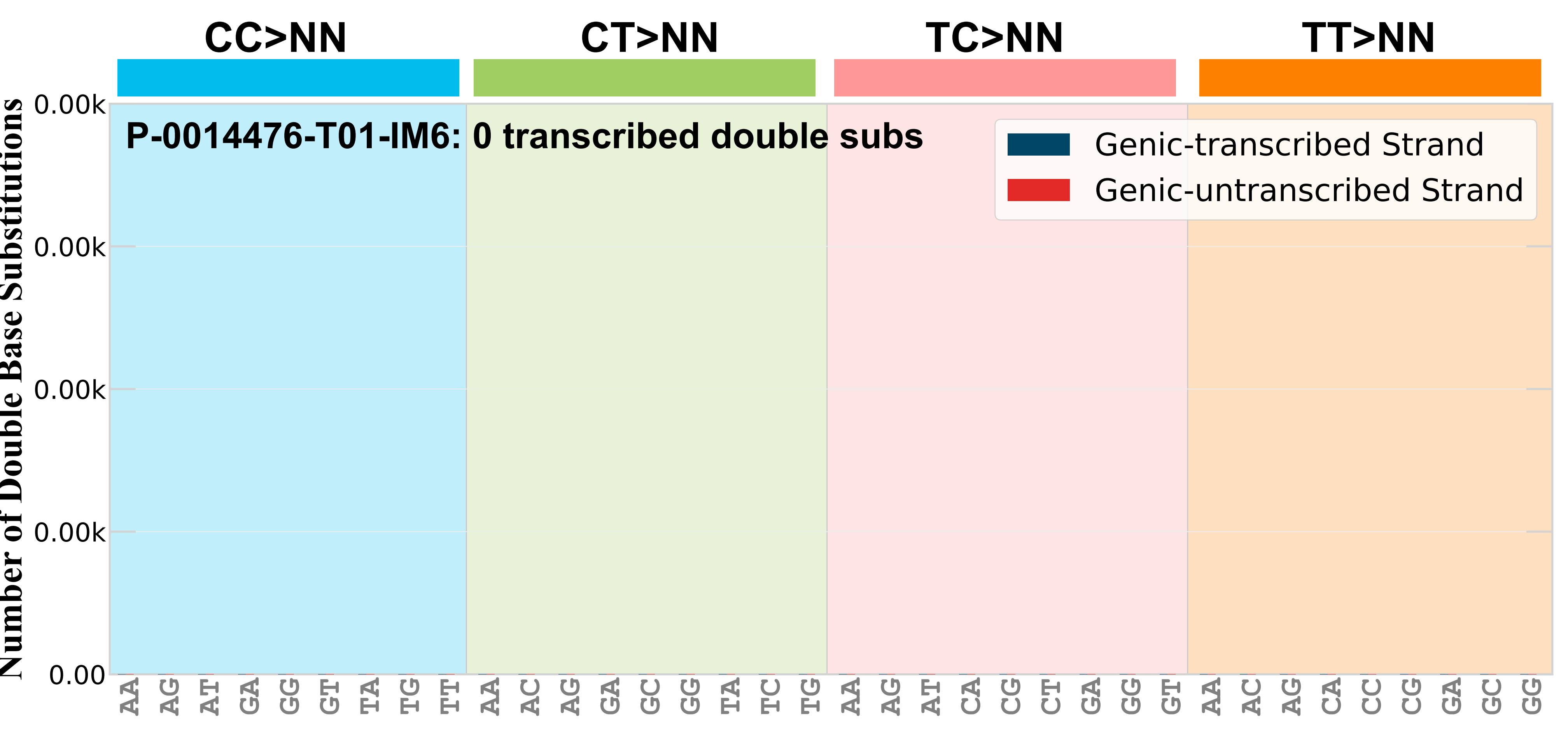




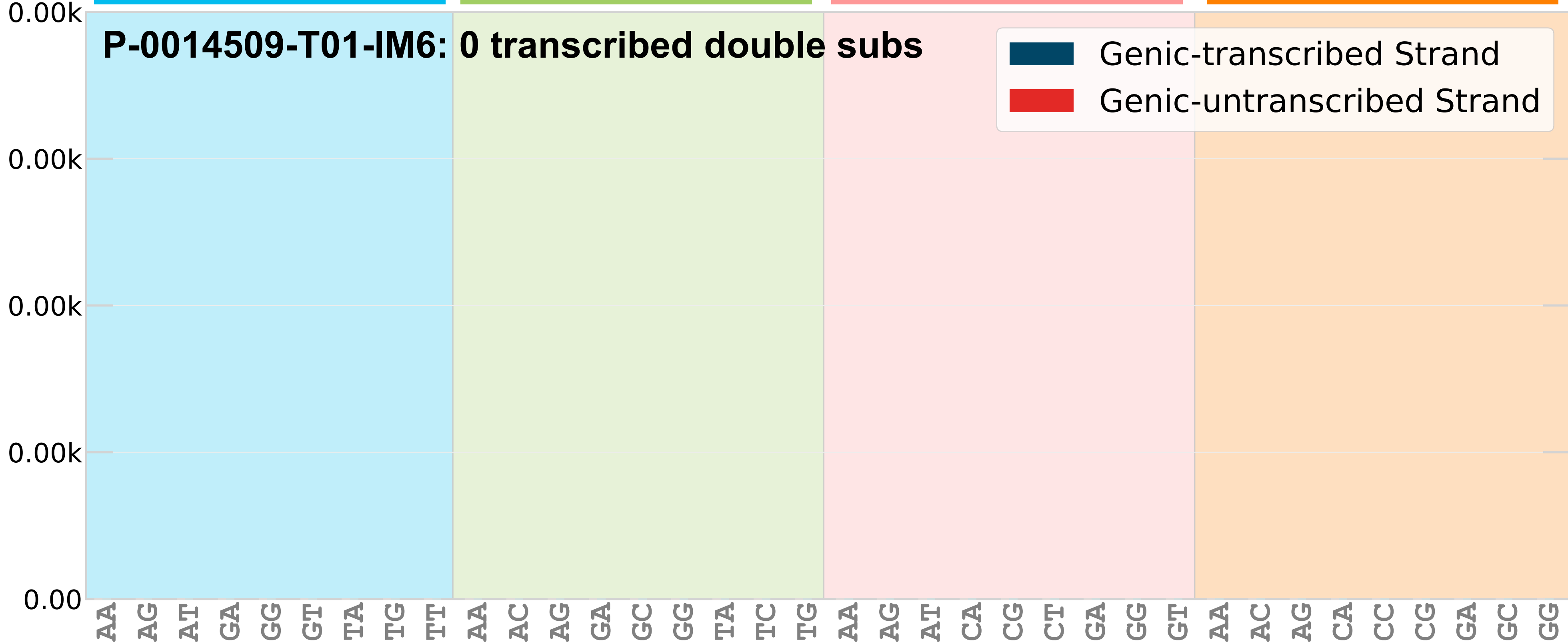


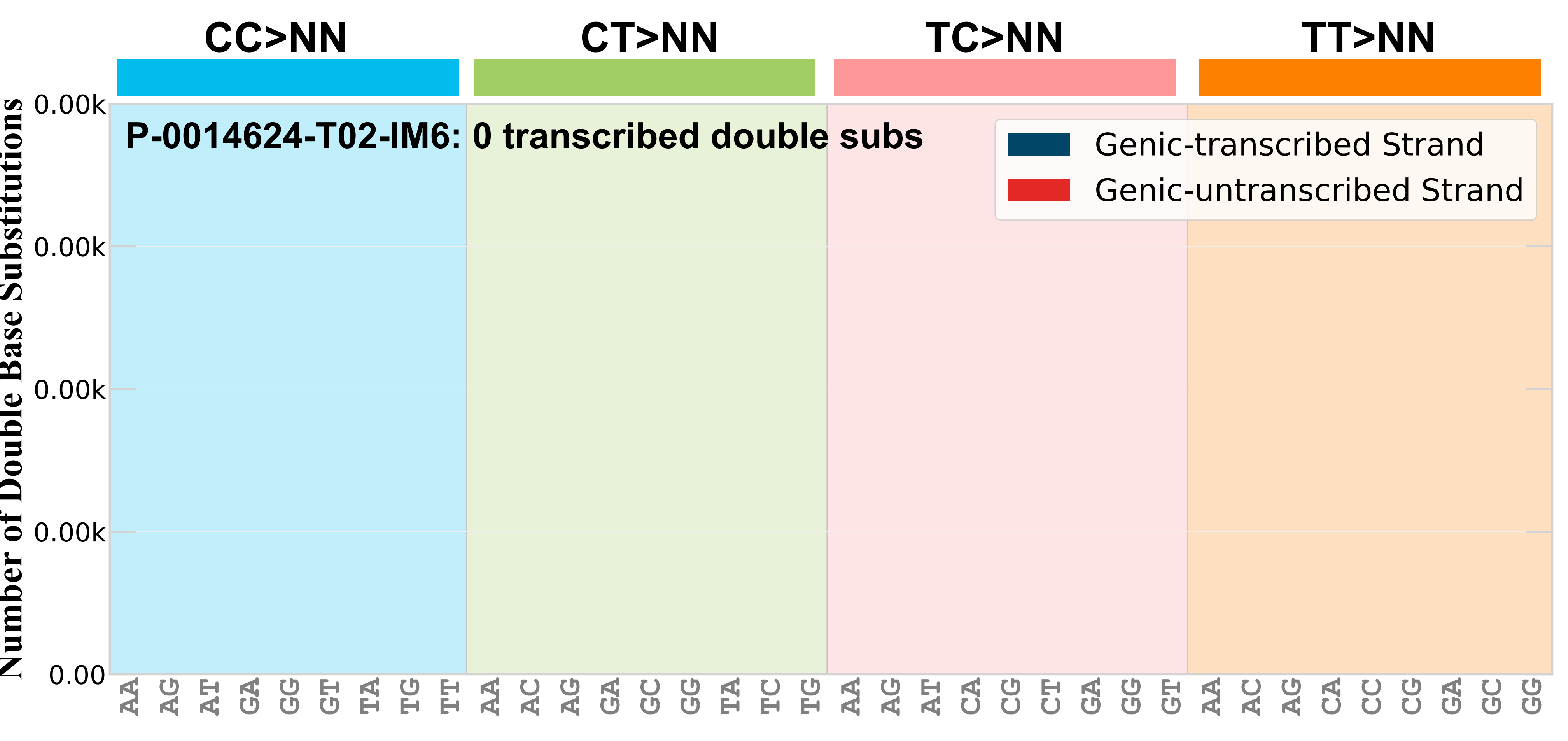
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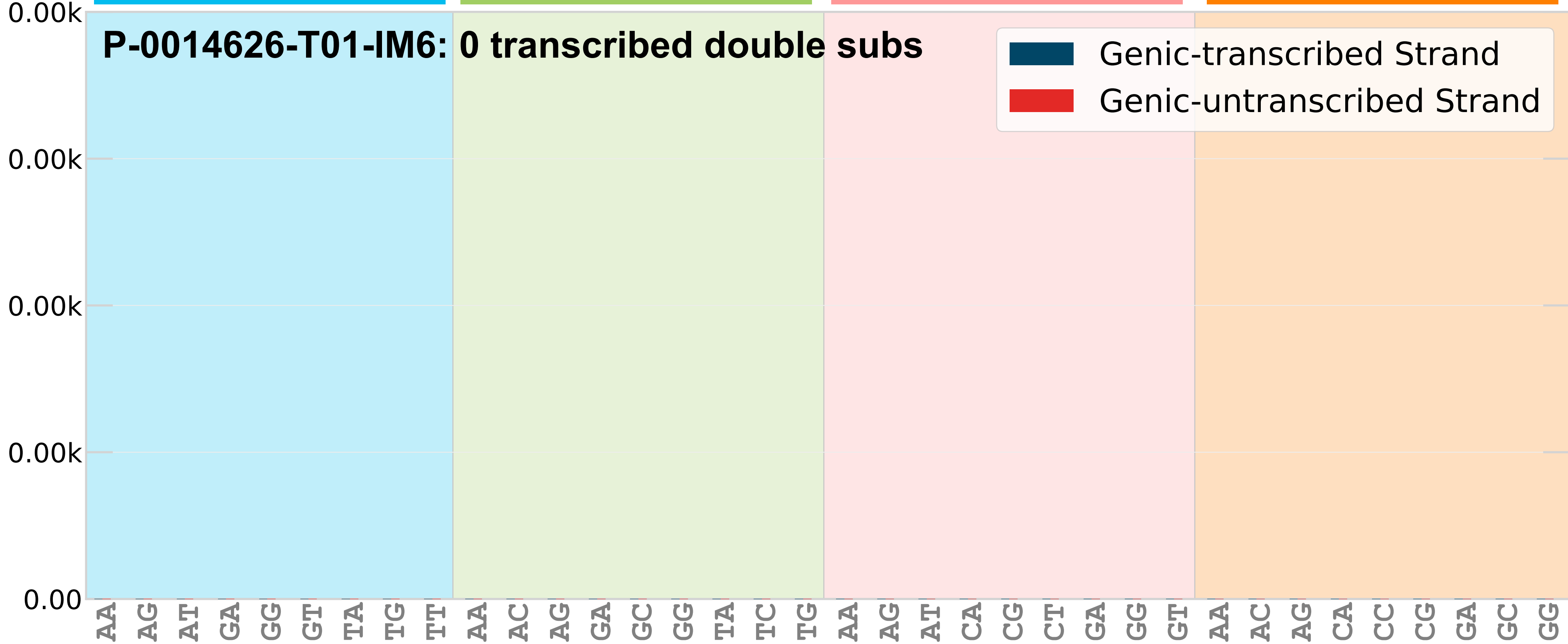


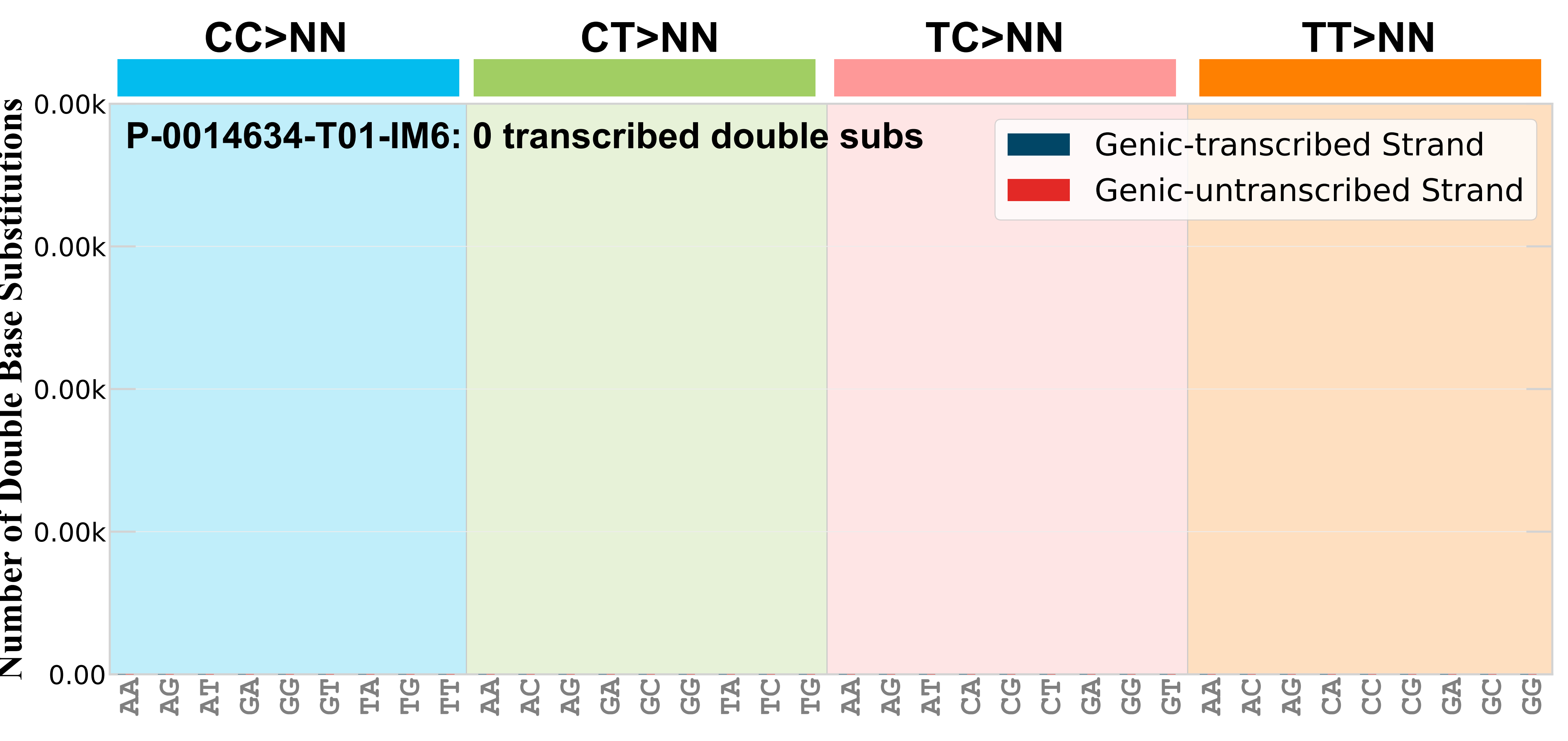
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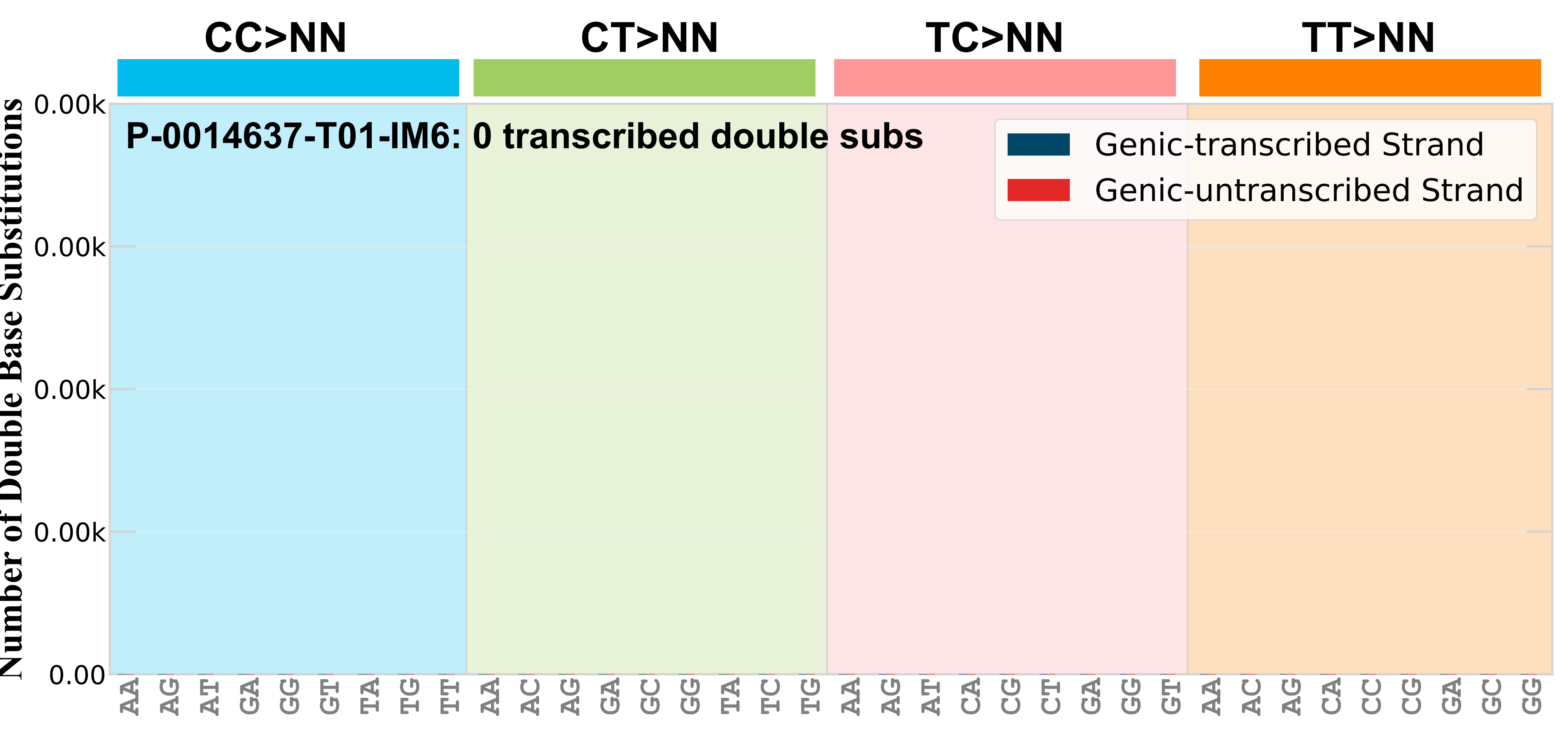


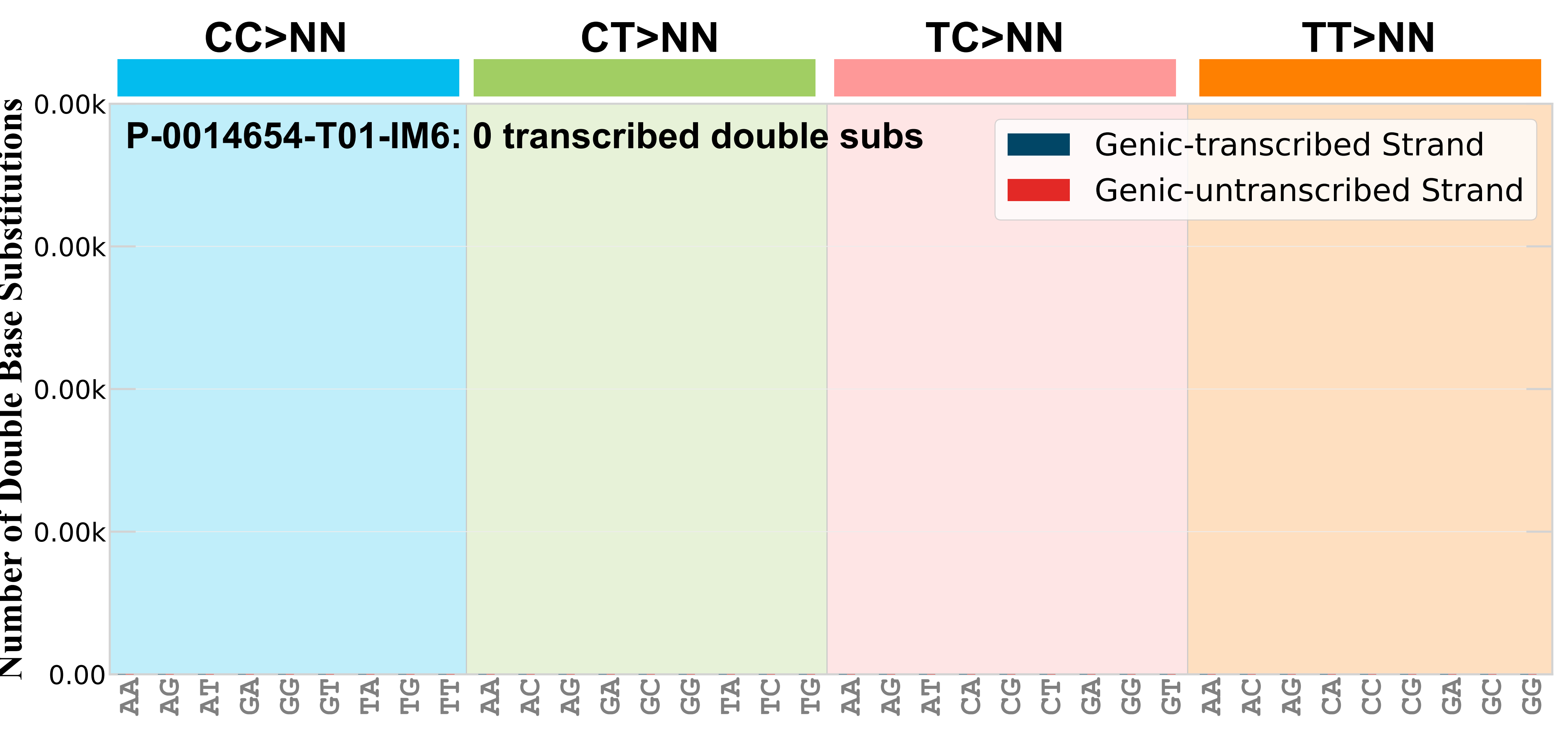


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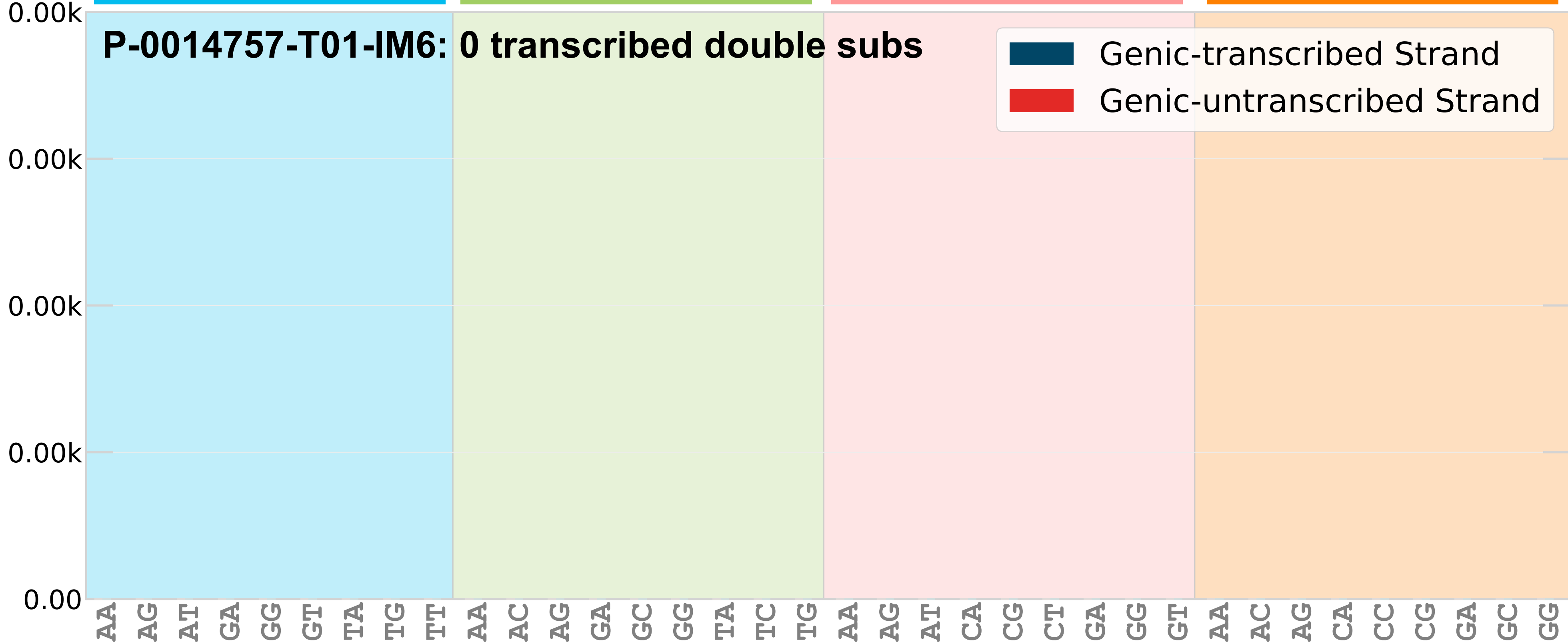




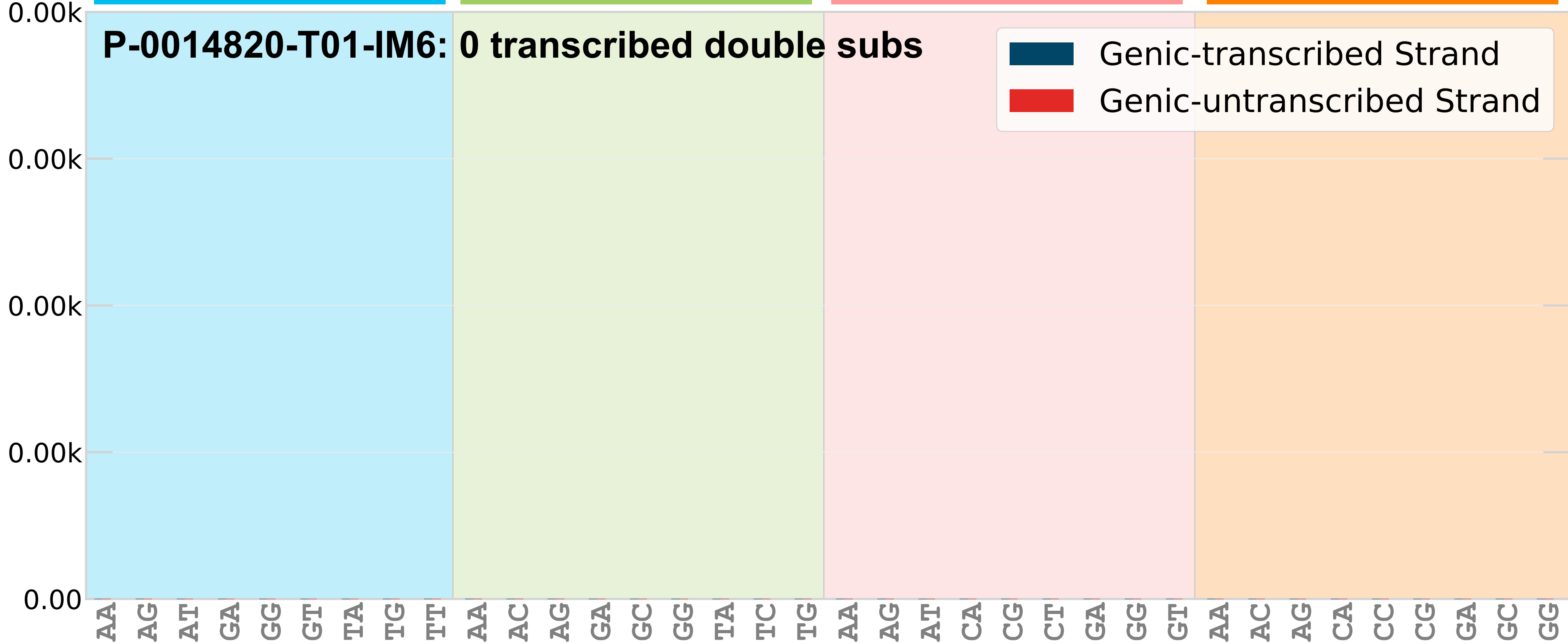


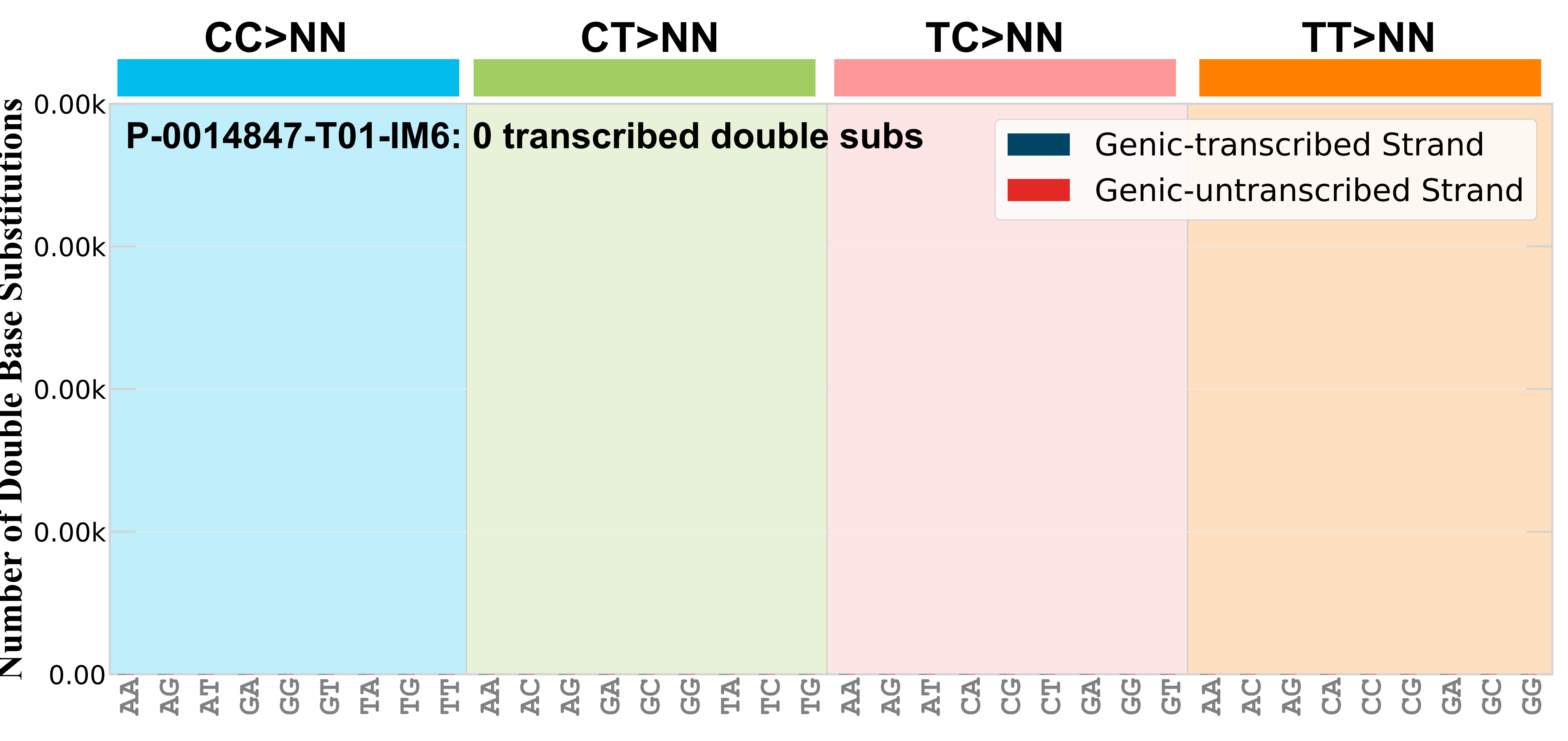


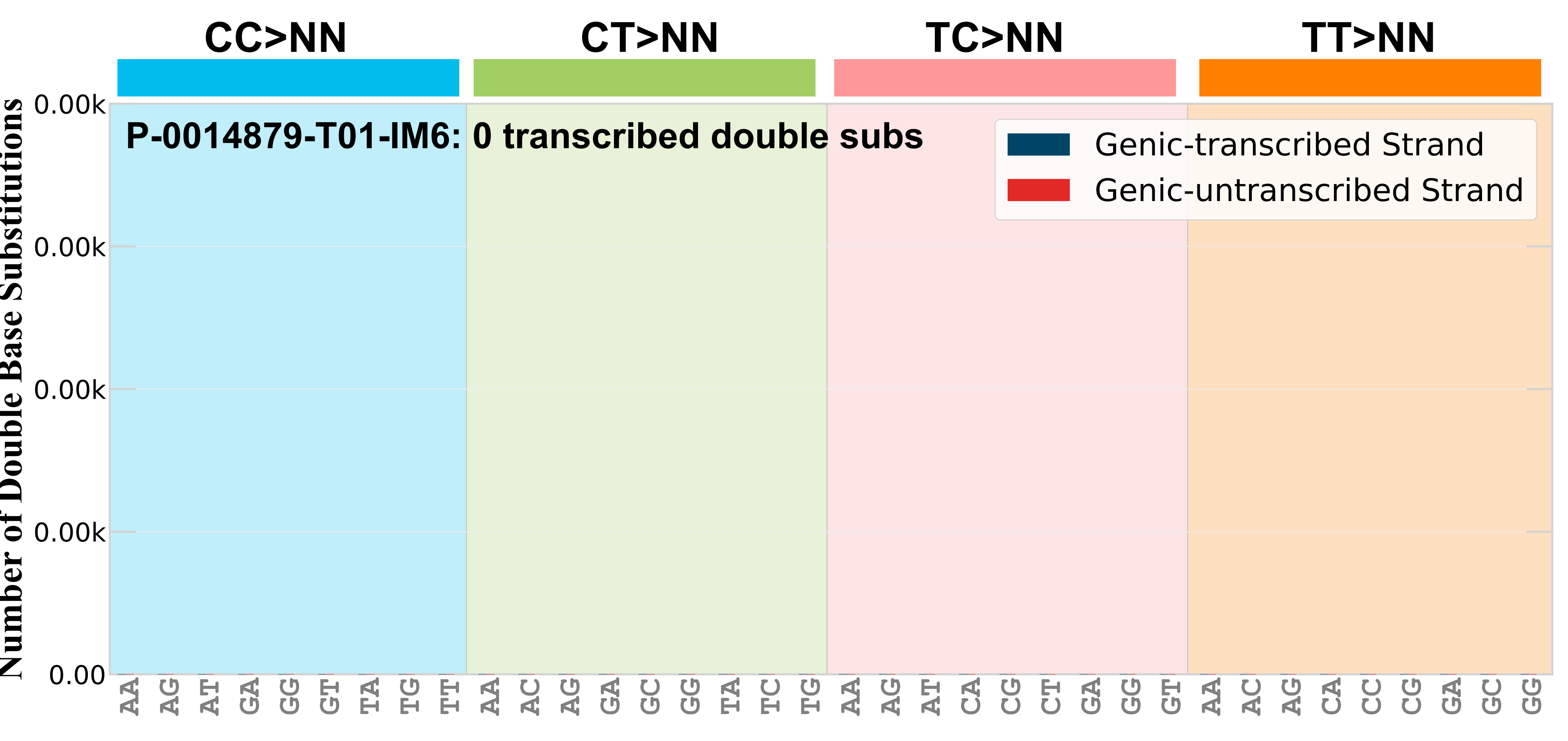
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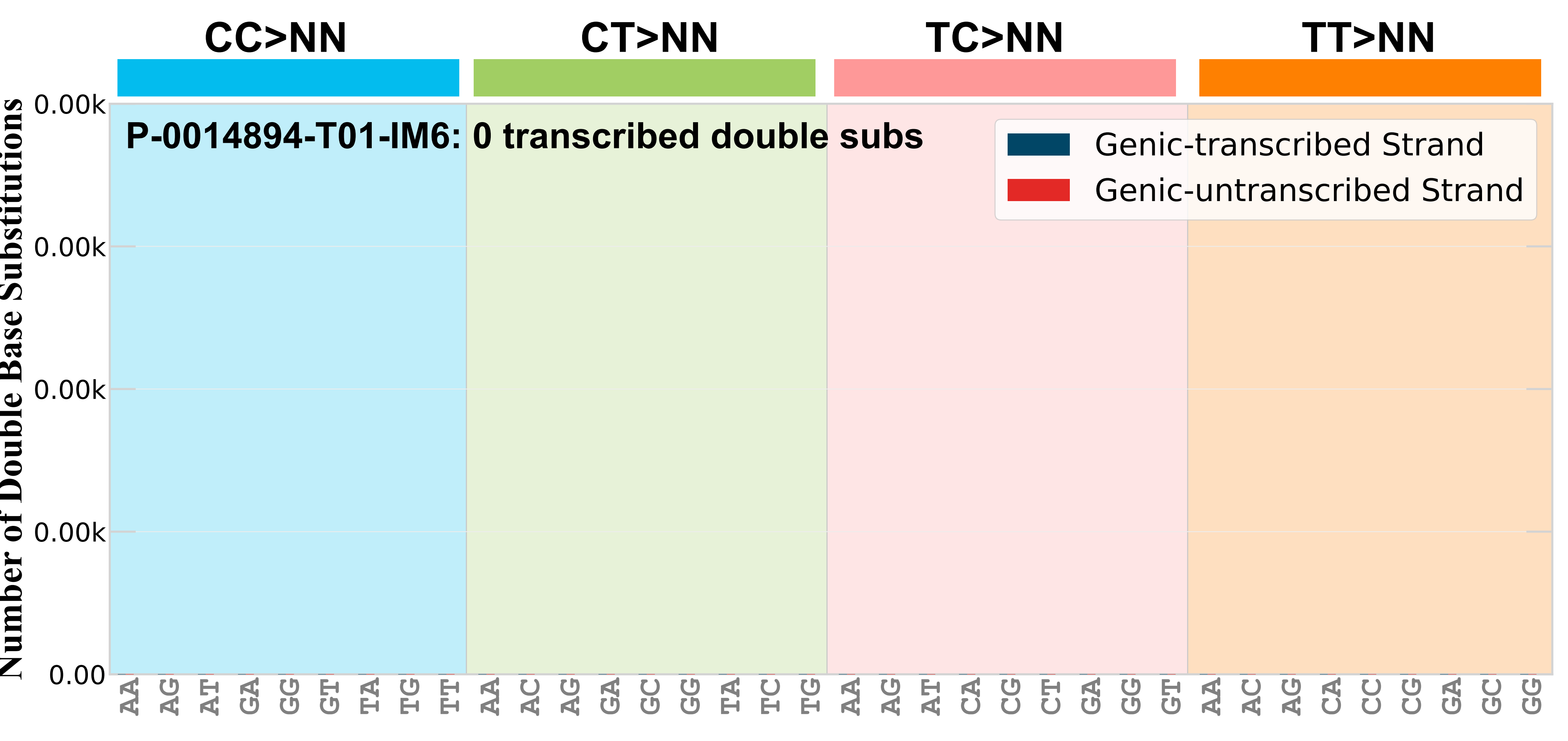


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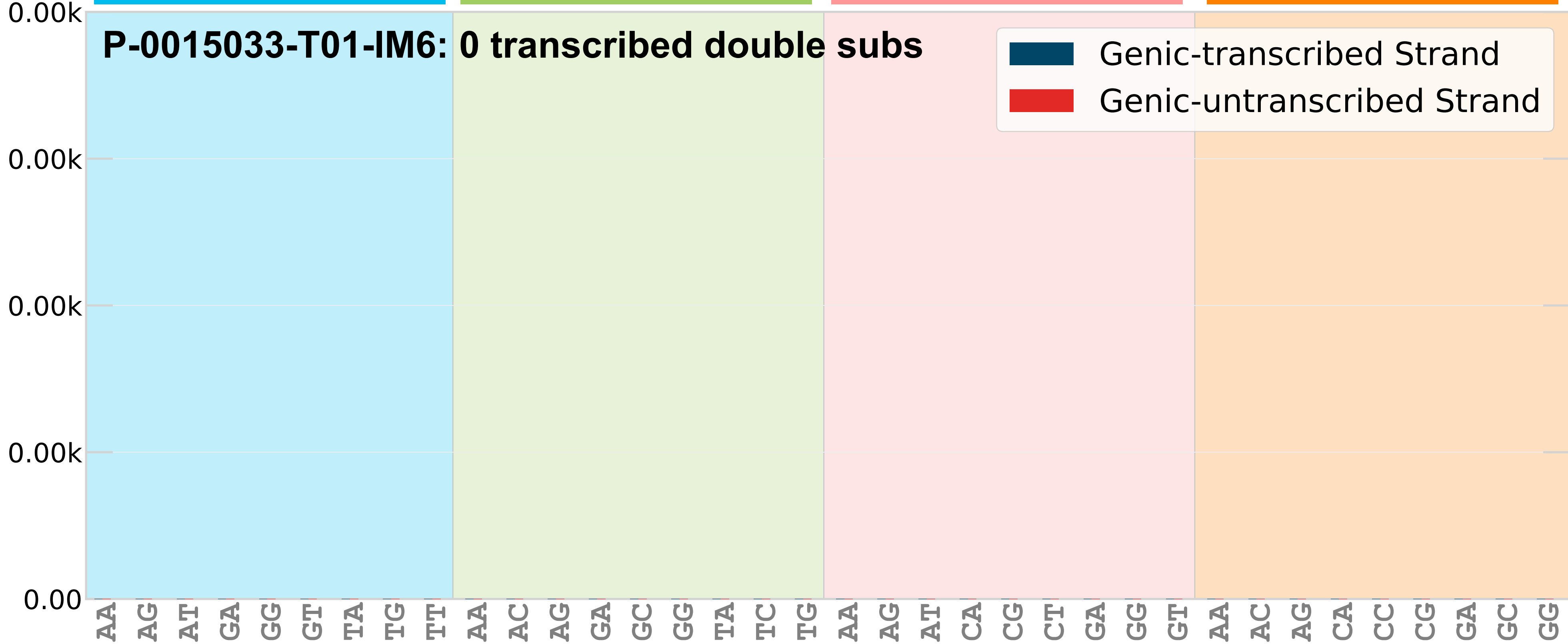




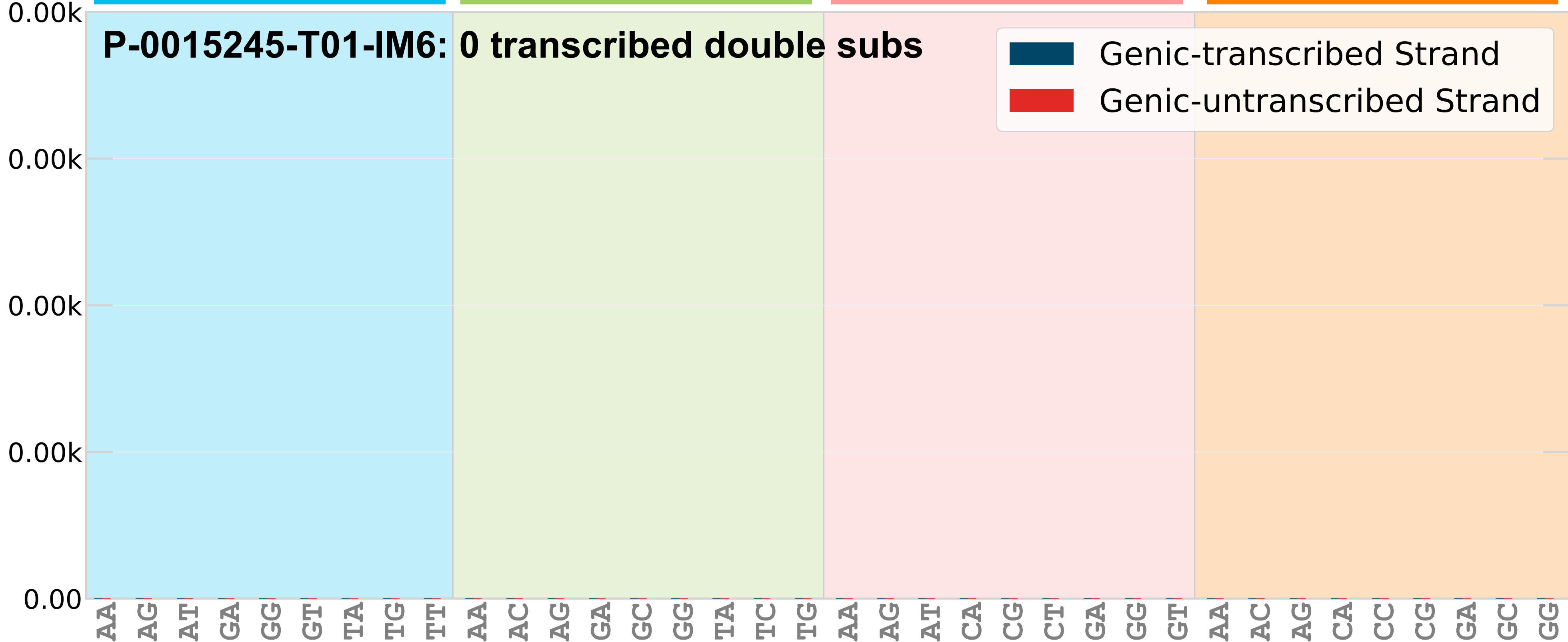




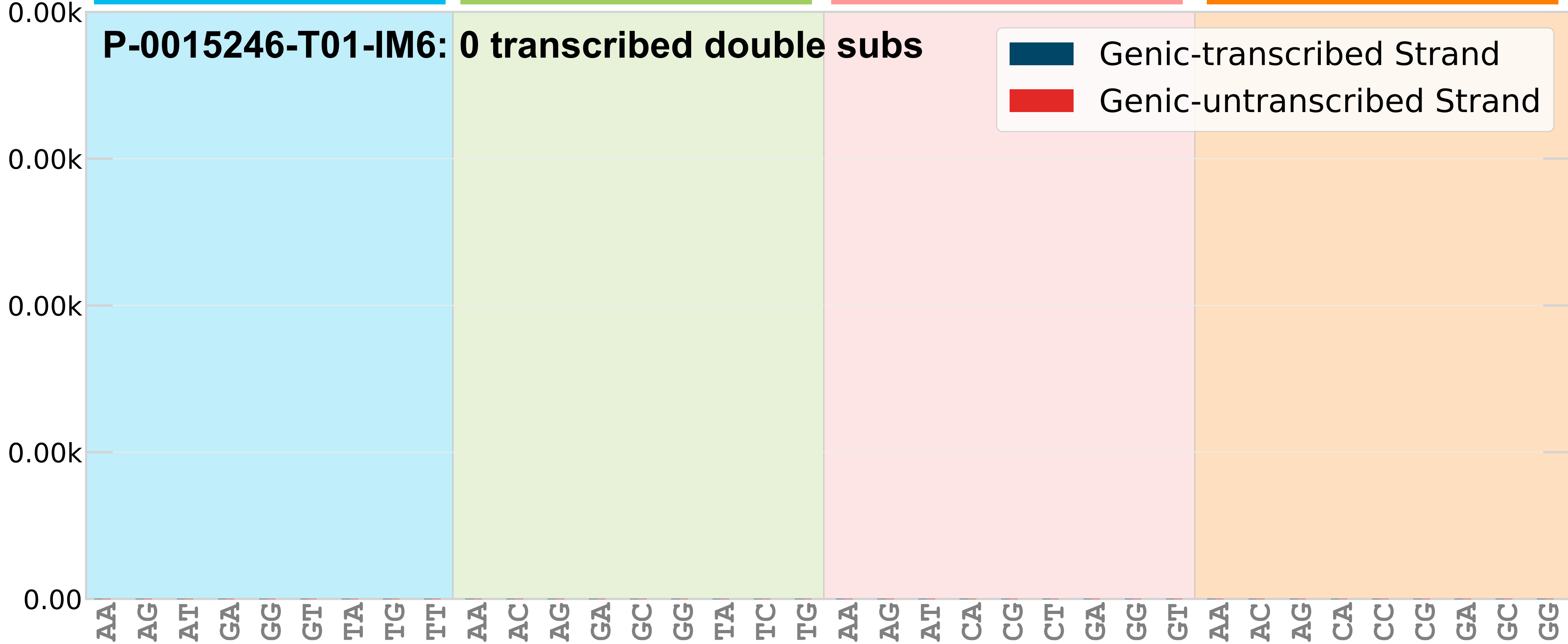
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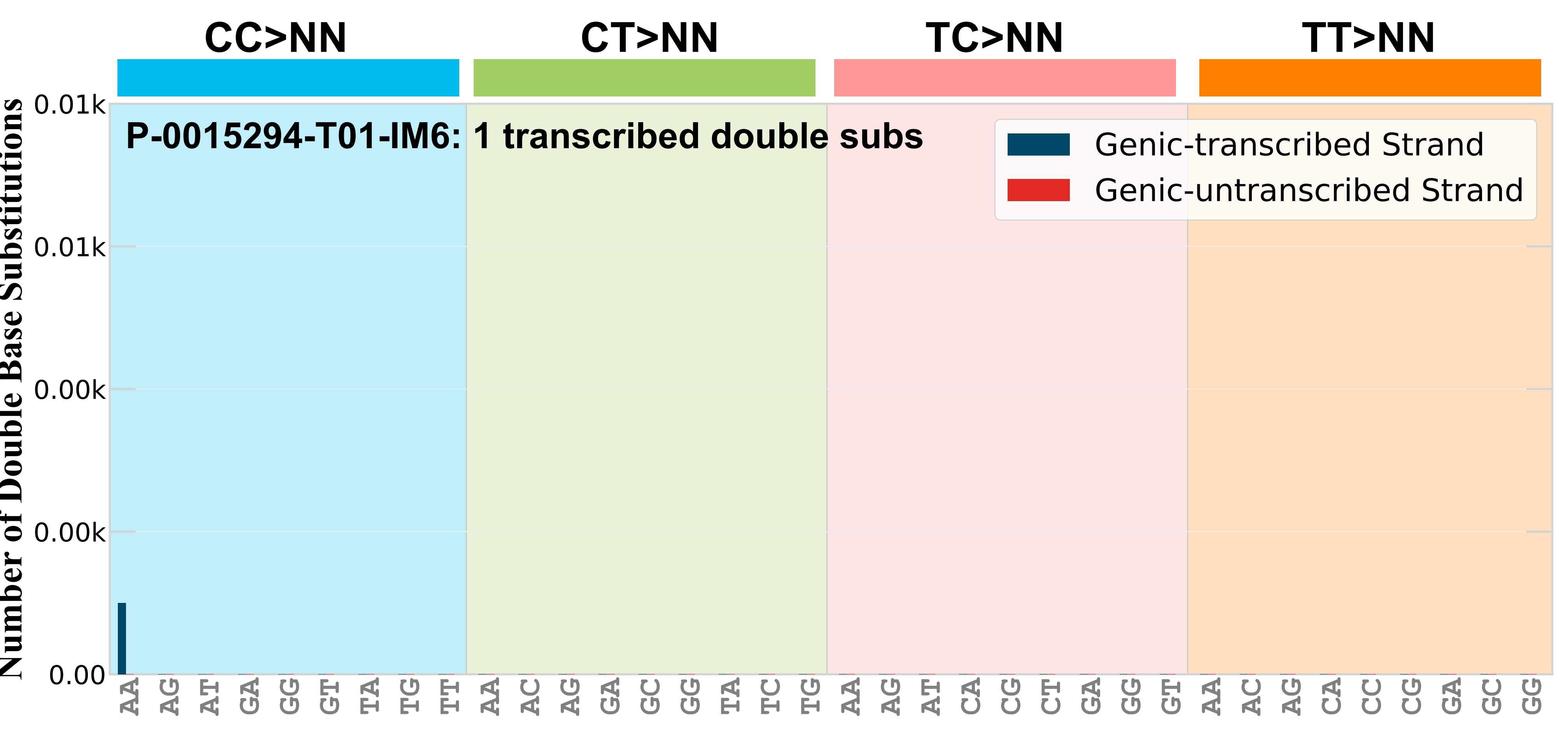


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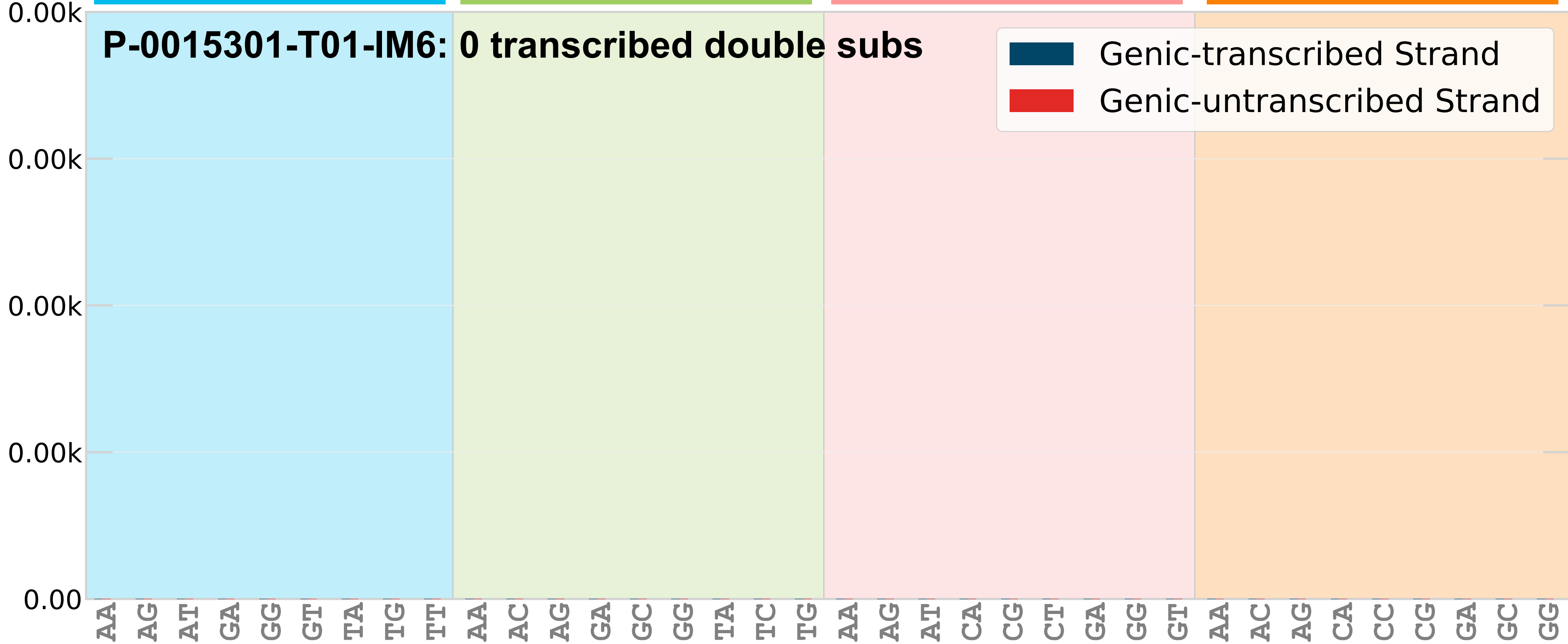


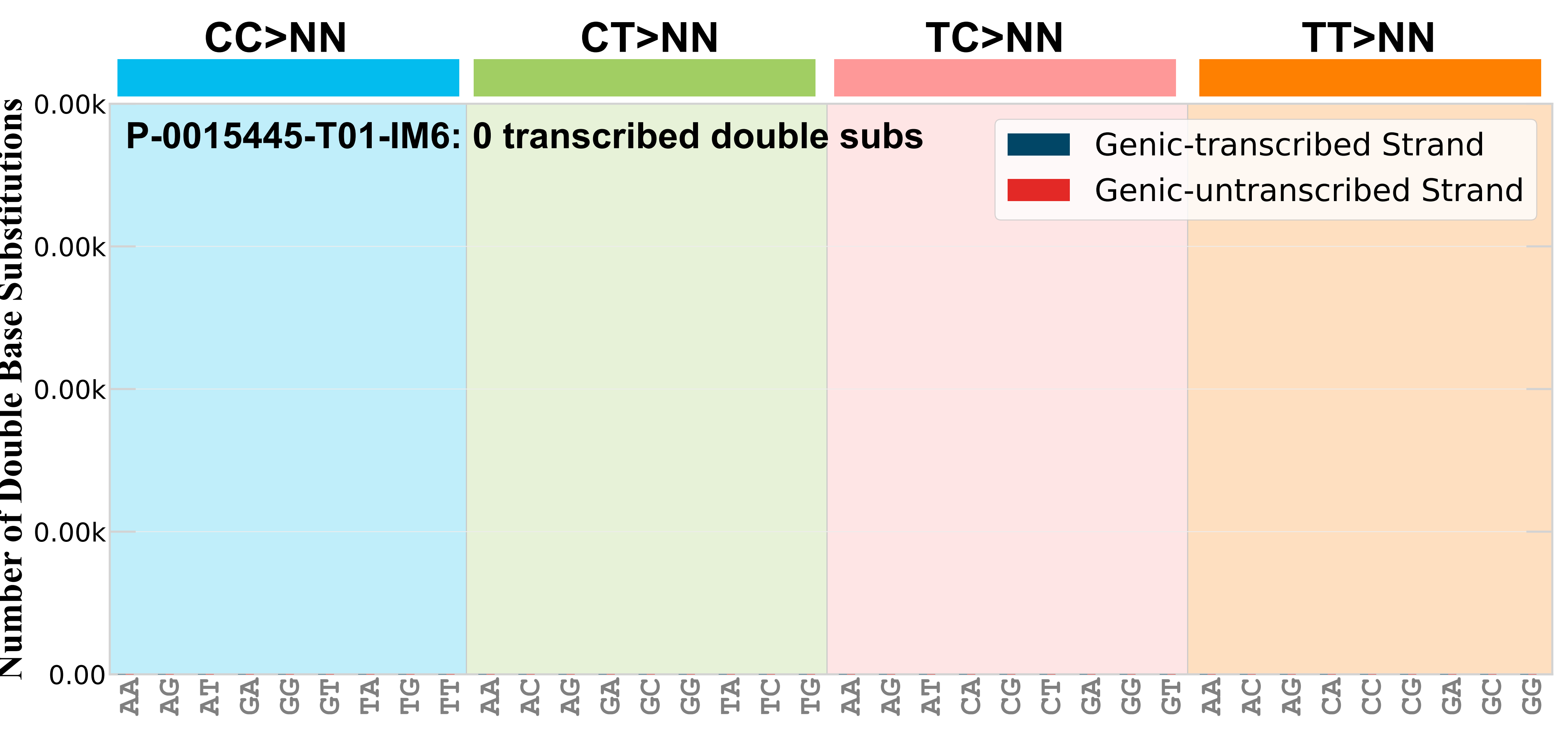
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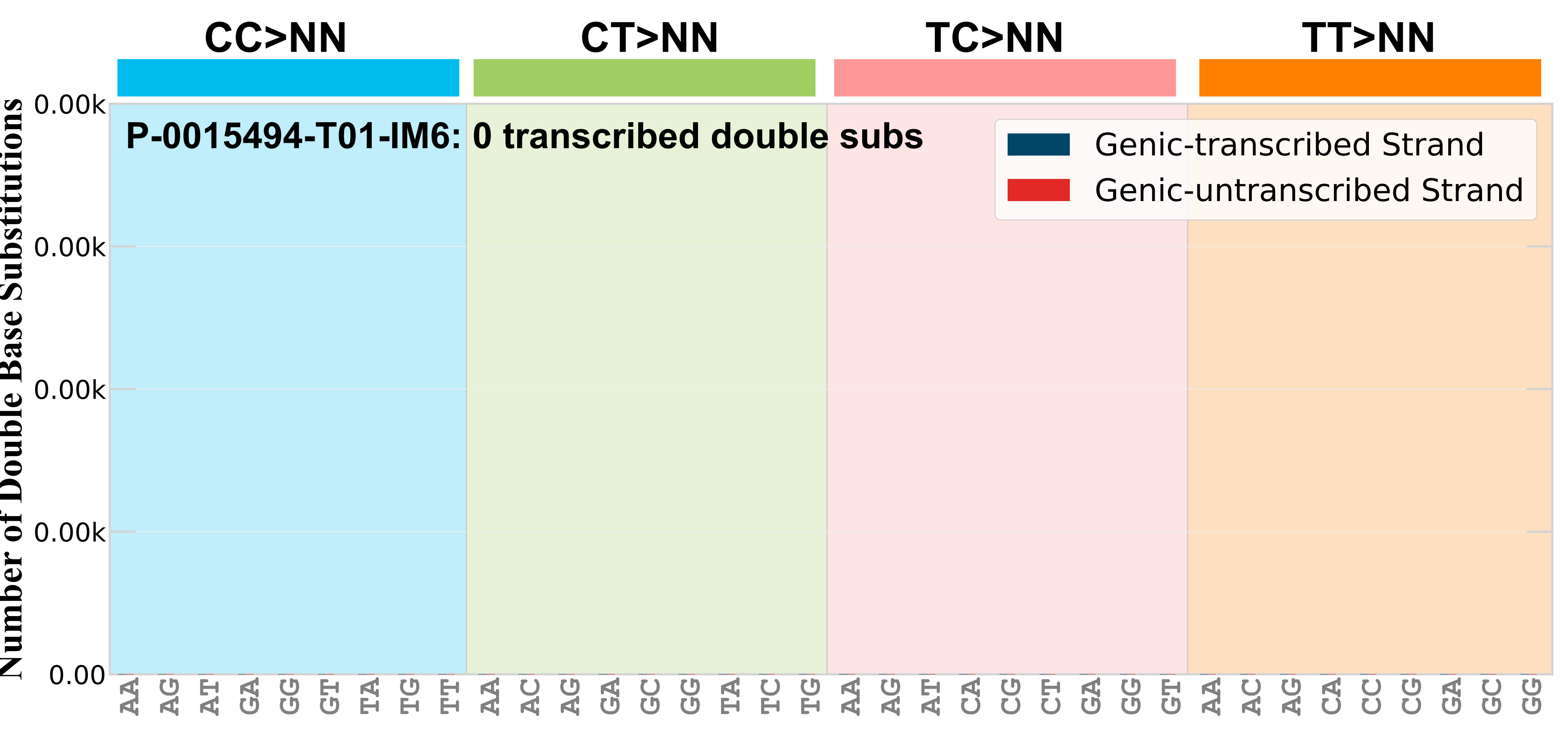




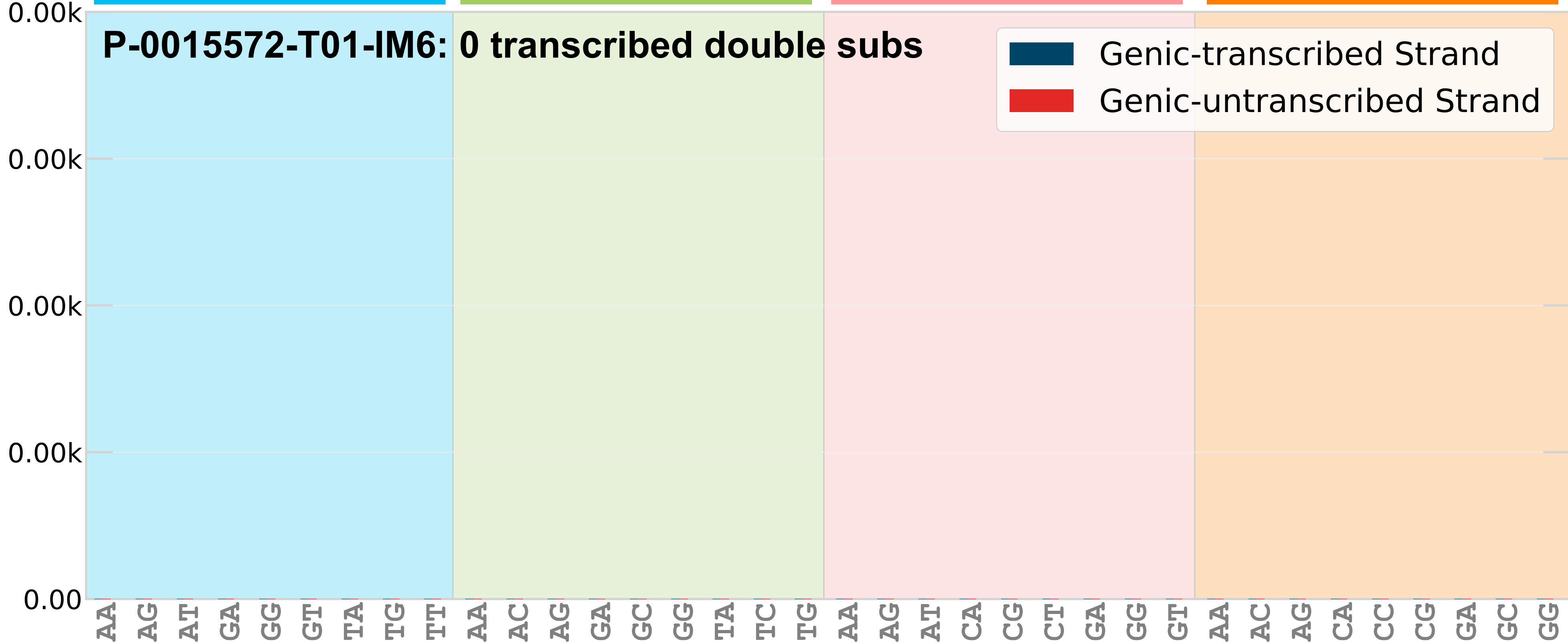
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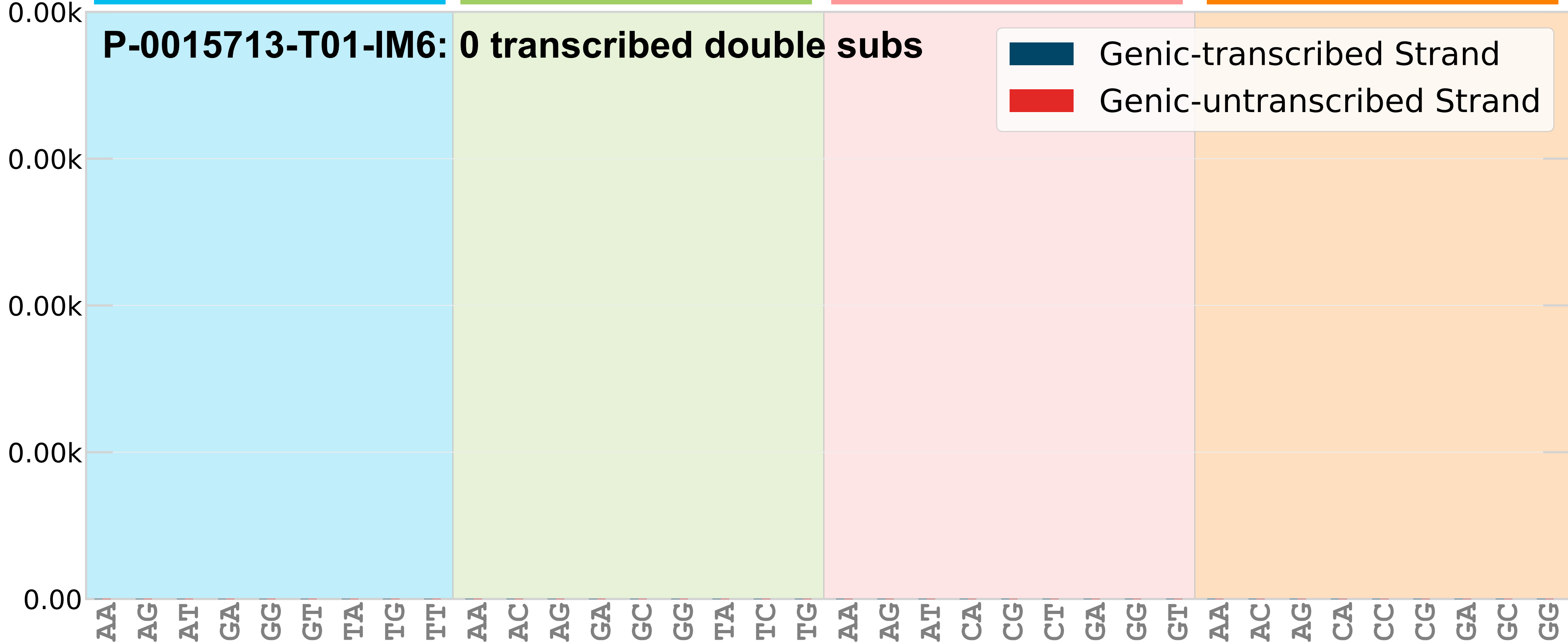


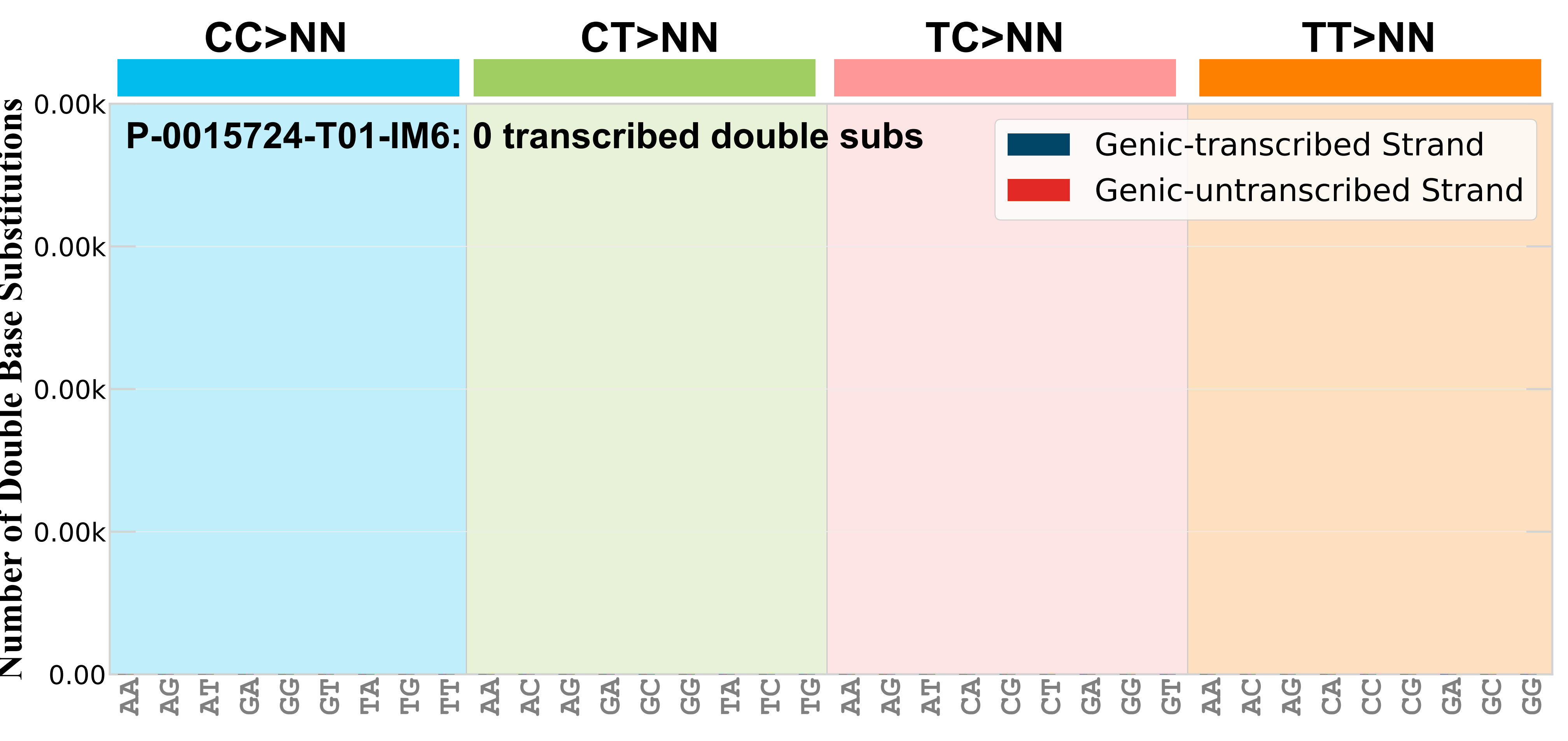


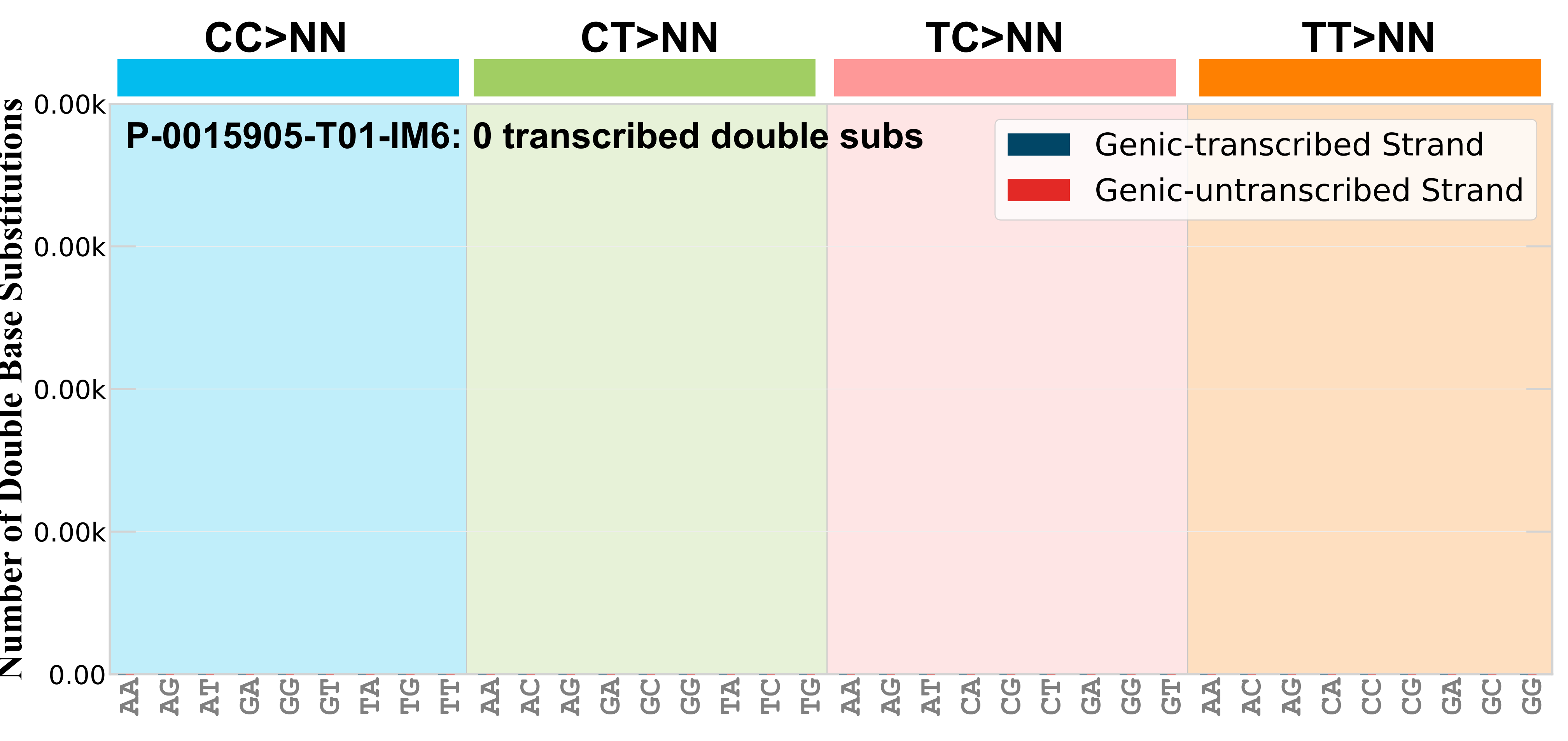
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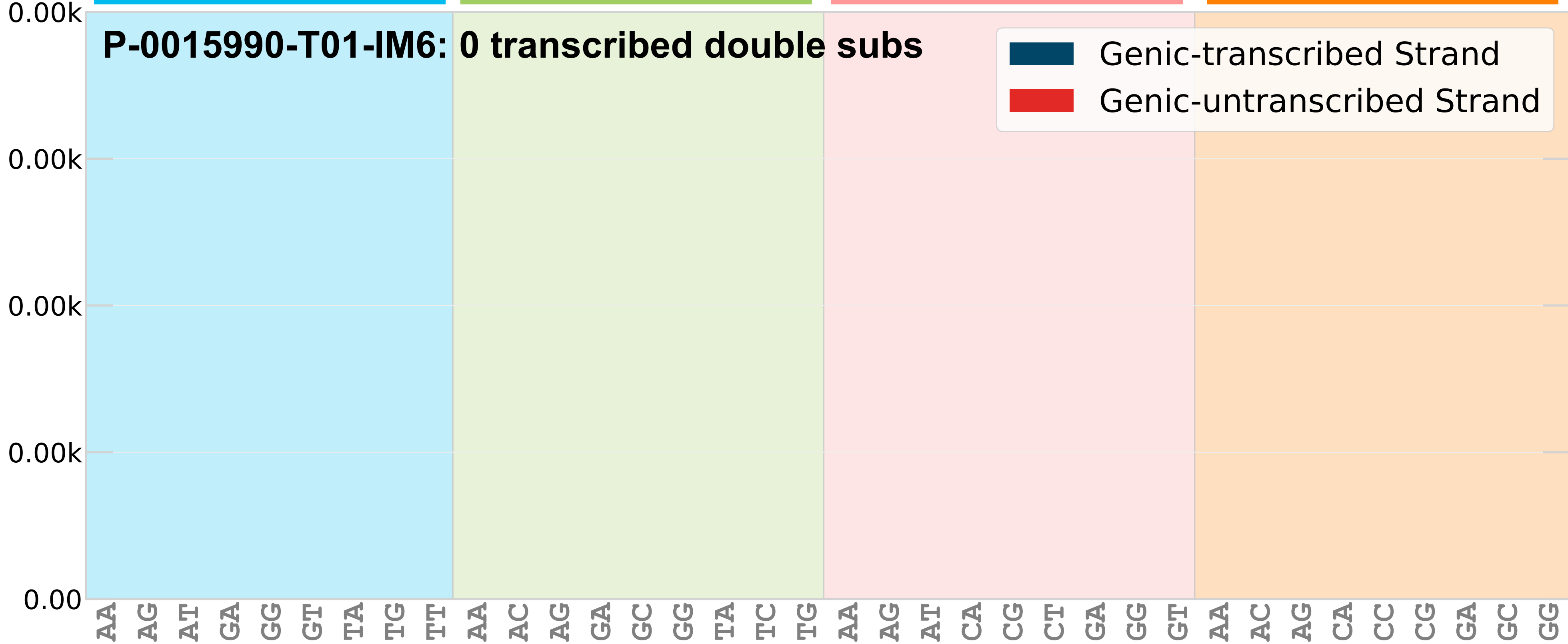
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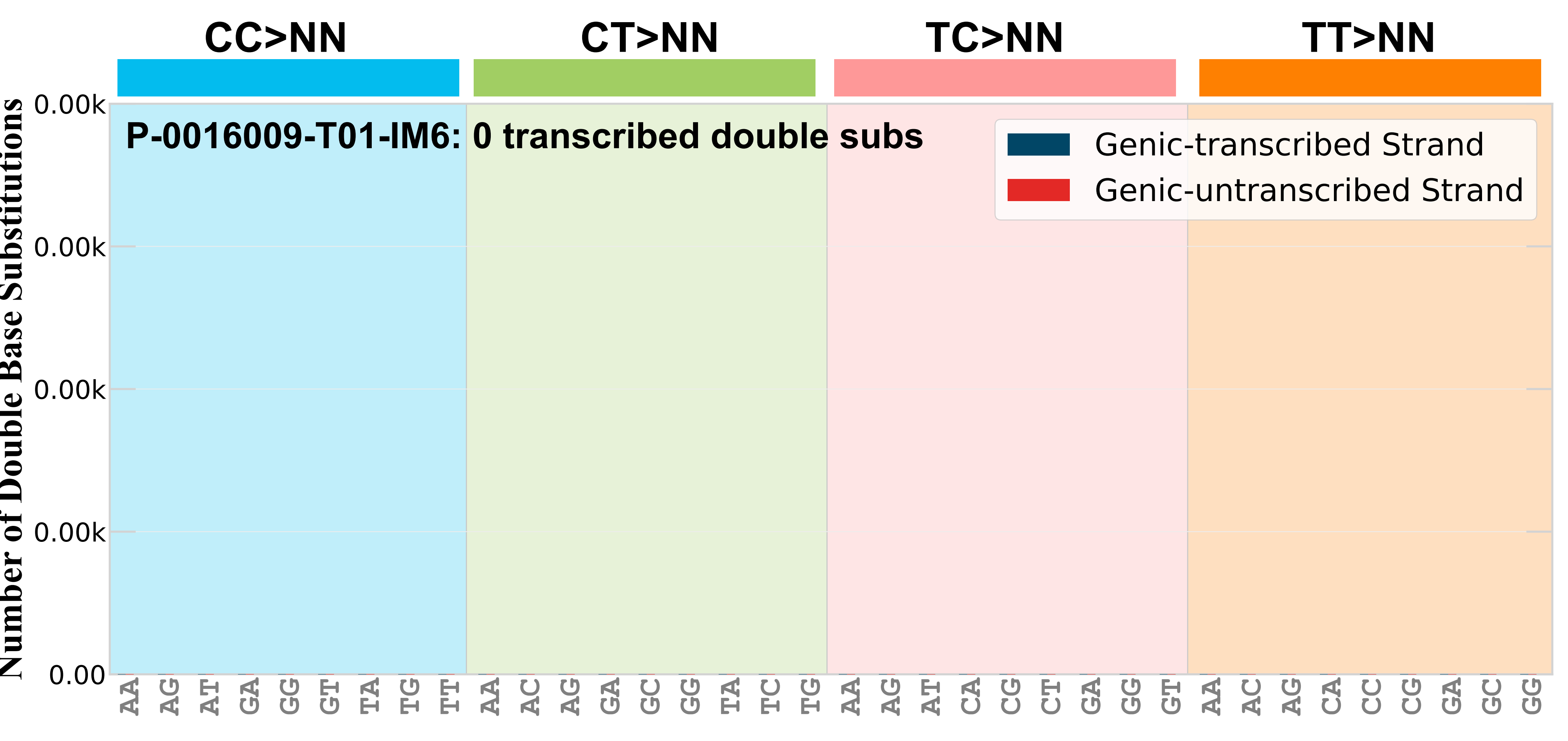




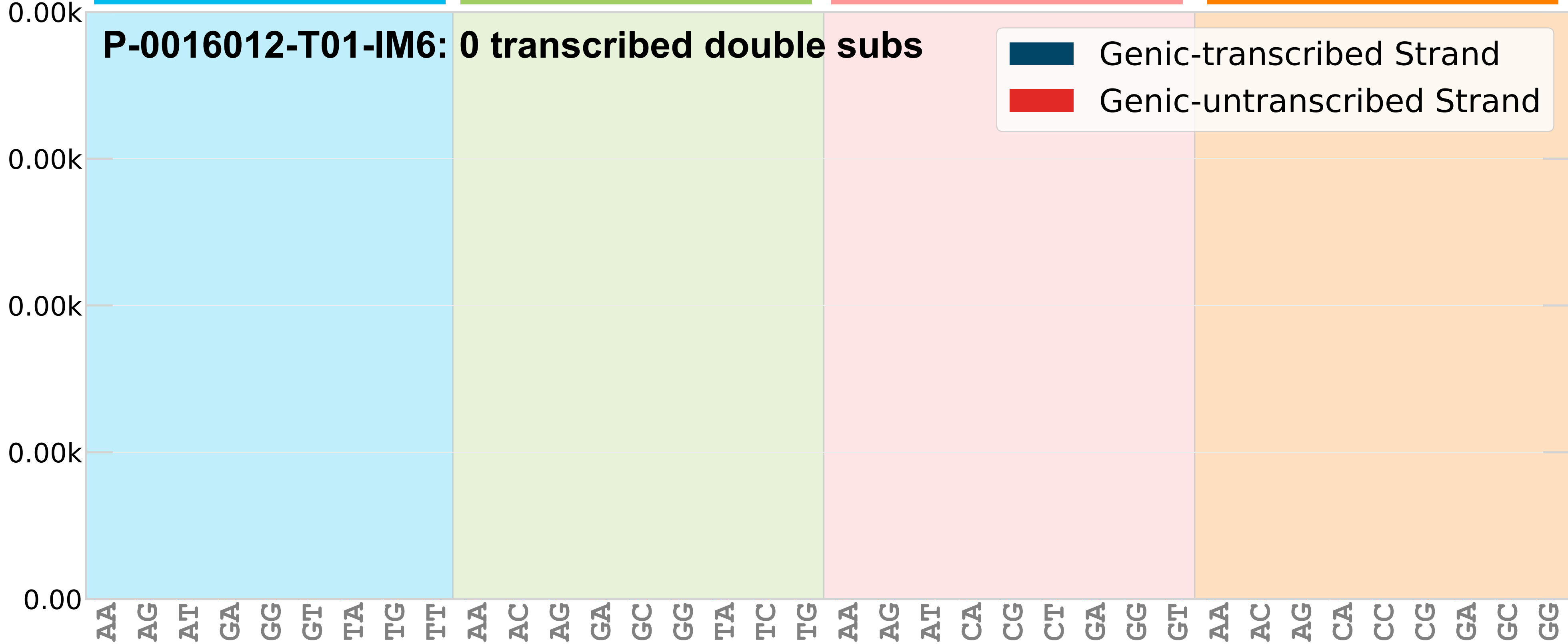


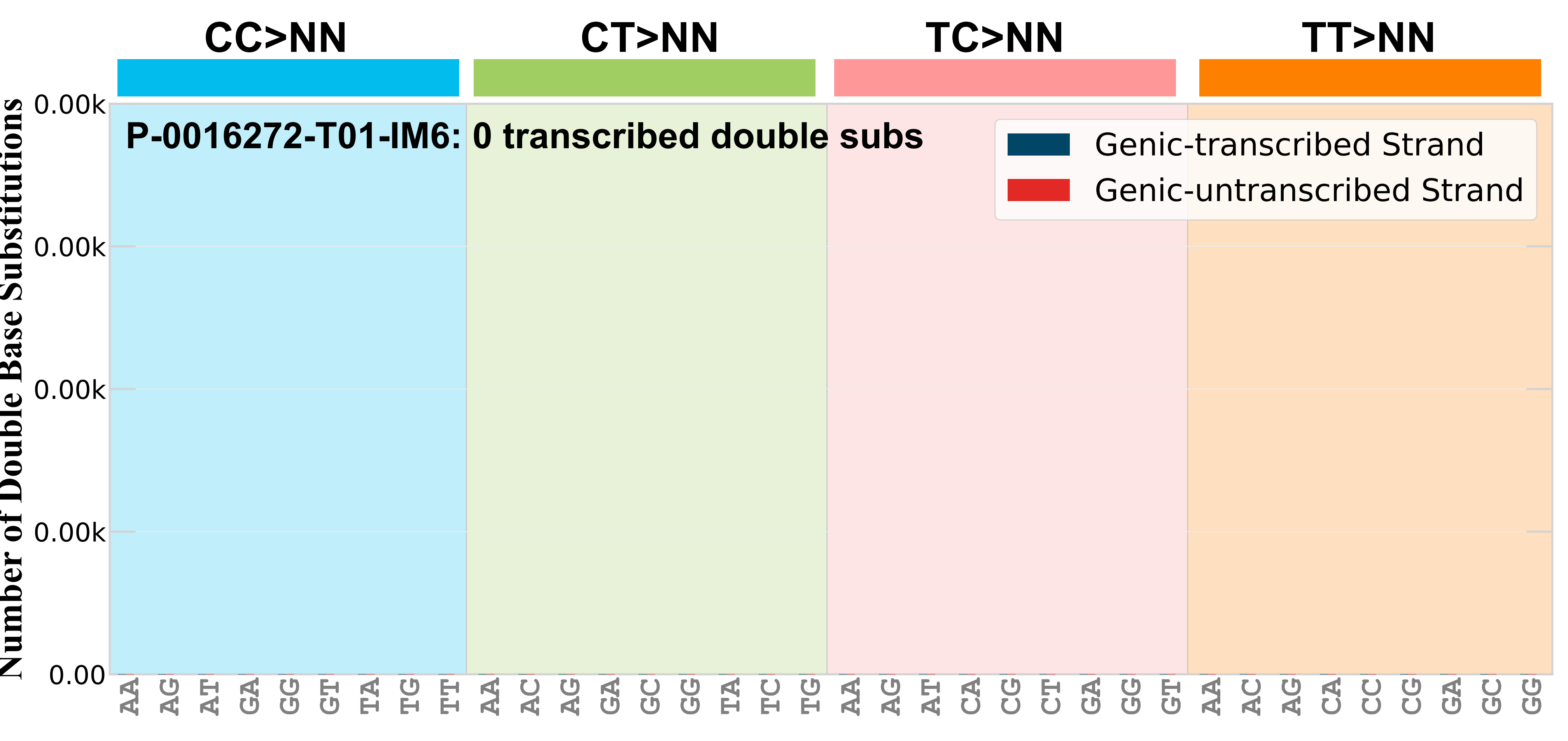
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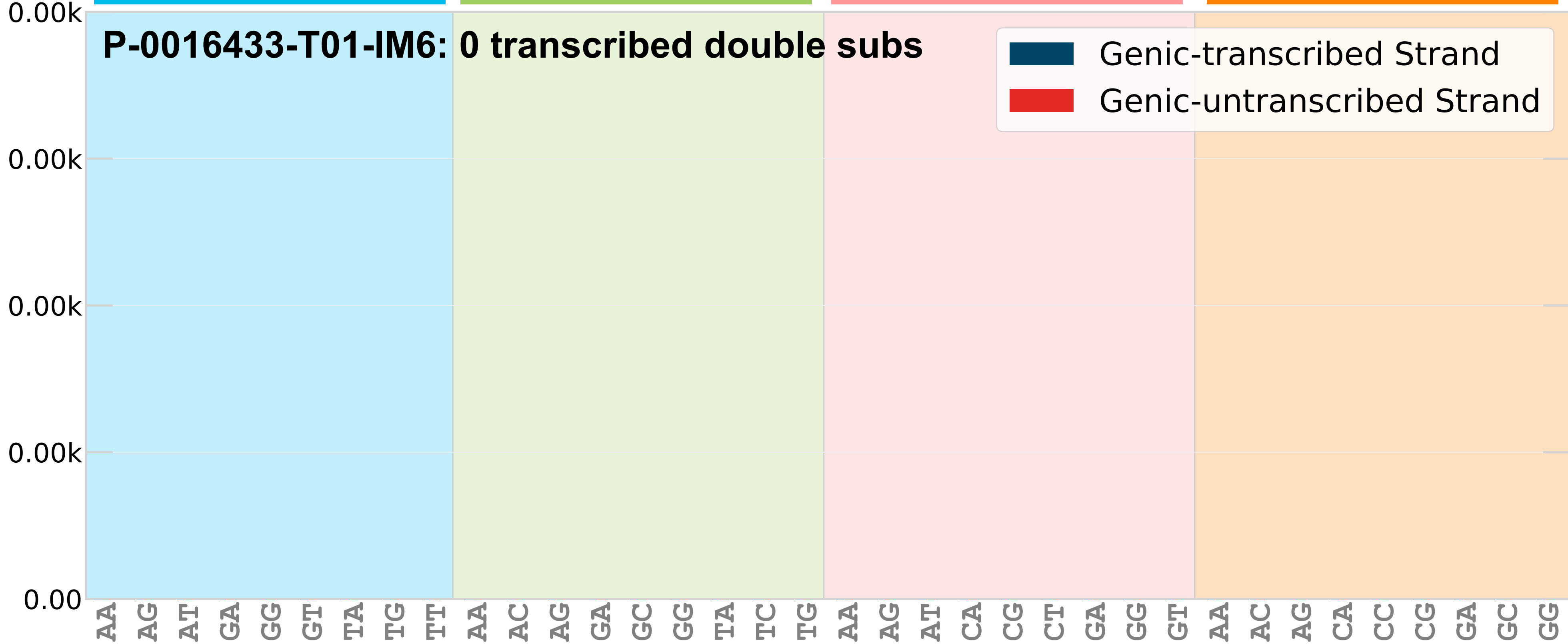


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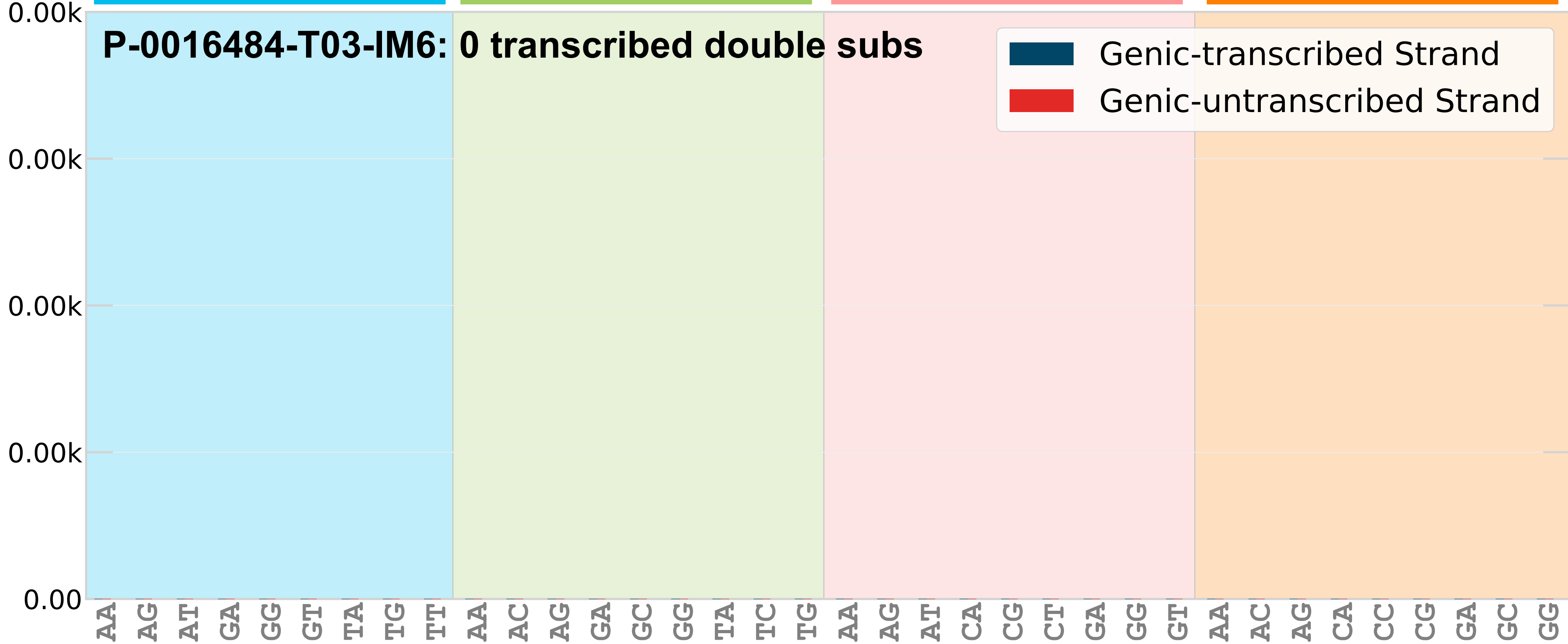


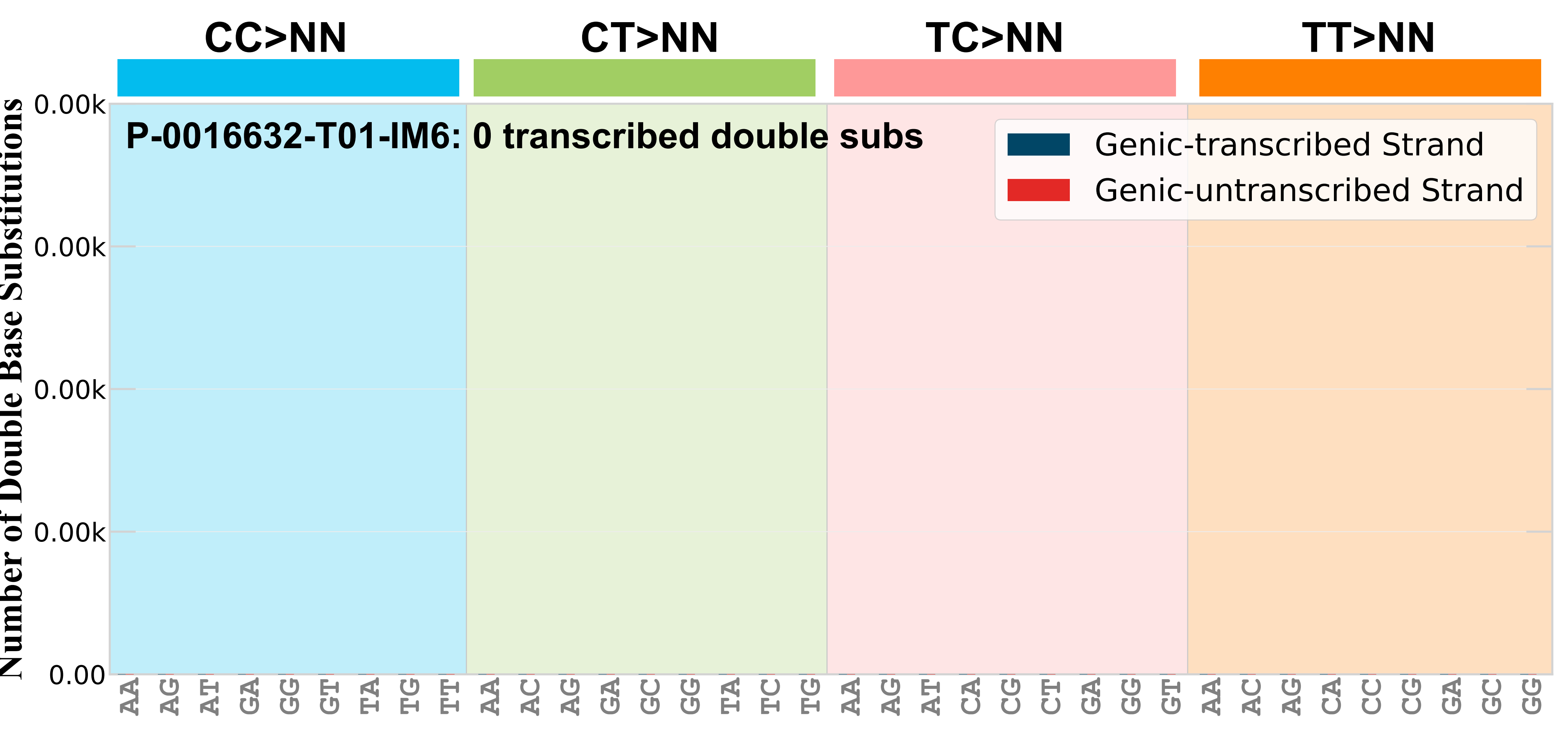


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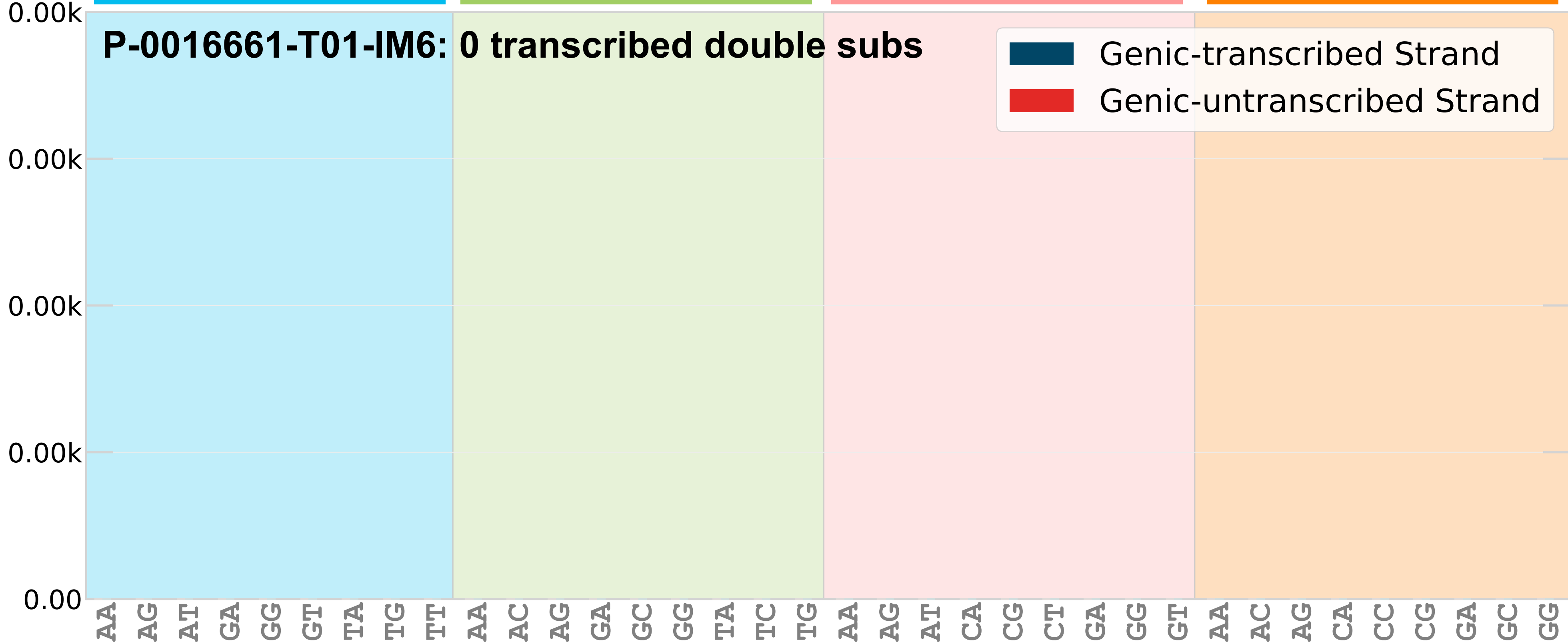


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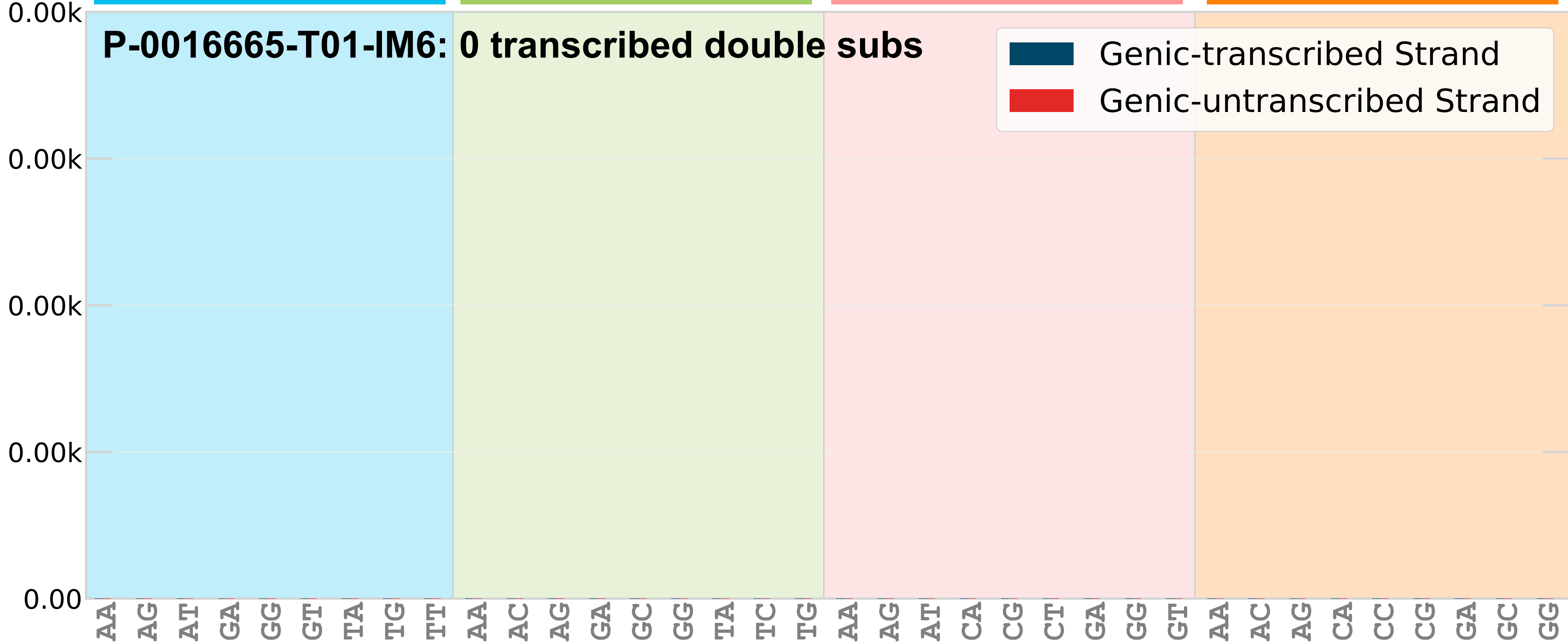


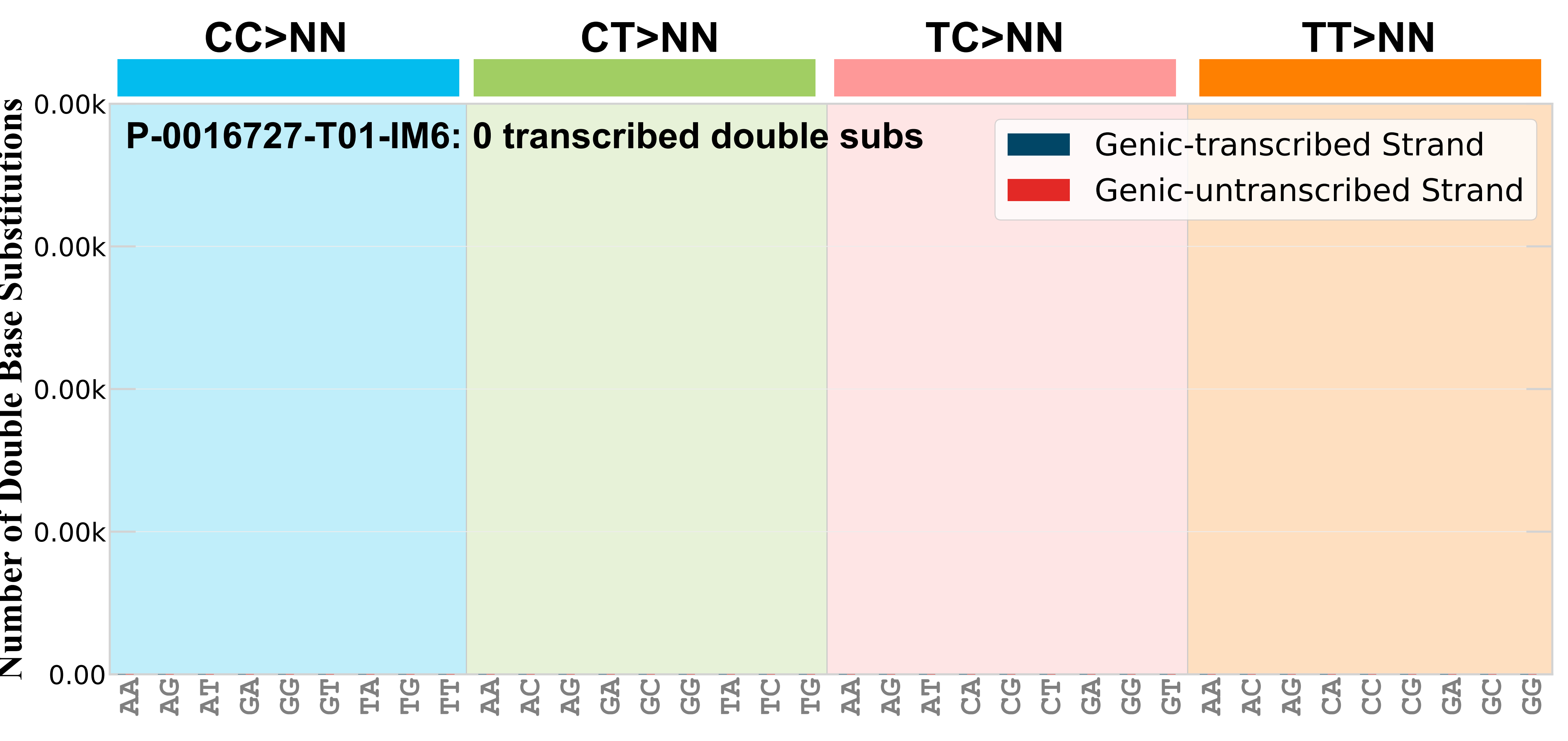


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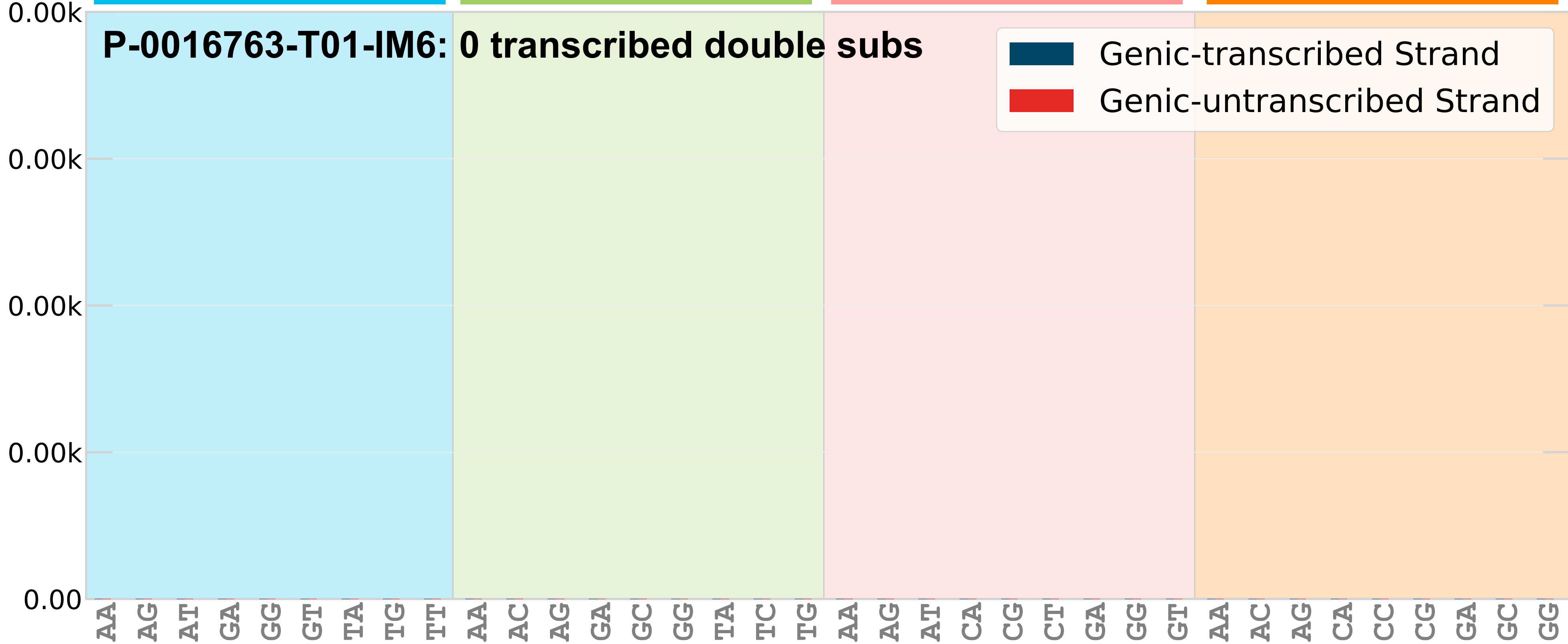


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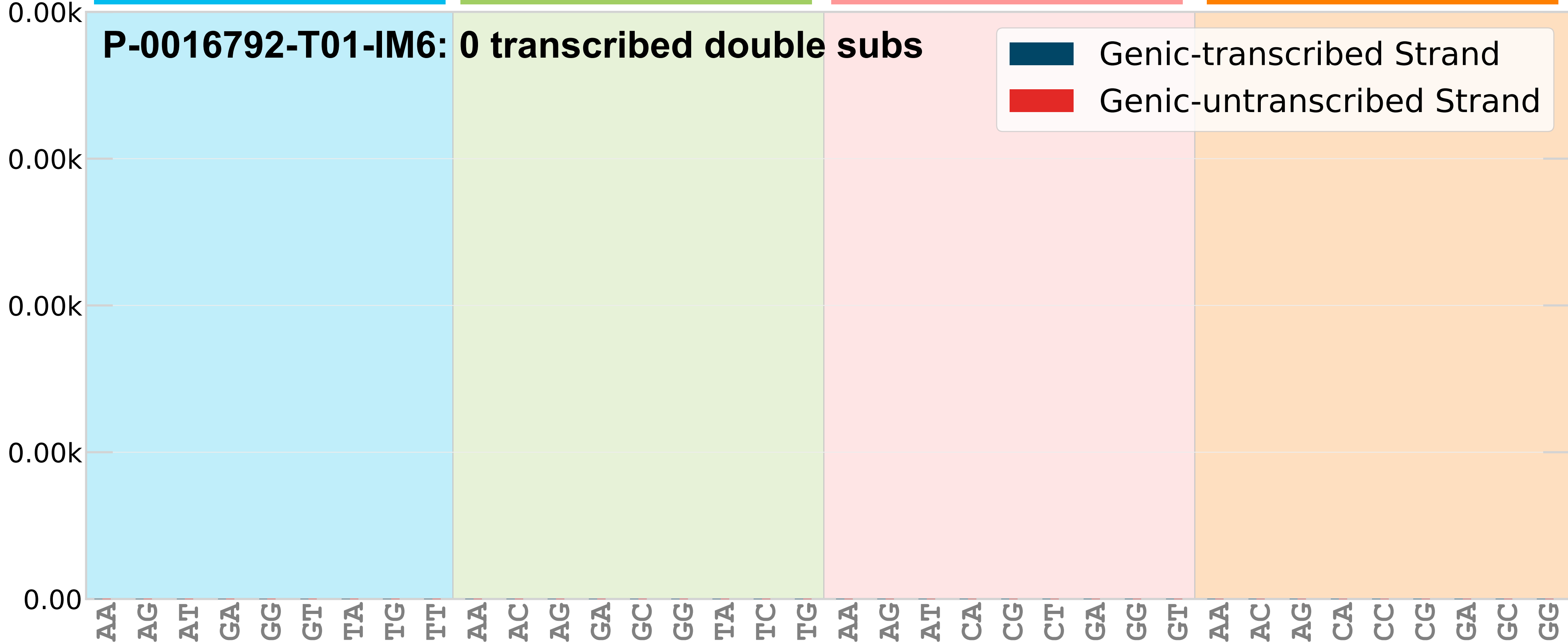




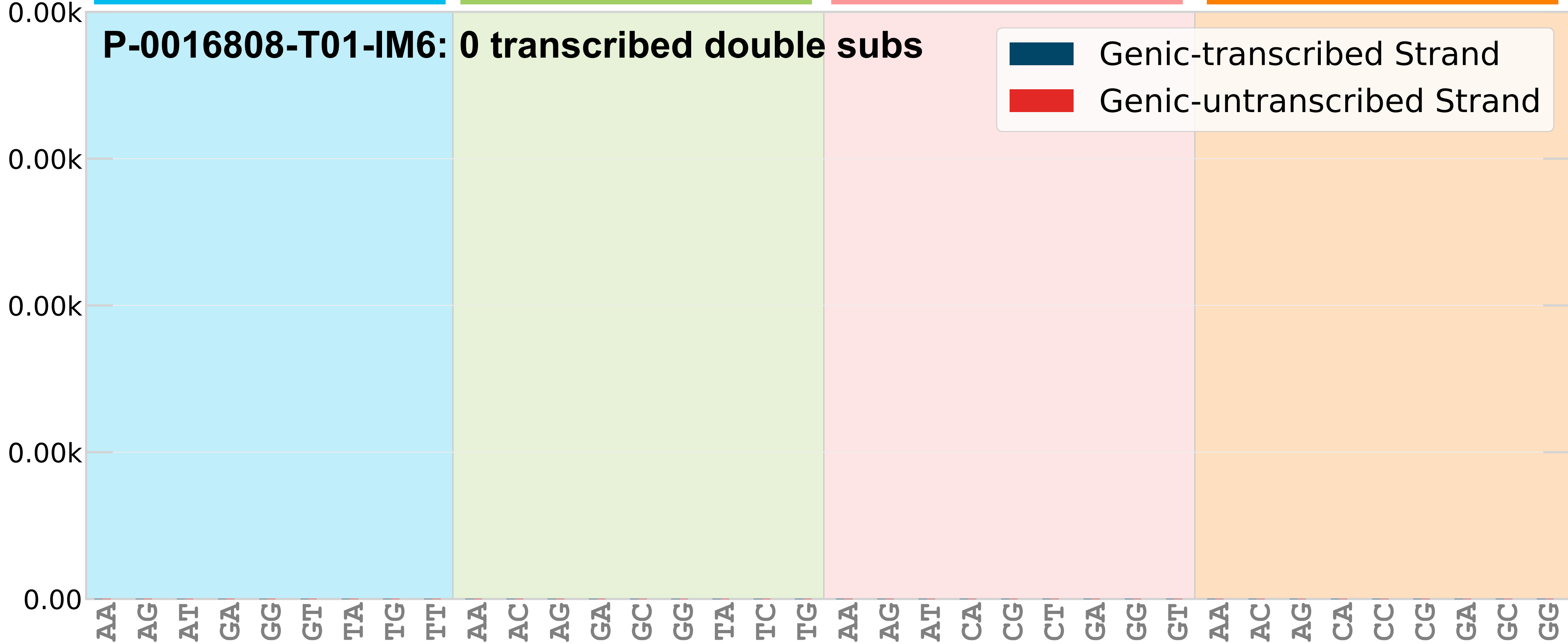
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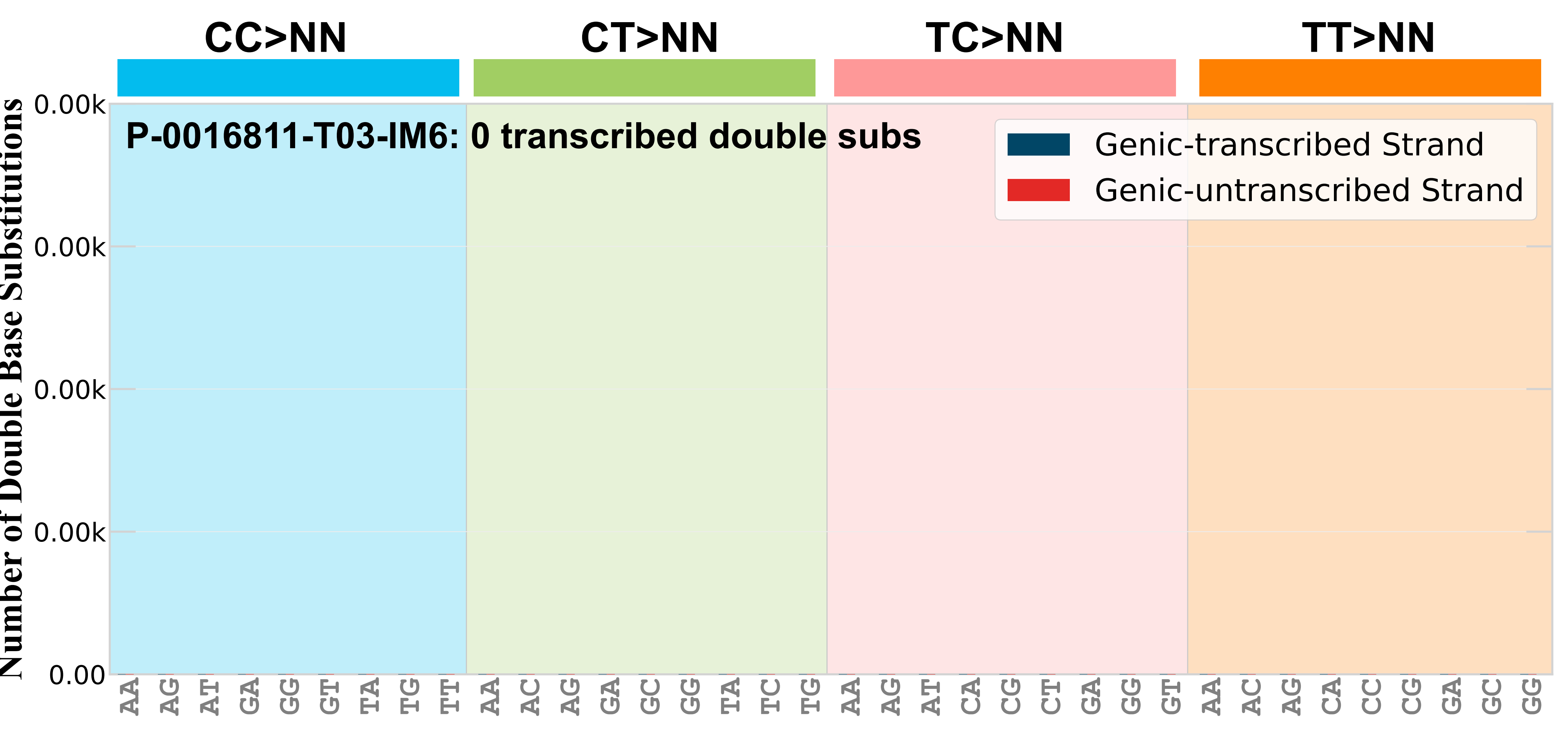


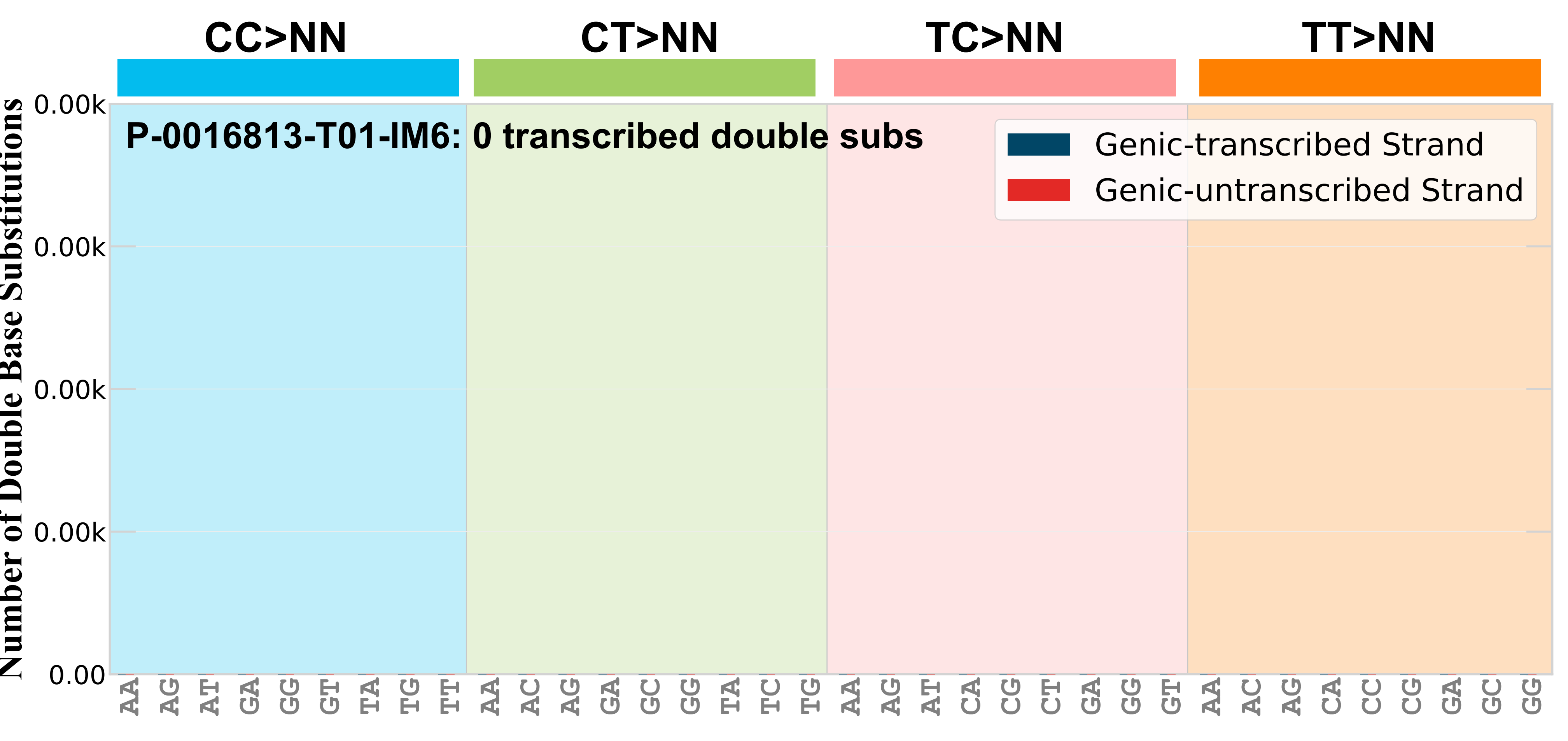
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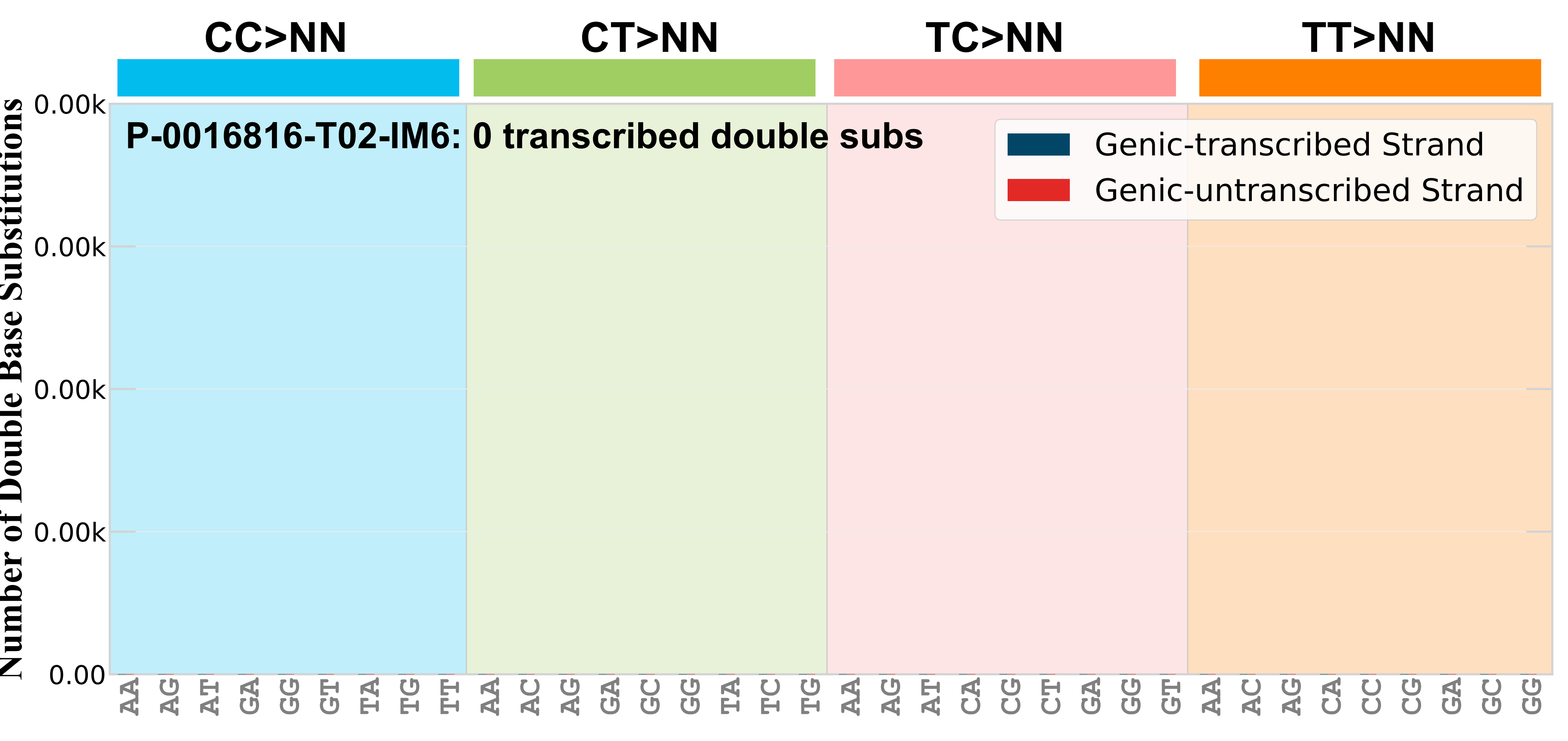


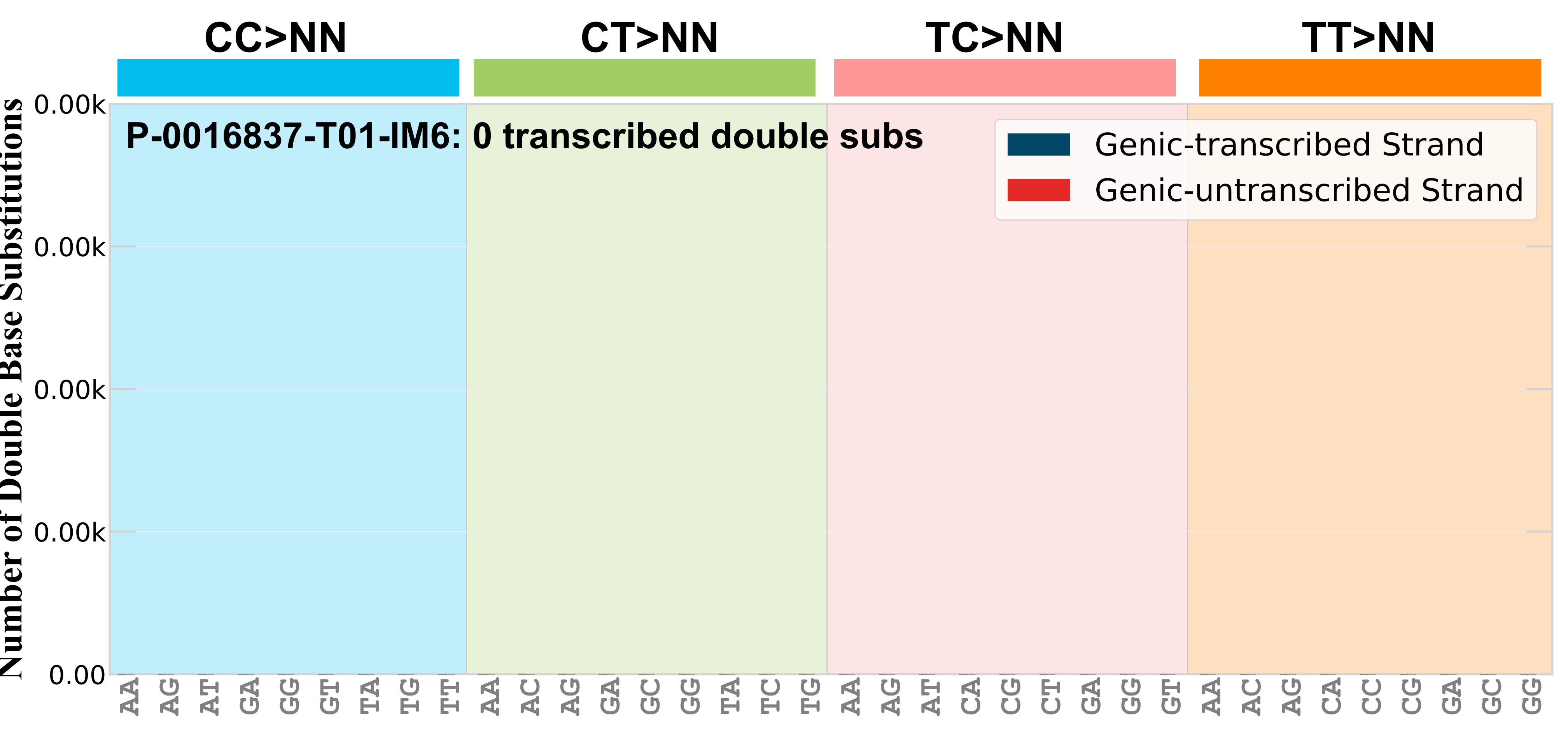
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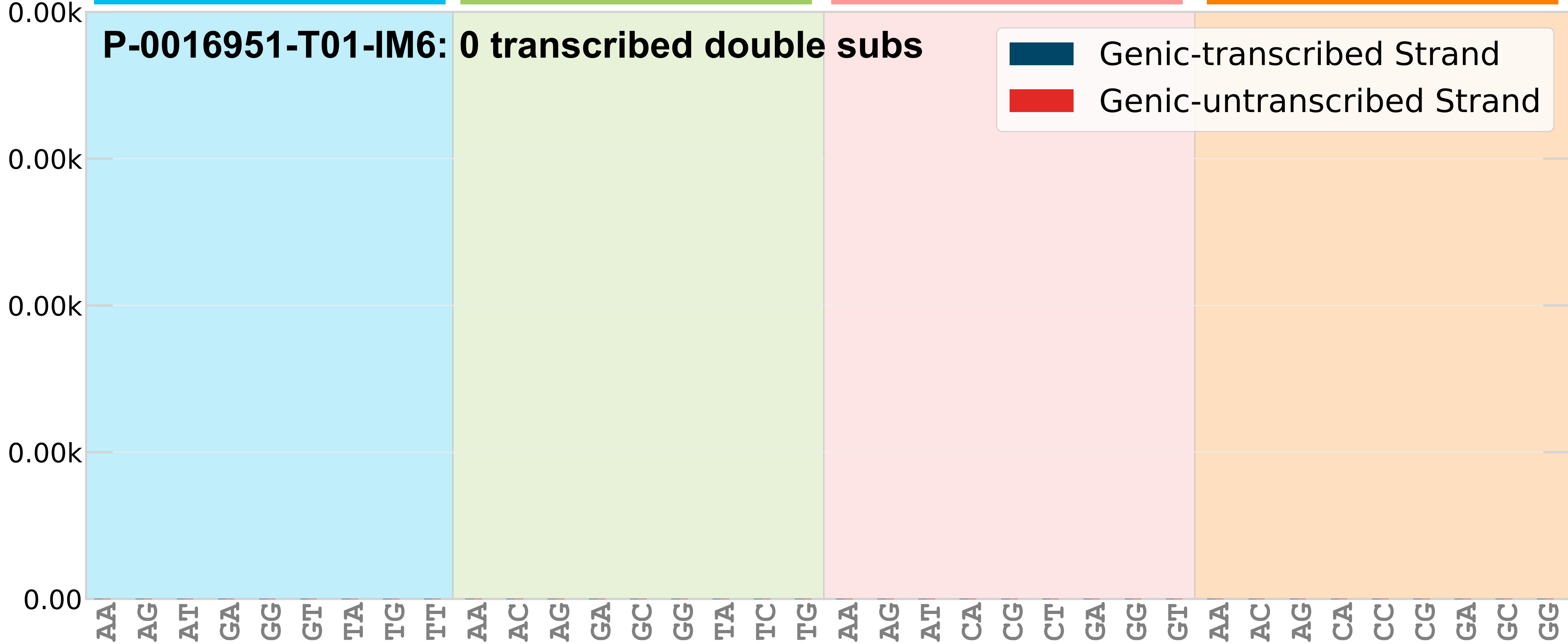




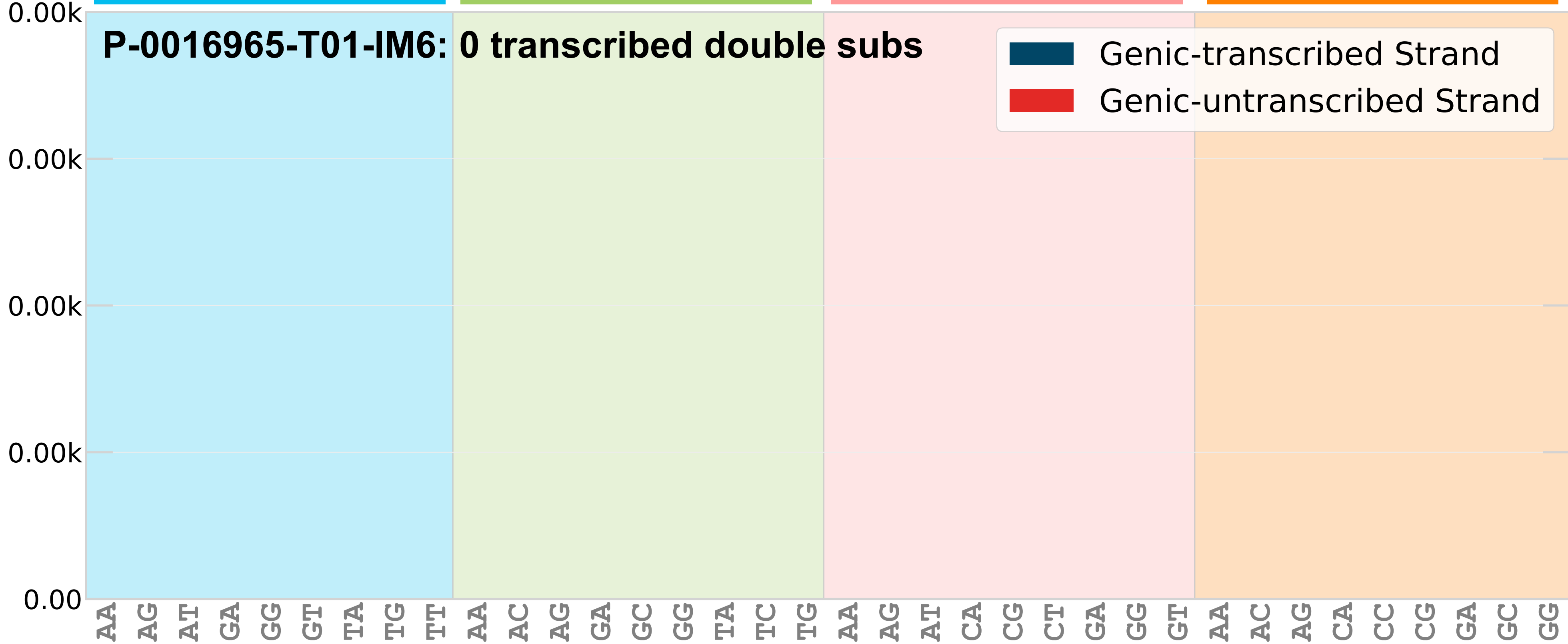


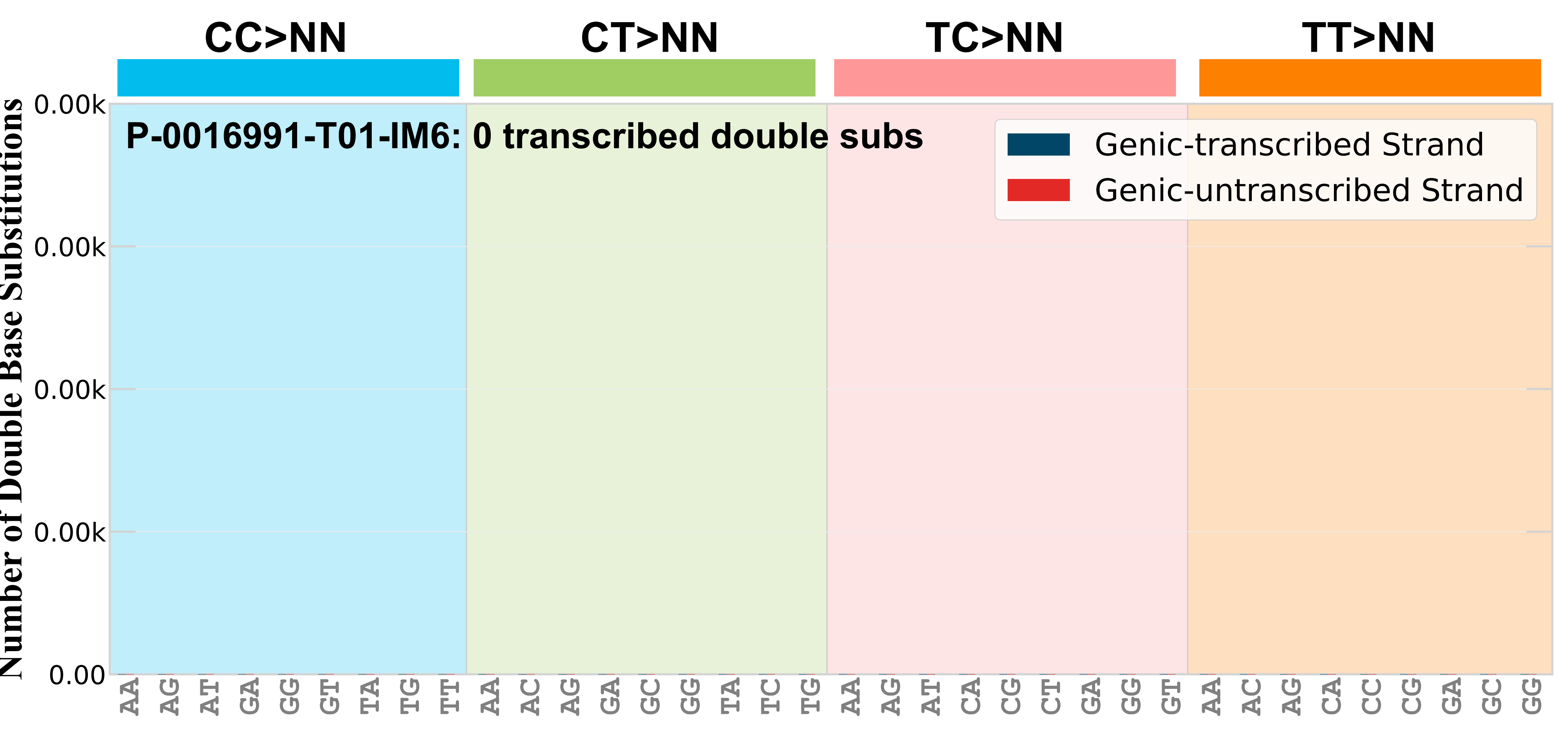


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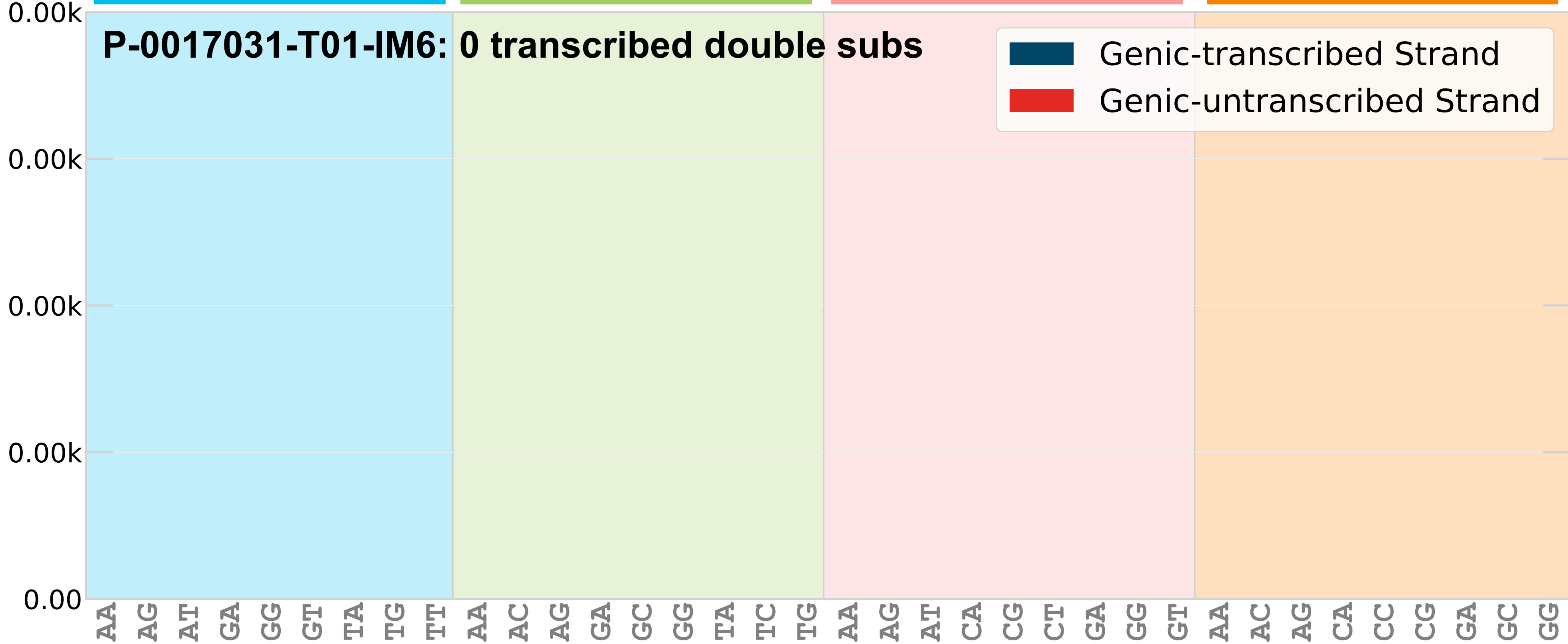


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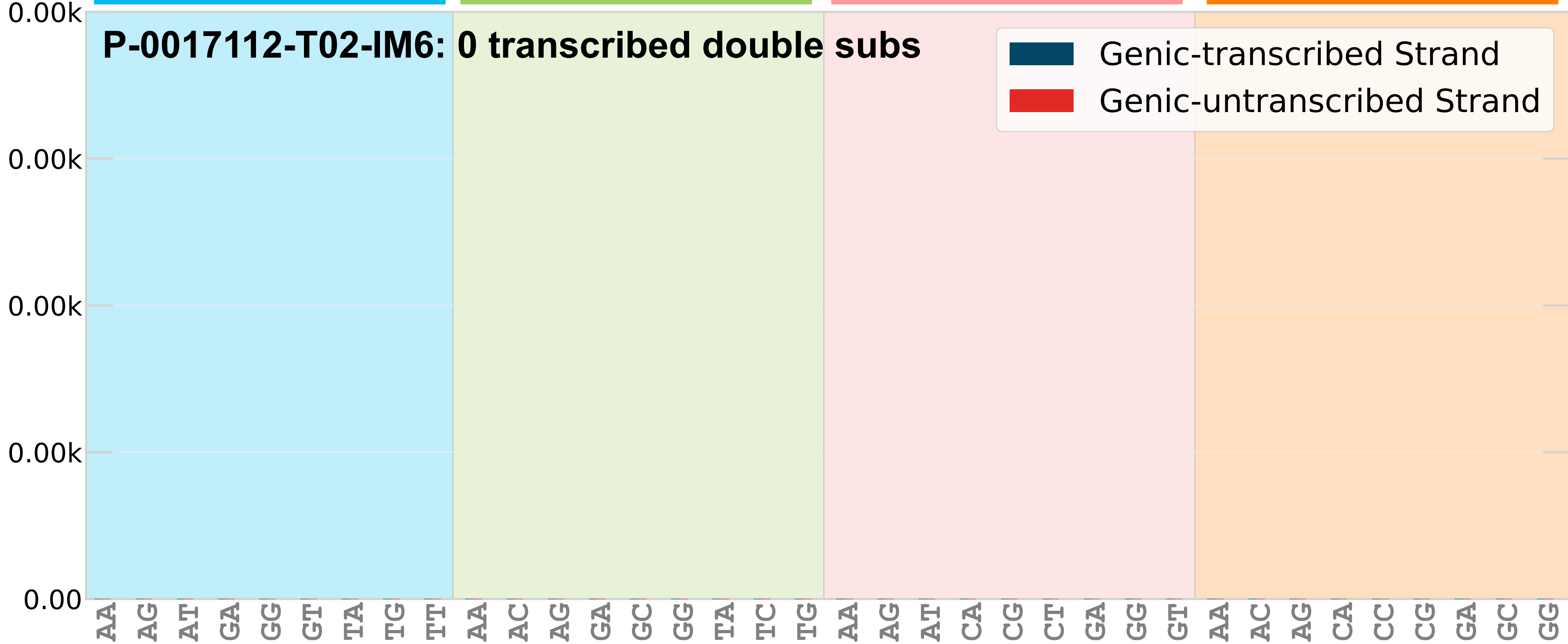




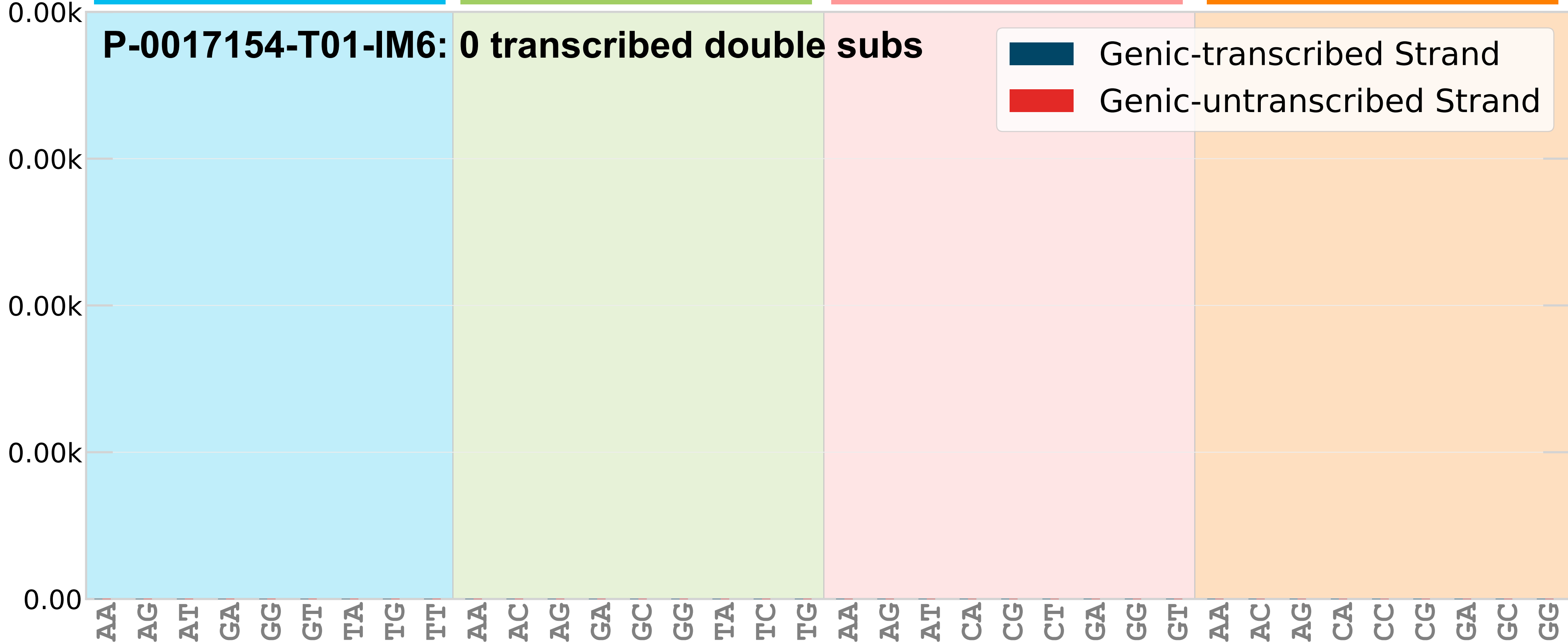
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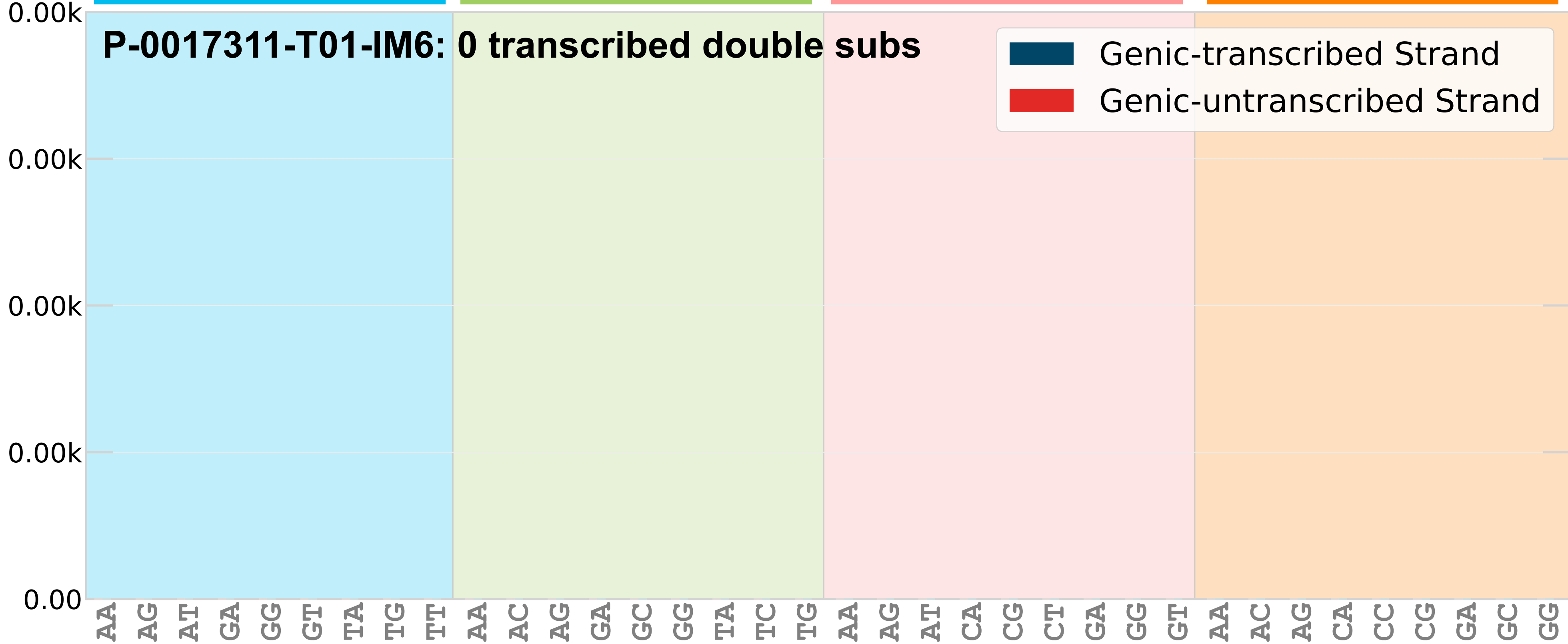
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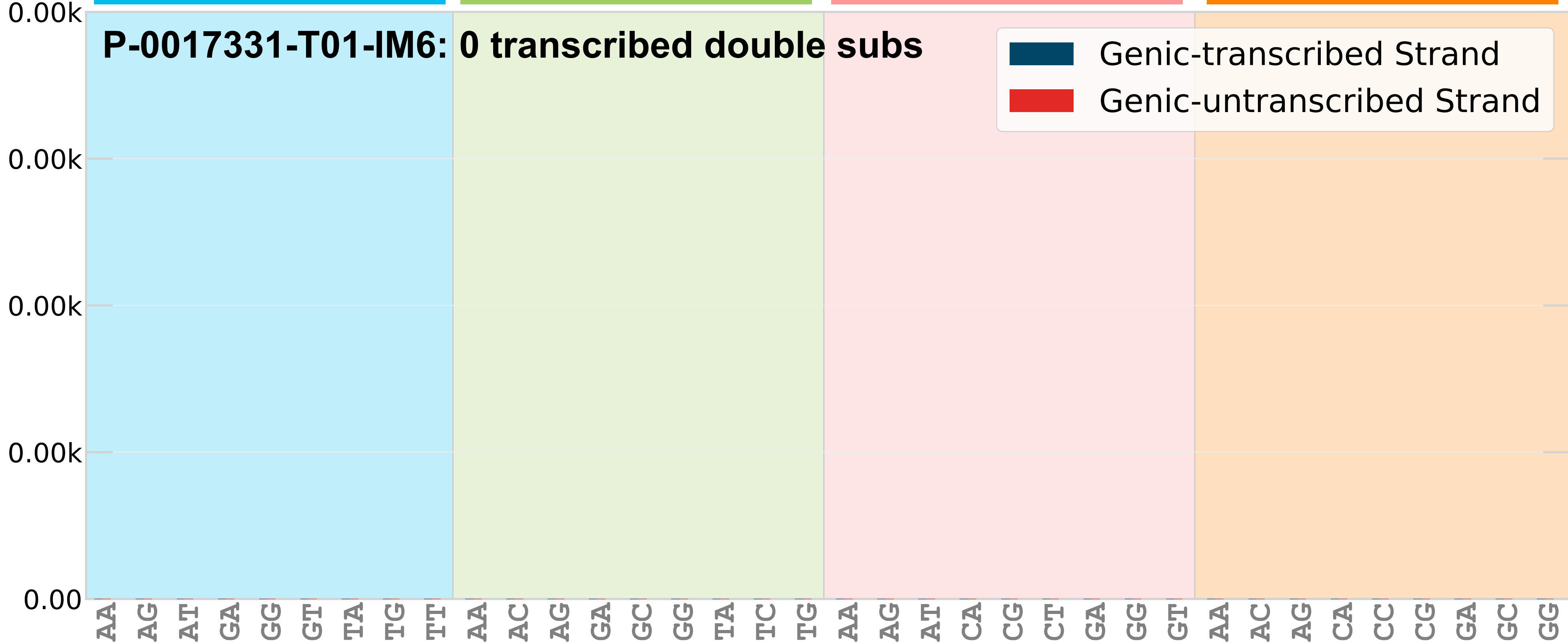
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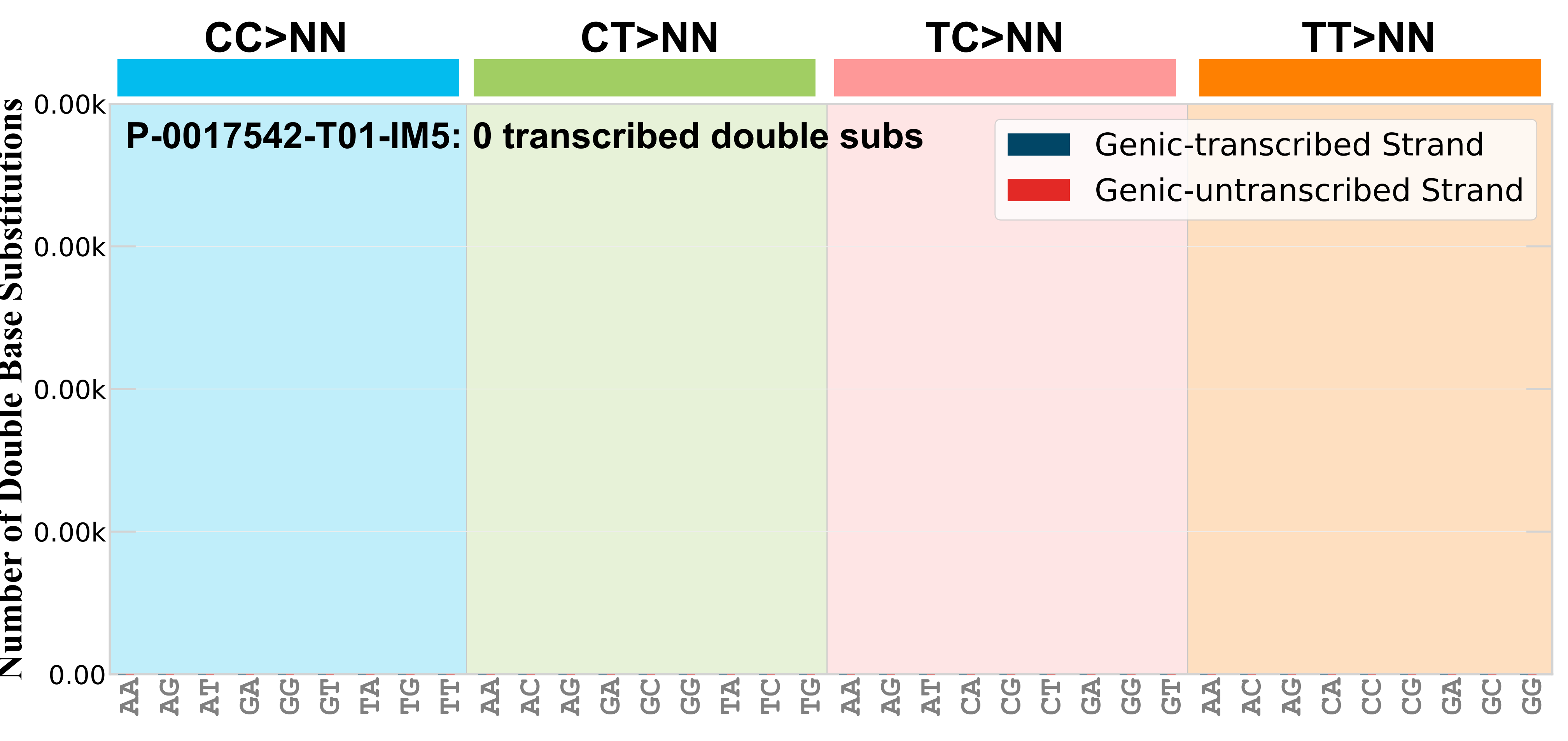


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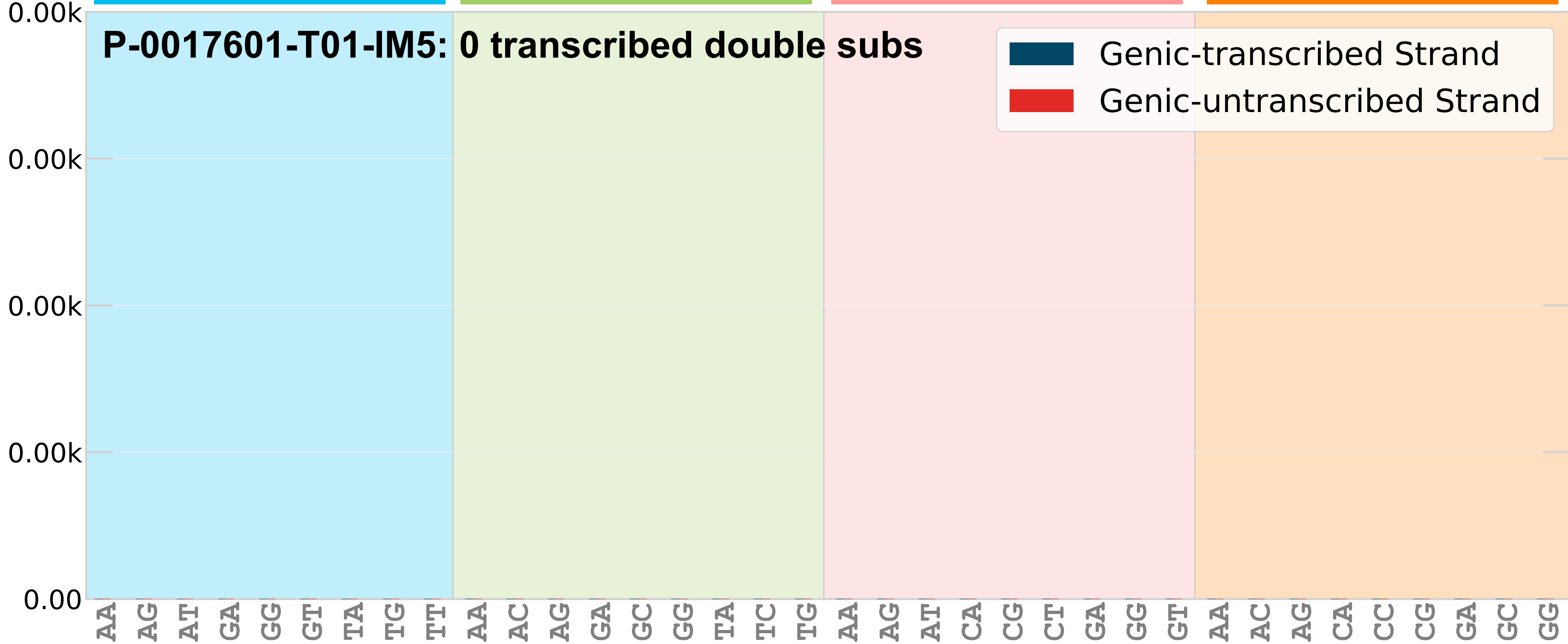


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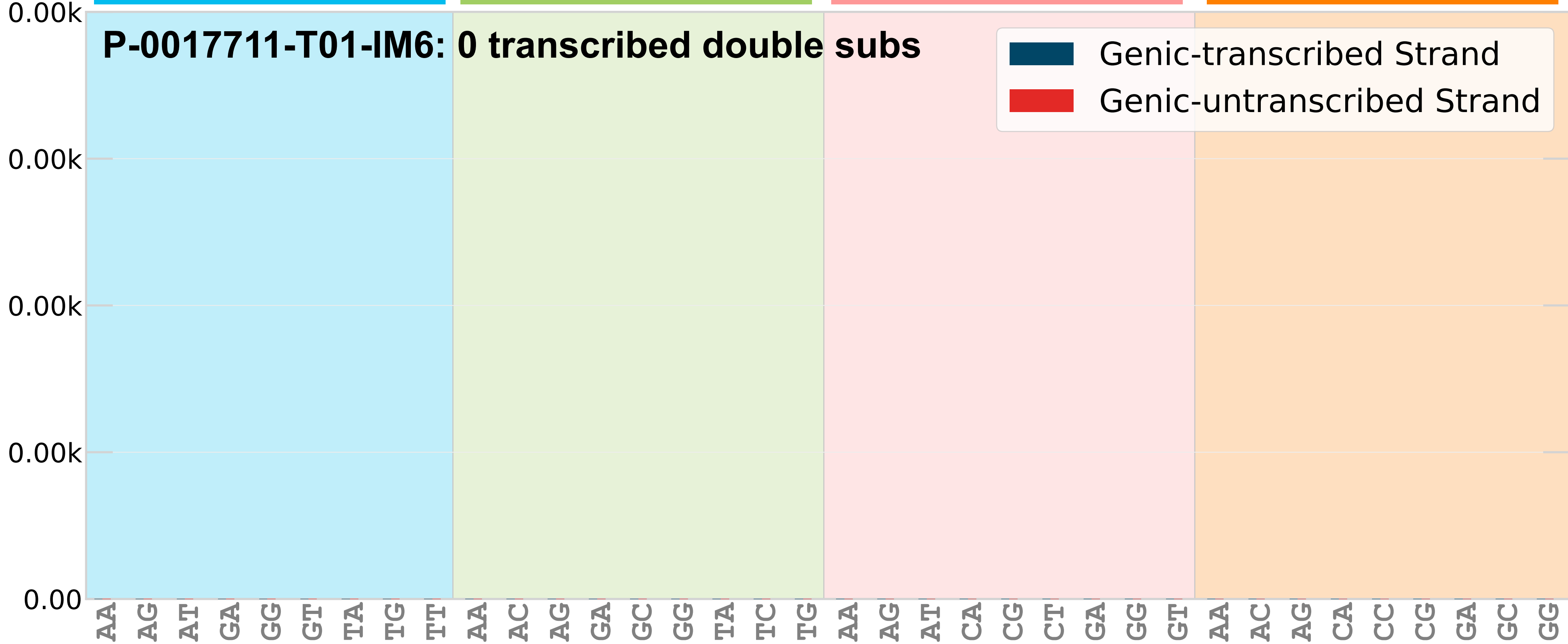




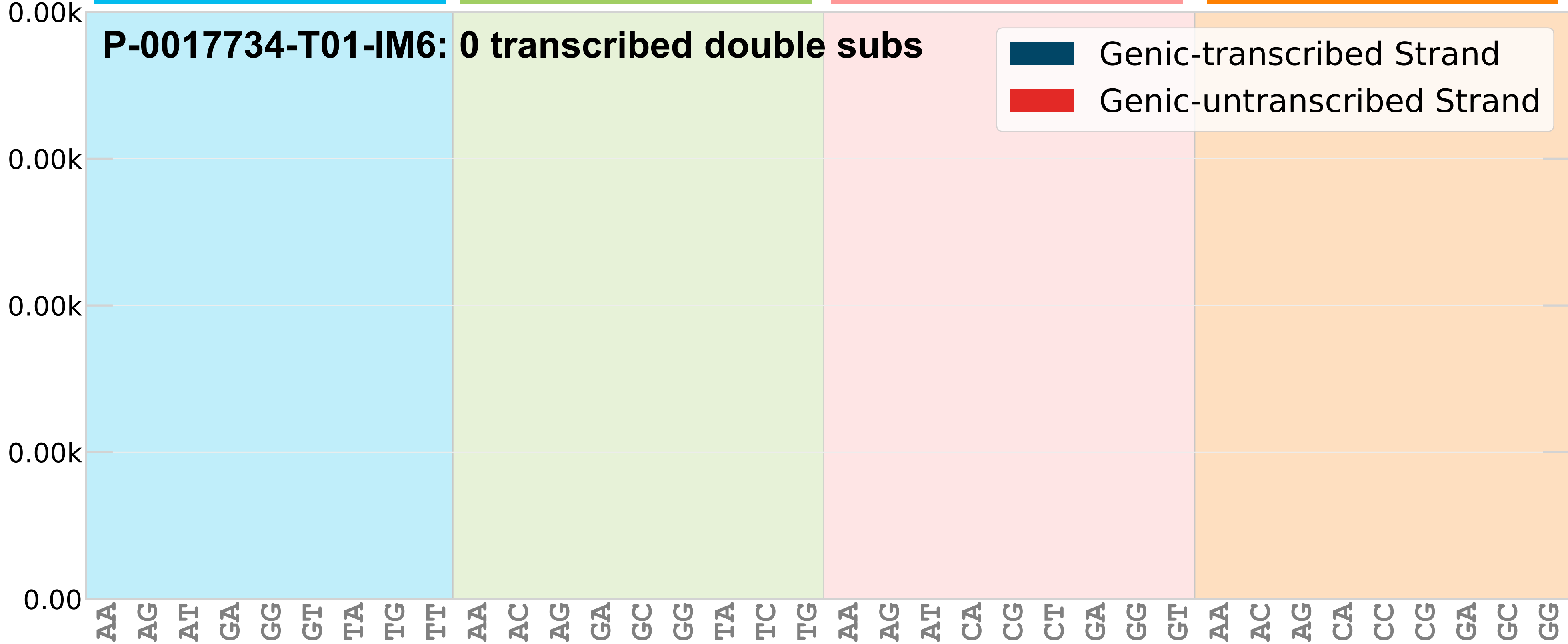
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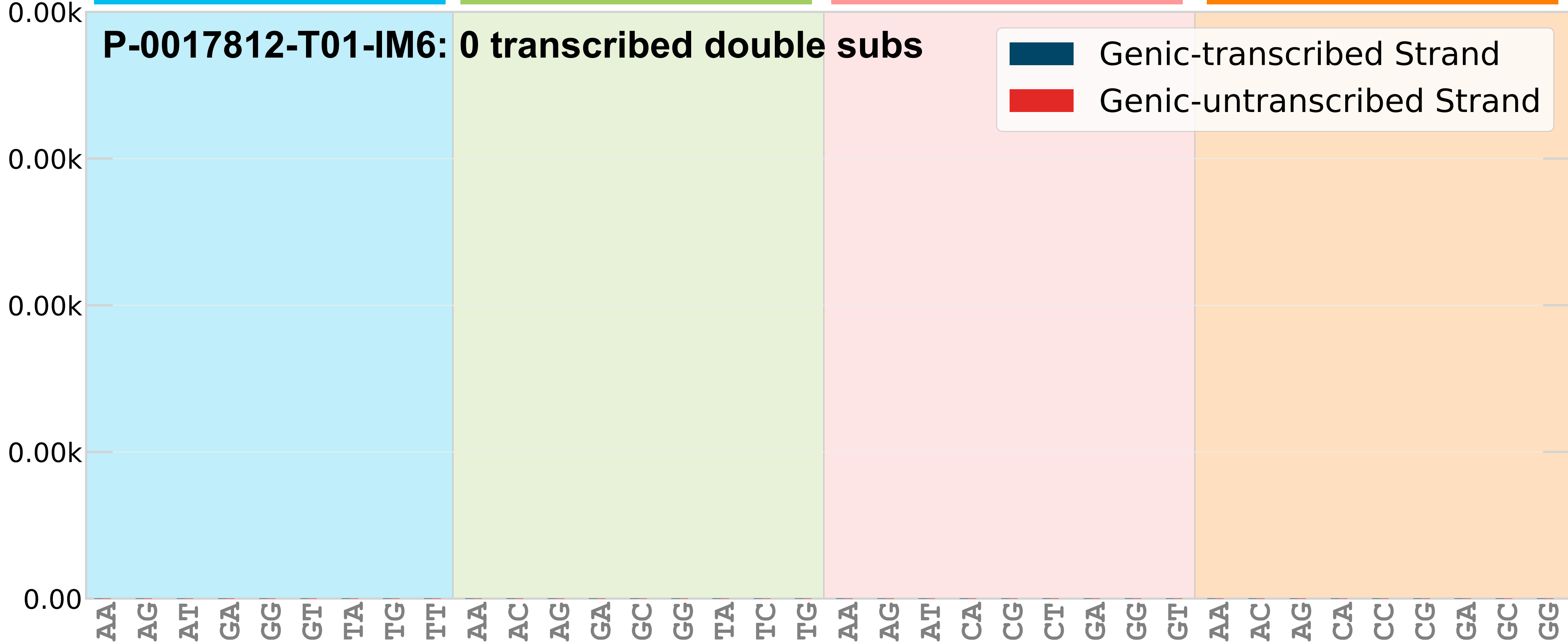
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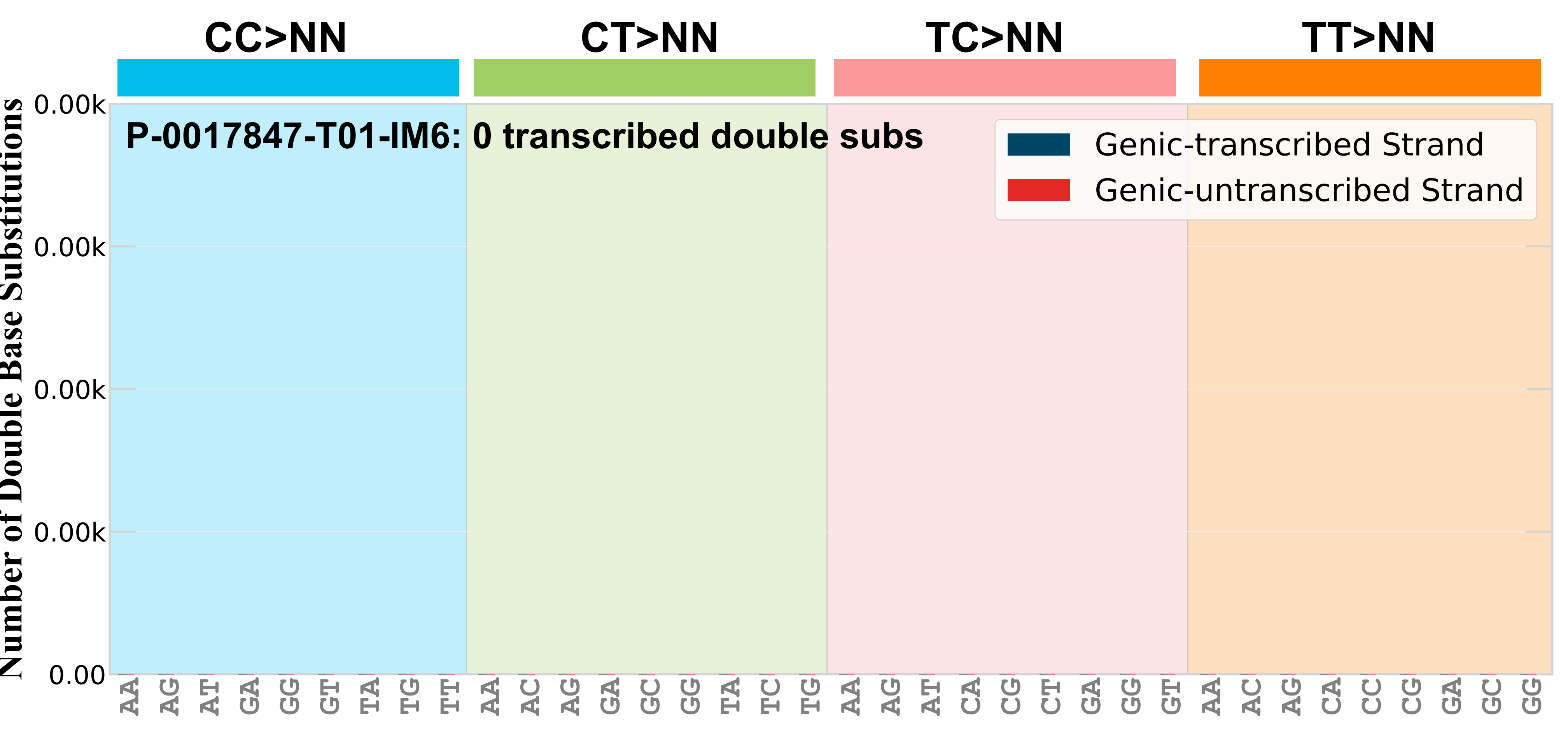


TT>NN



TT>NN





Number of Double Base Substitutions

CC>NN

CT>NN

TC>NN

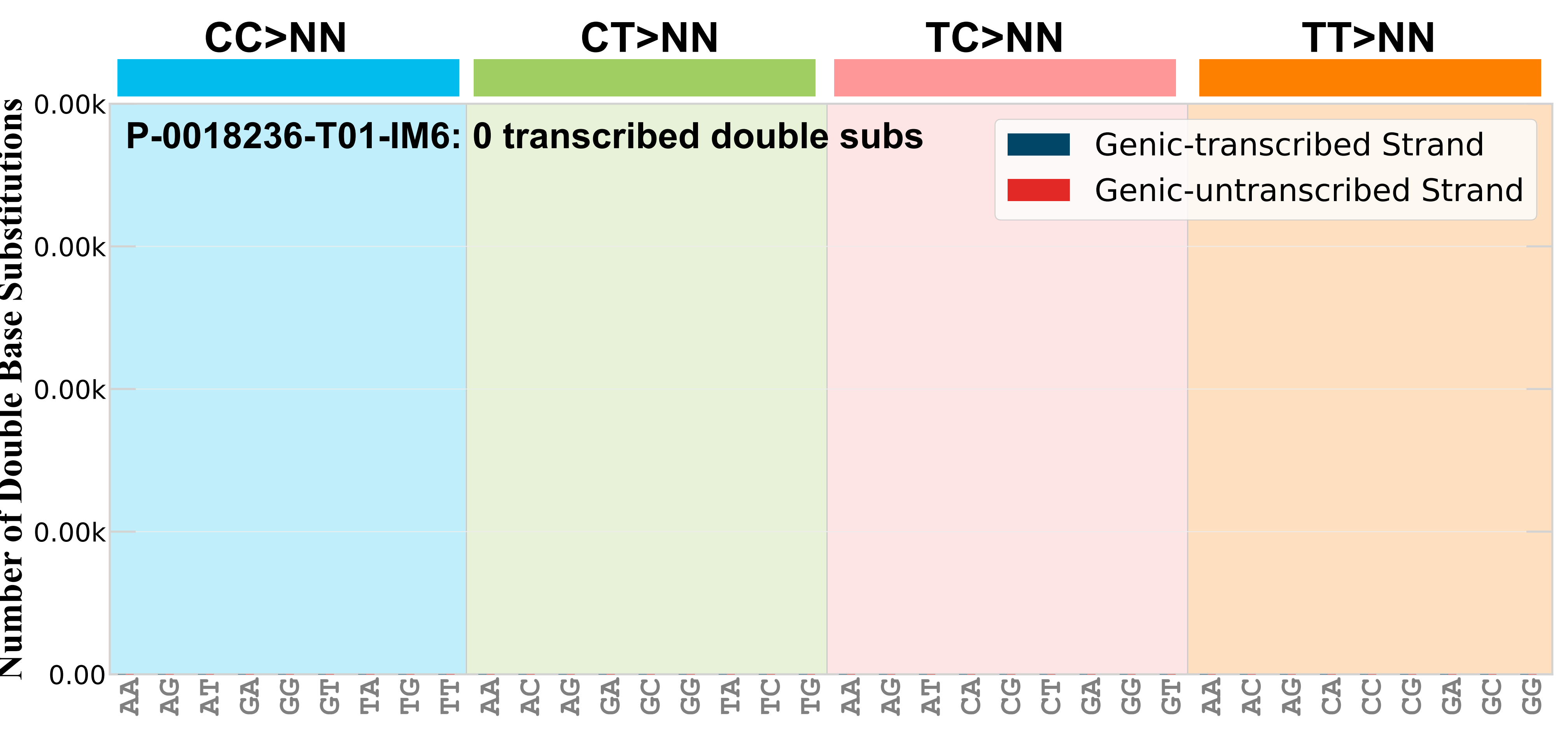
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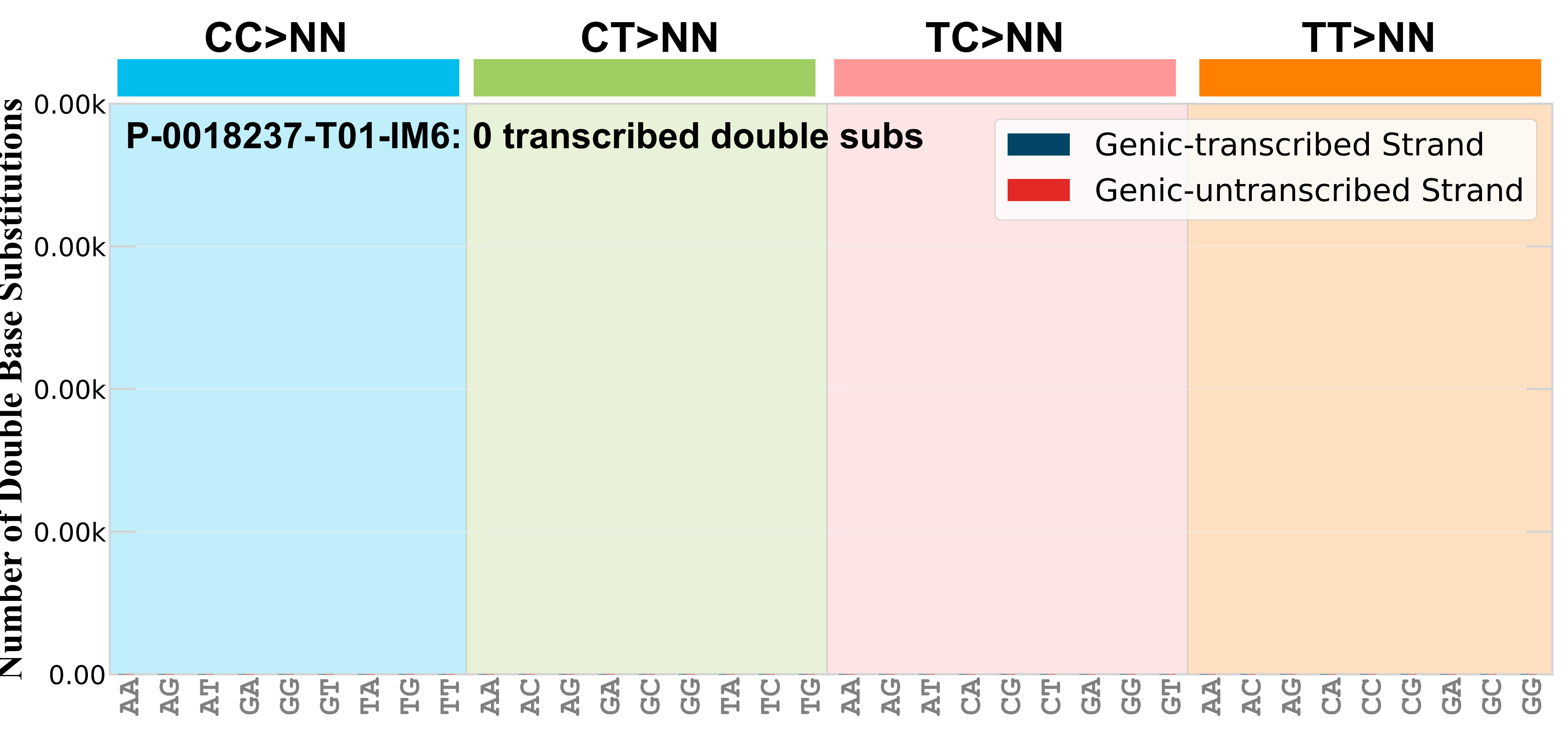
P-0018134-T01-IM6: 0 transcribed double subs

Genic-transcribed Strand

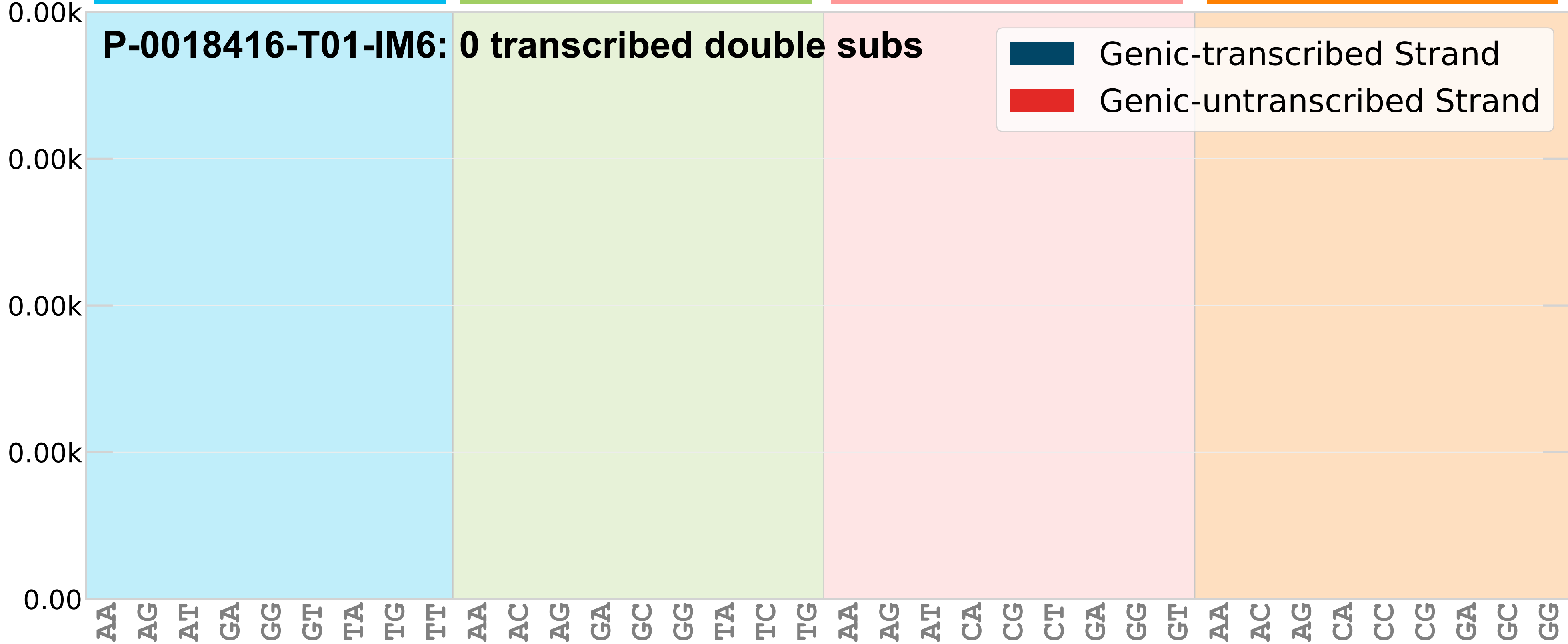
Genic-untranscribed Strand

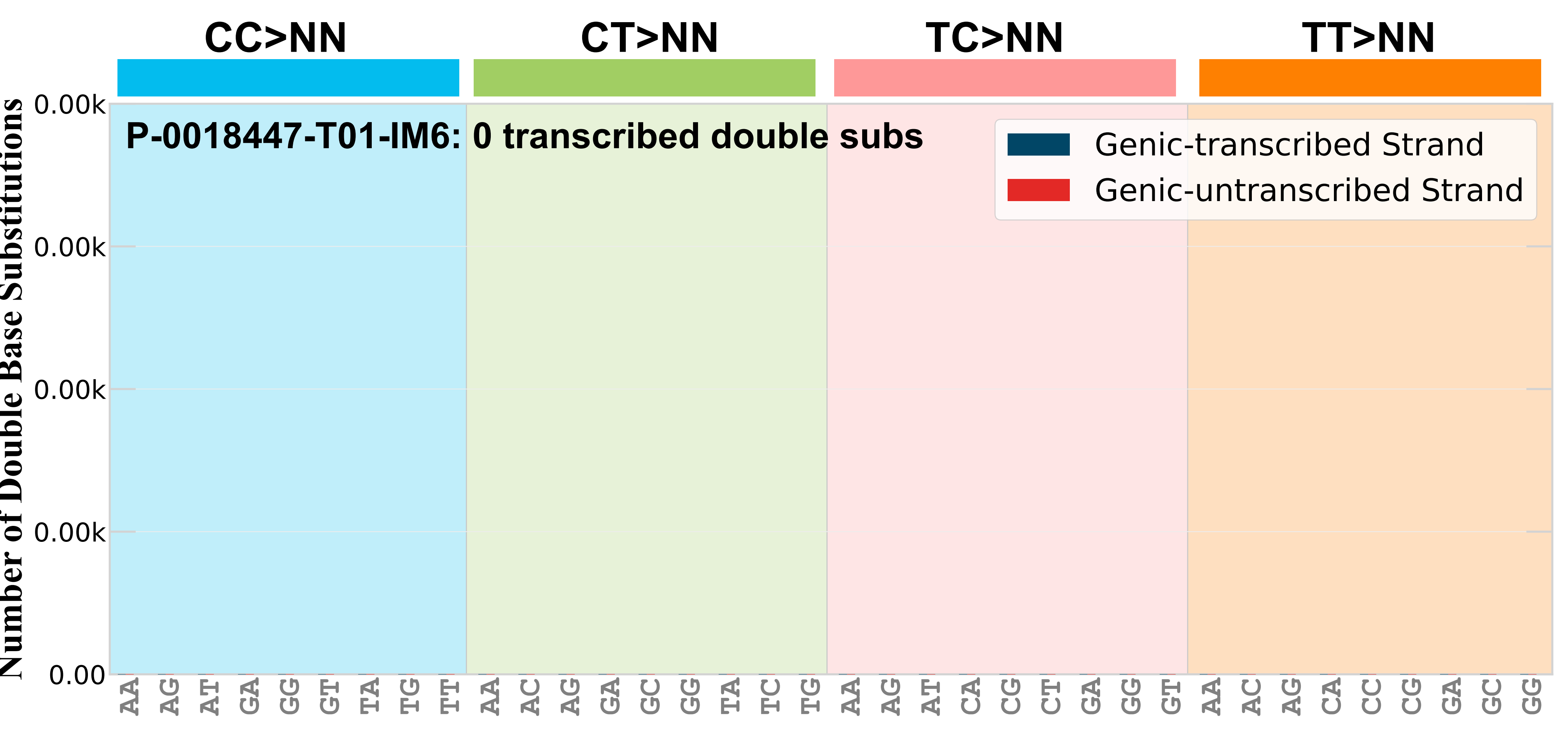
AA AG AT GA GG GT TA TG TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG CT GA GG GT AA AC AG CA CC CG GA GC GG



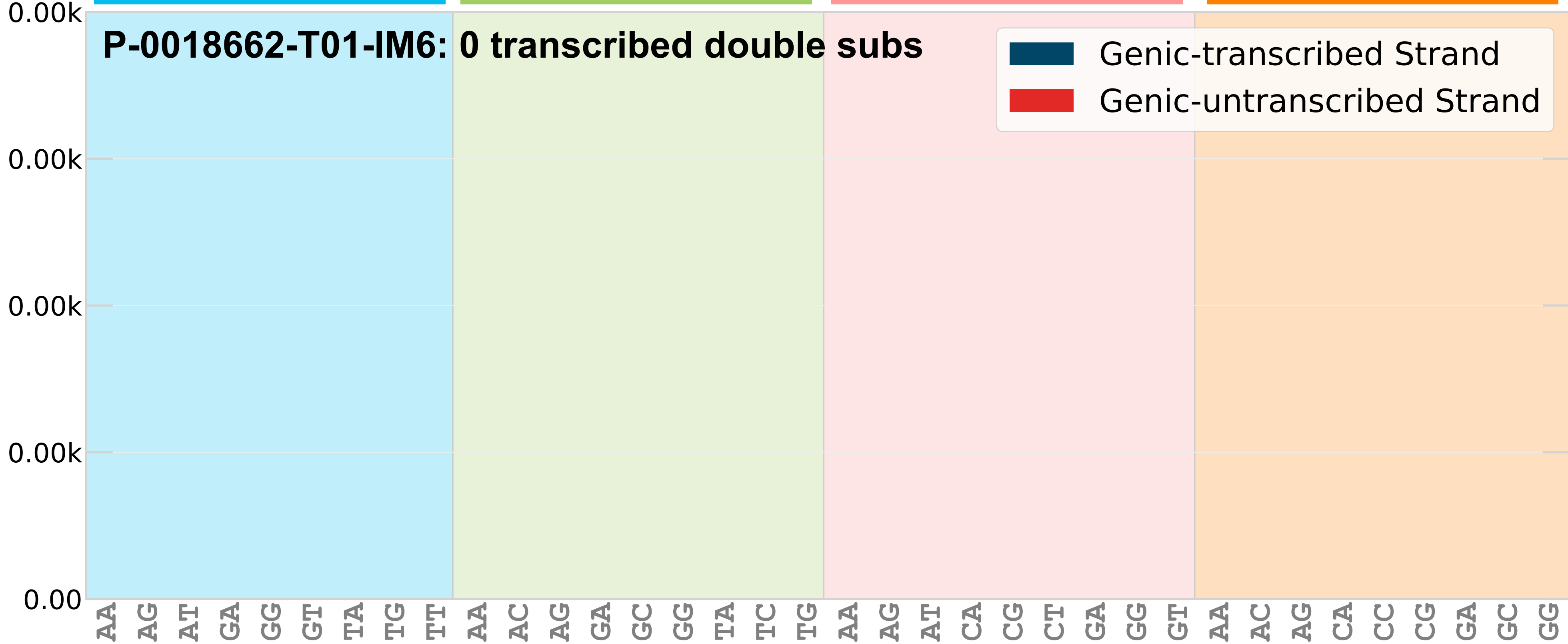


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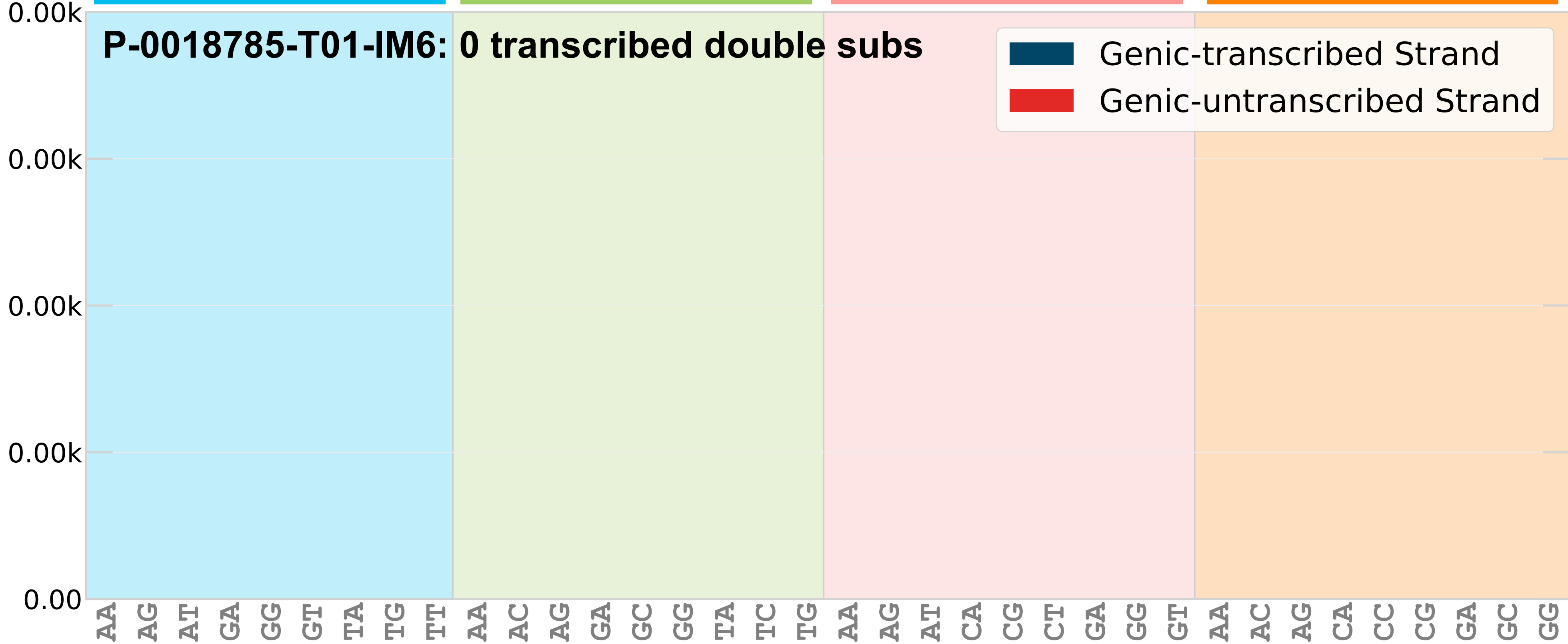


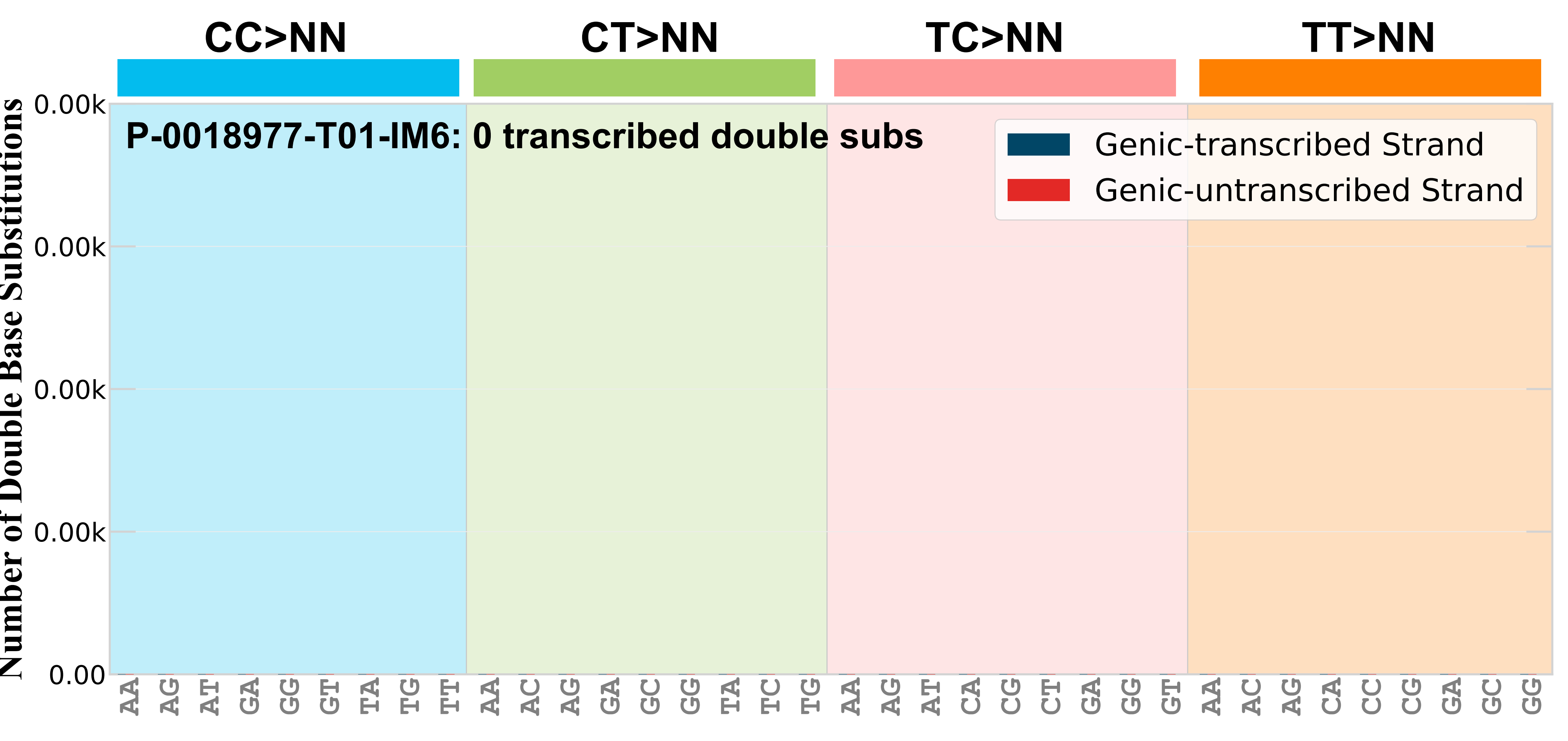


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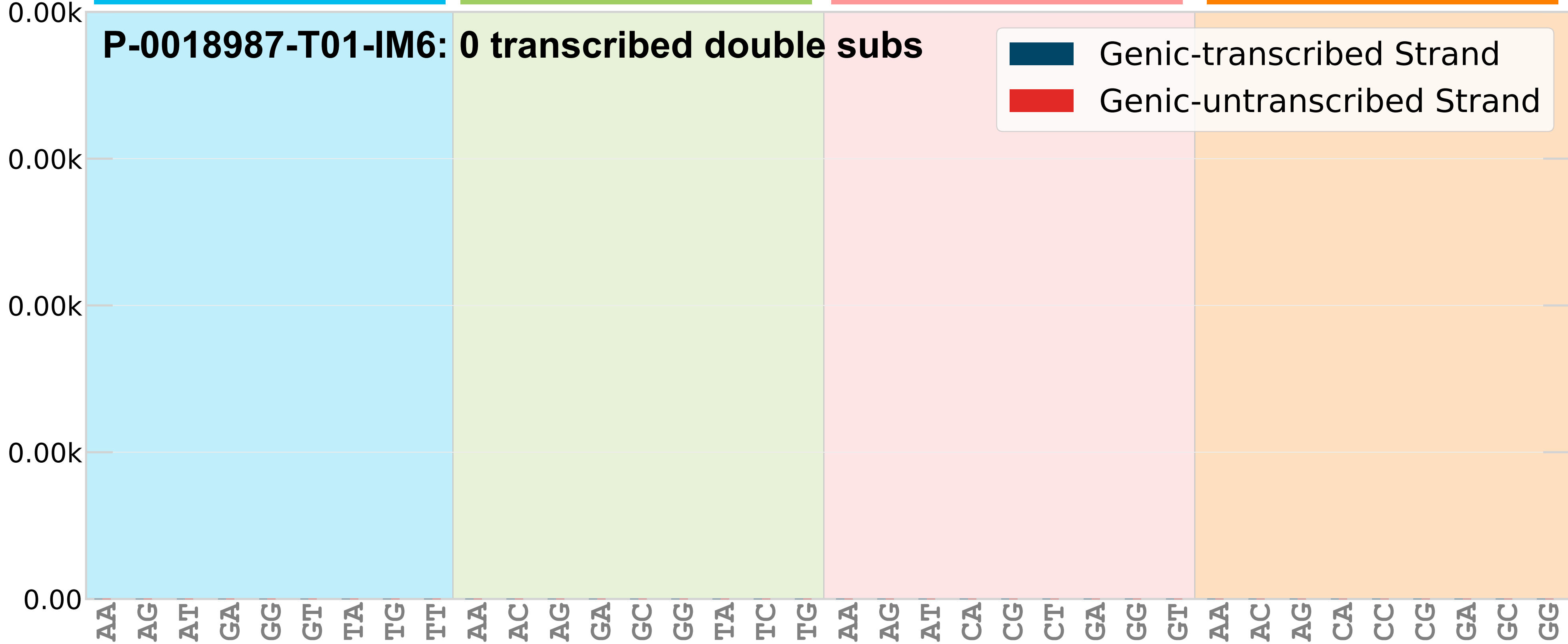


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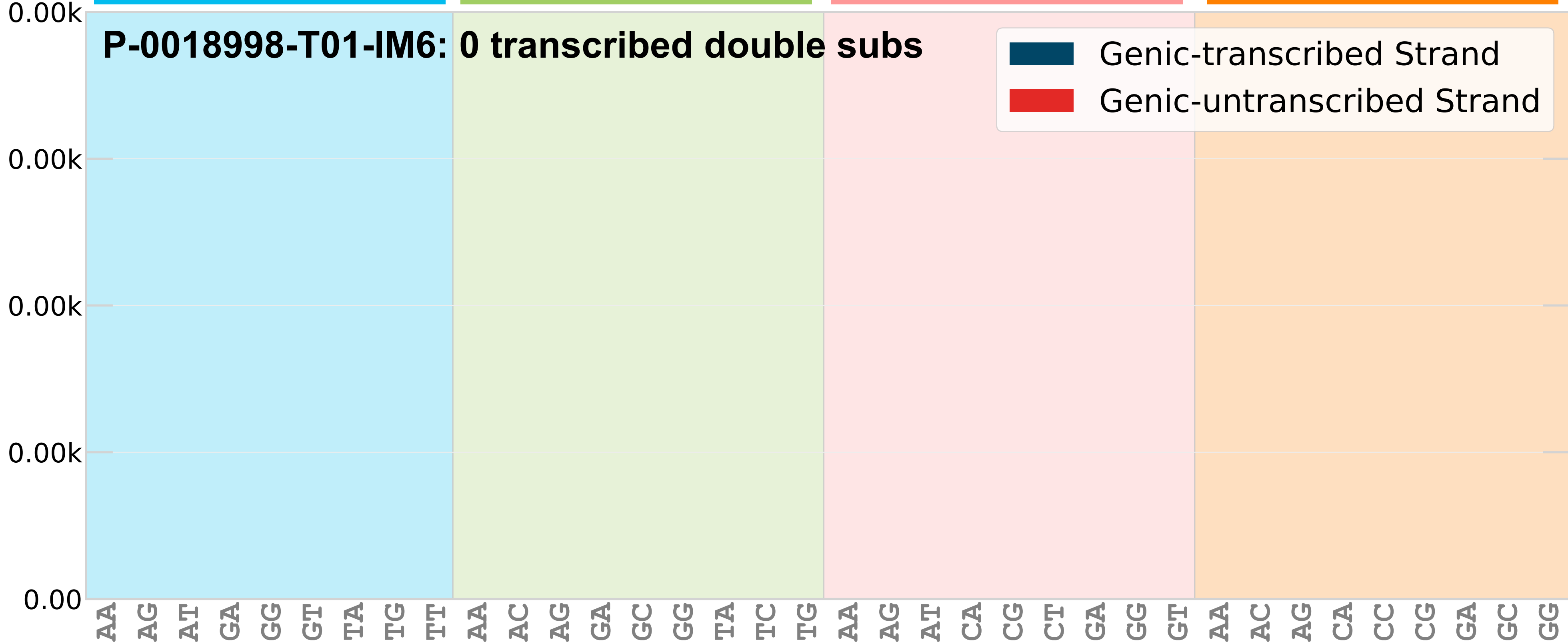




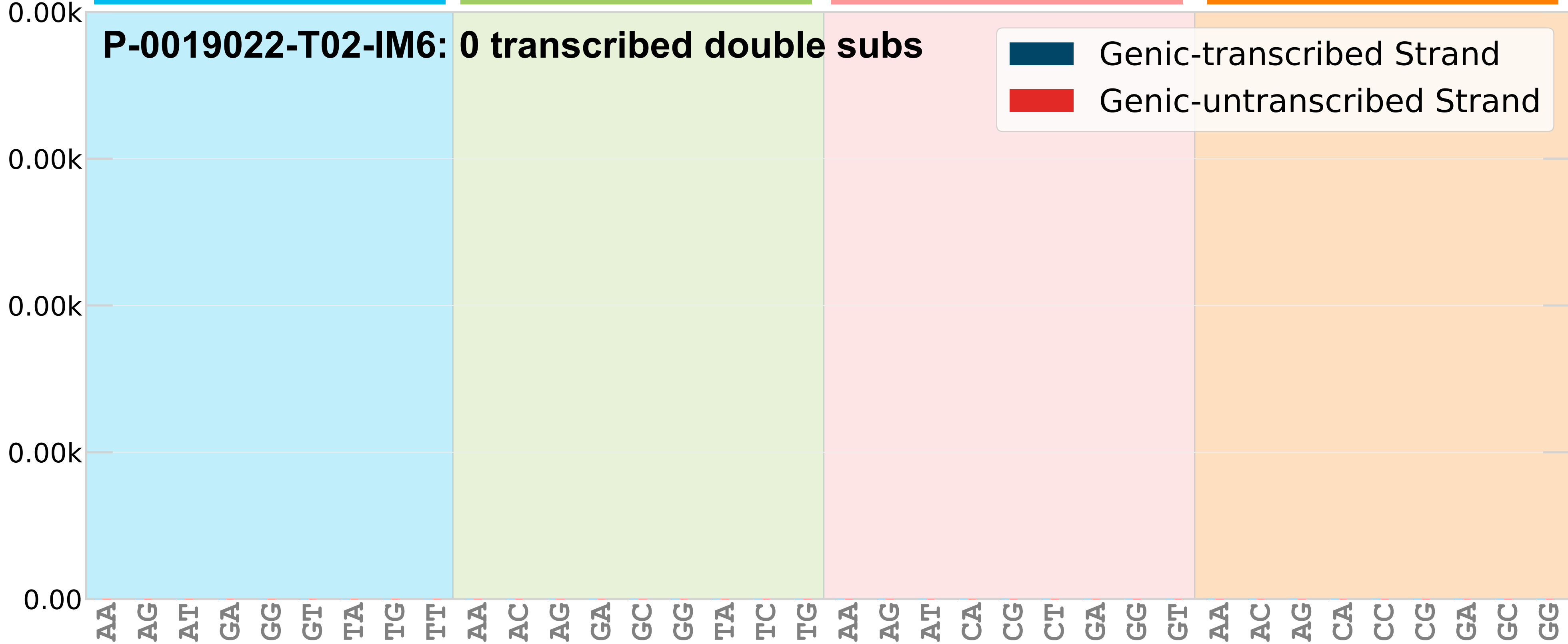
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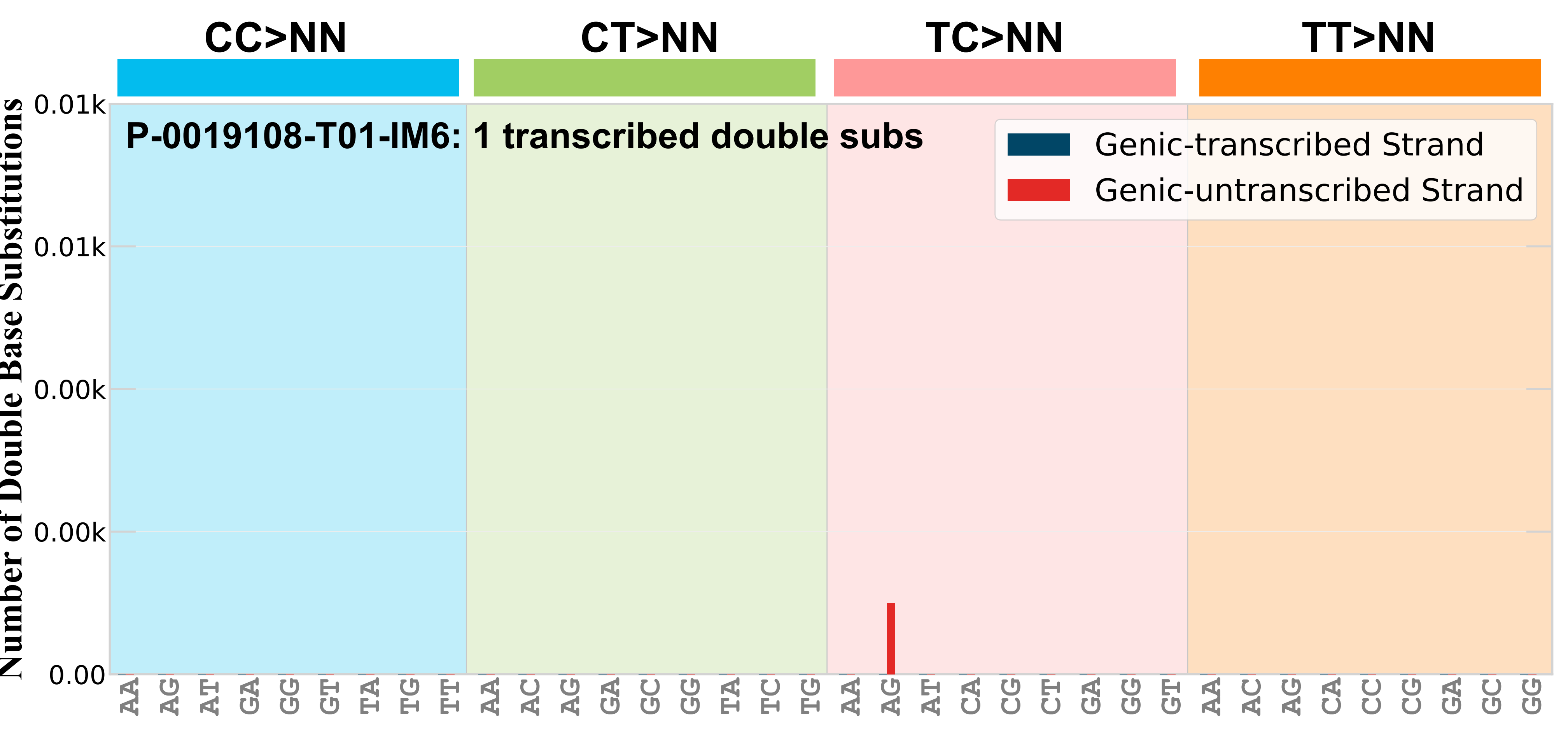


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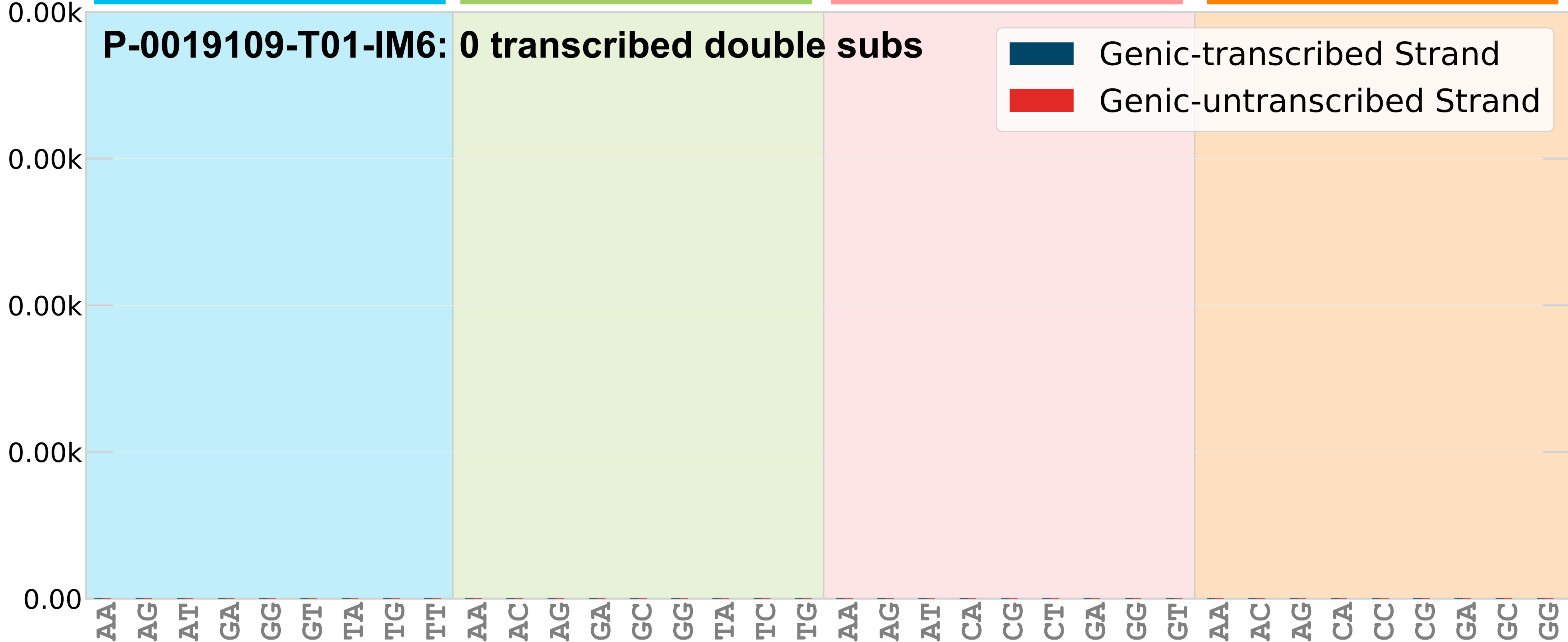


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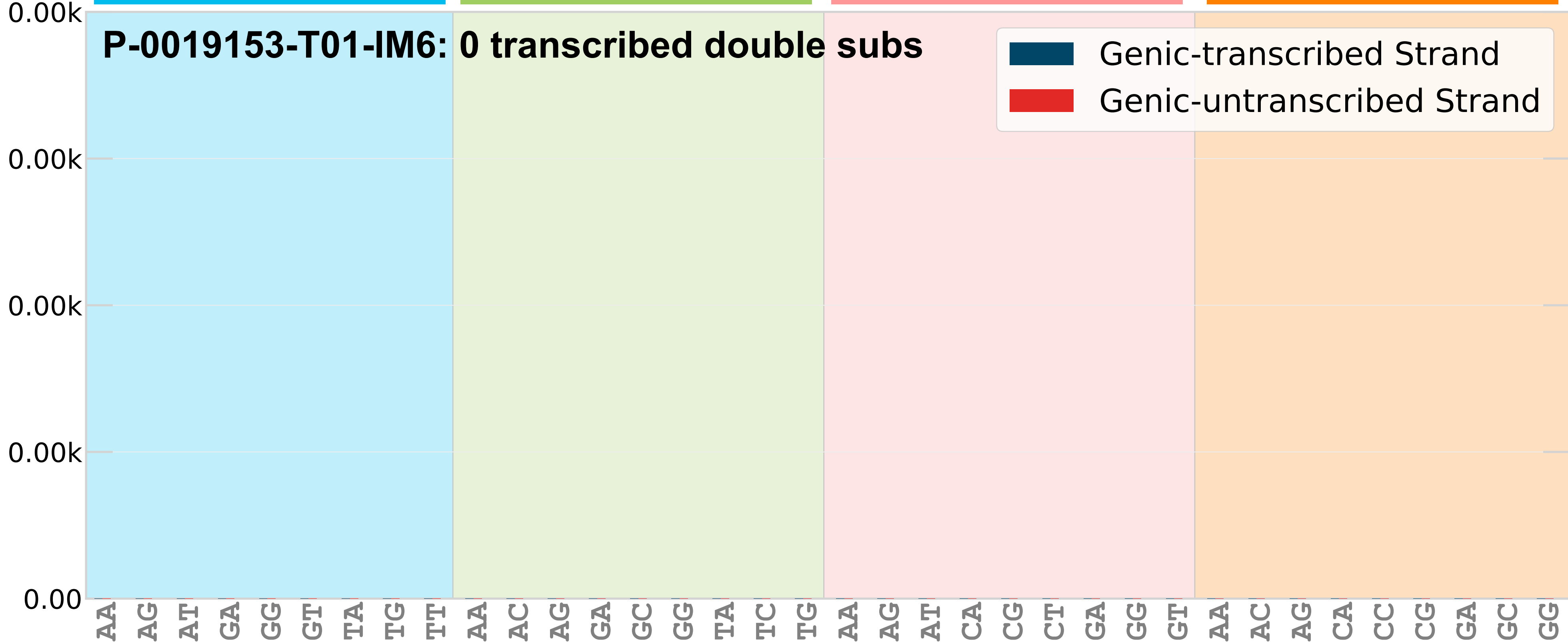


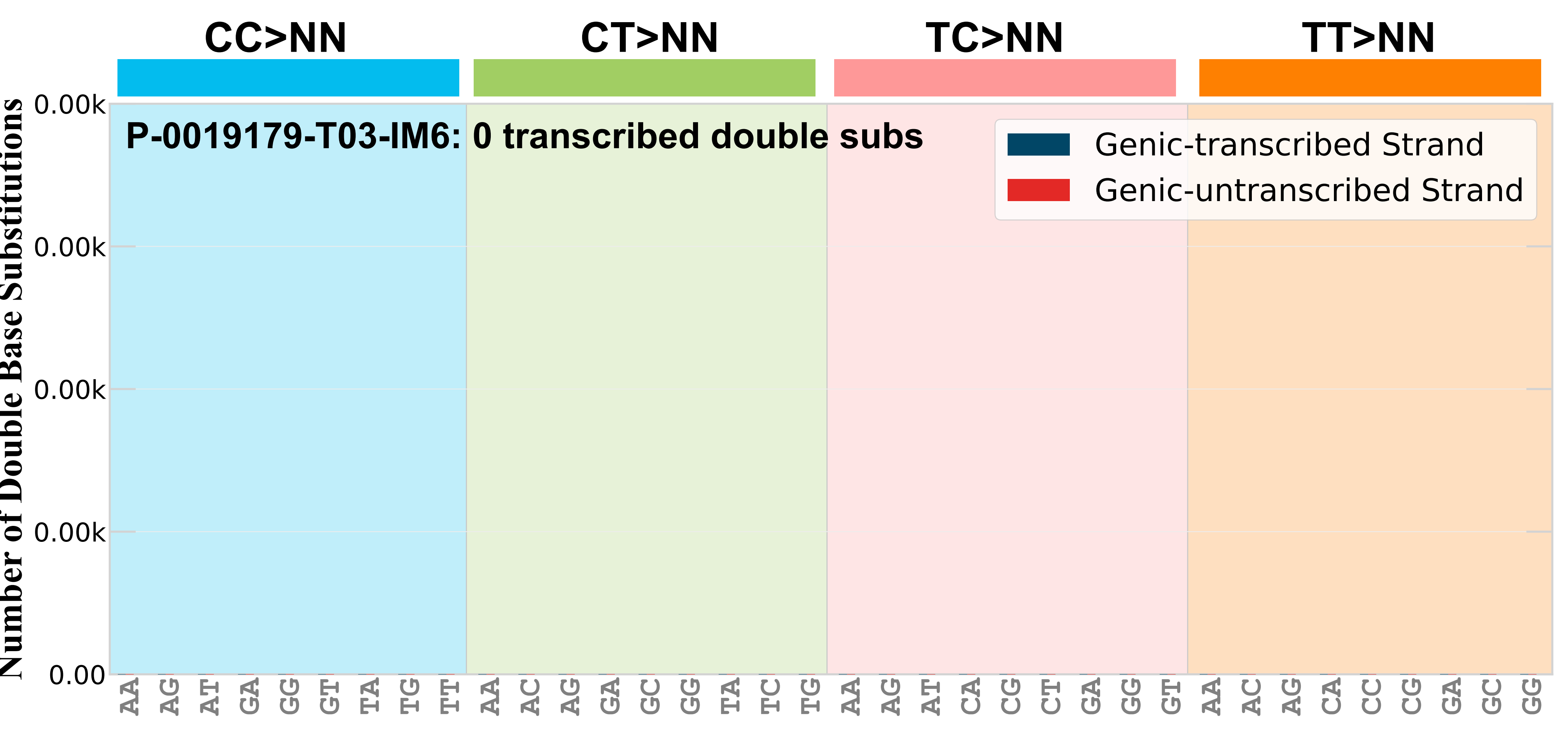


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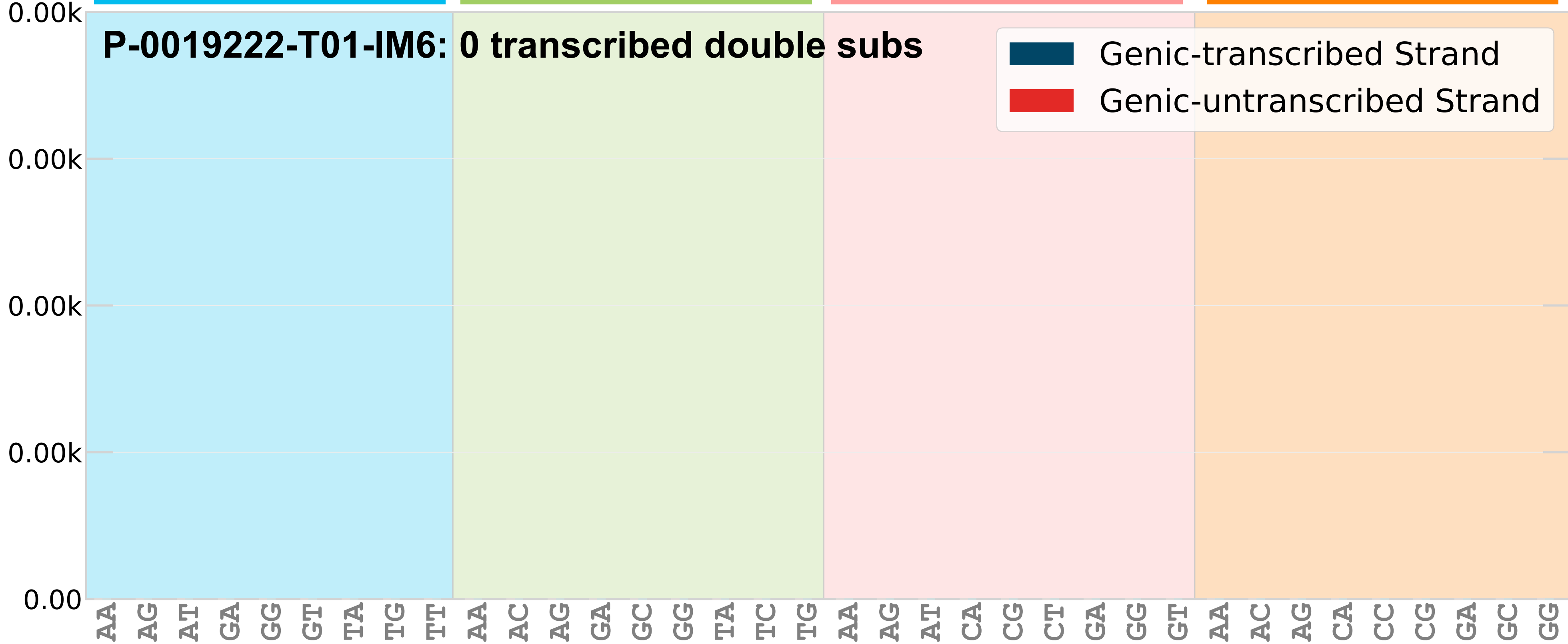


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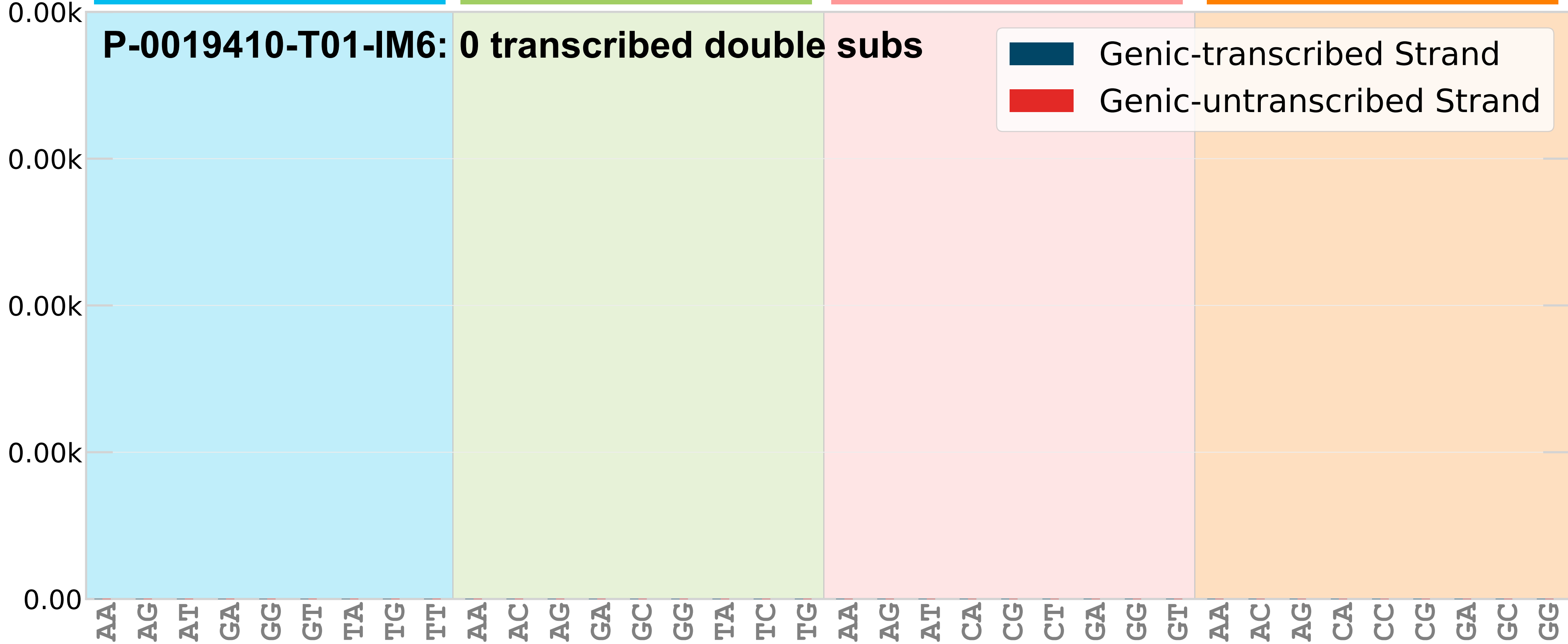




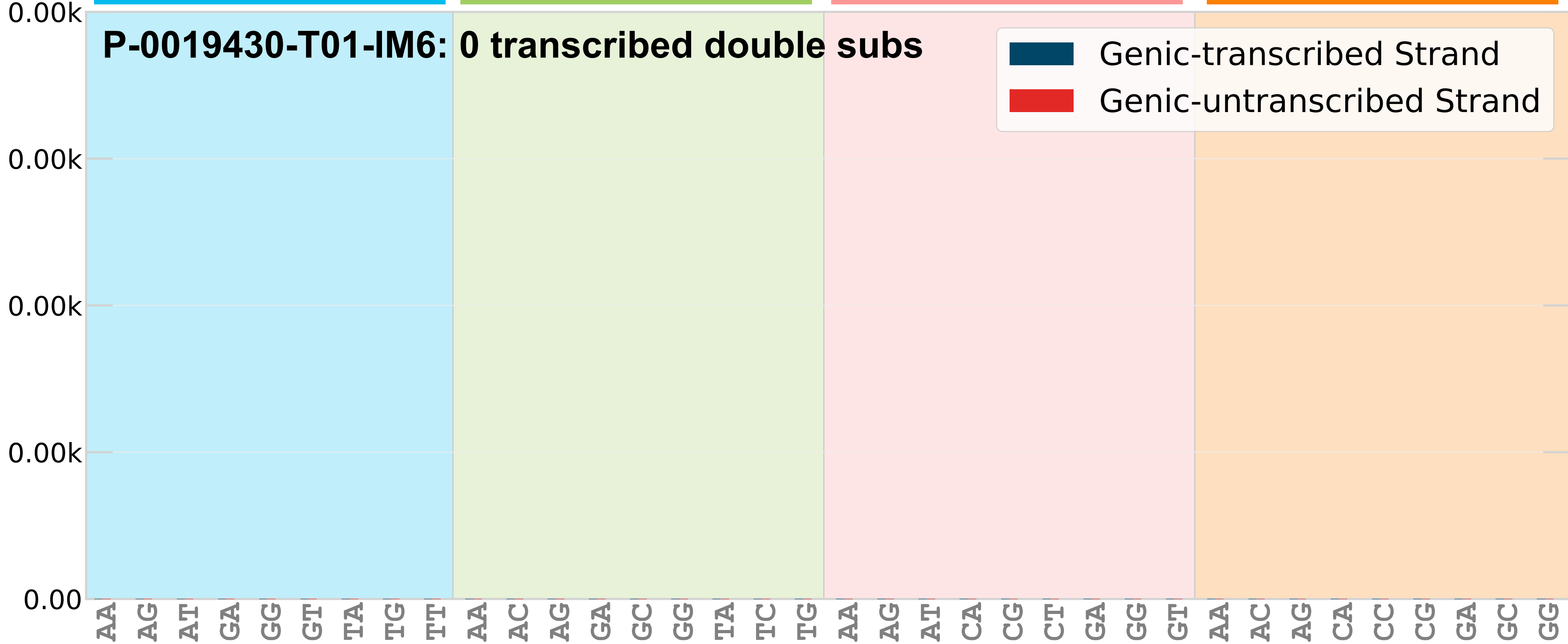
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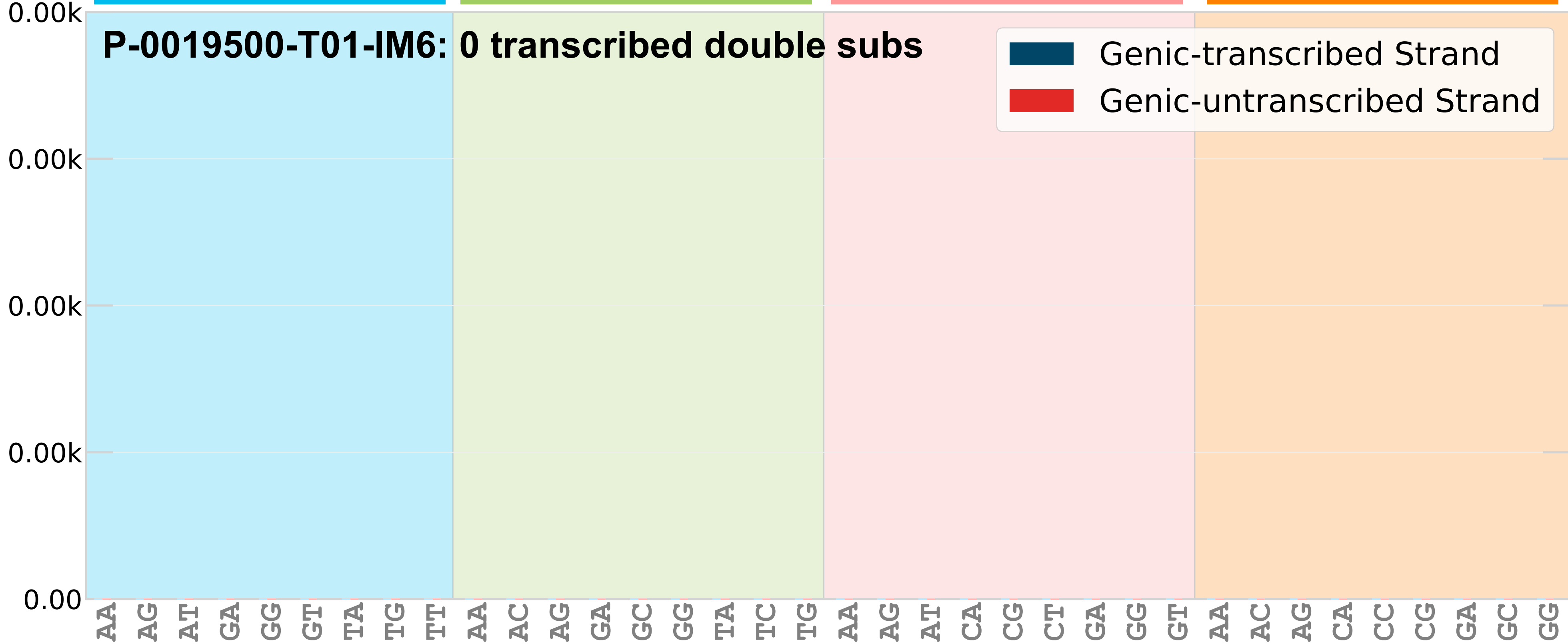
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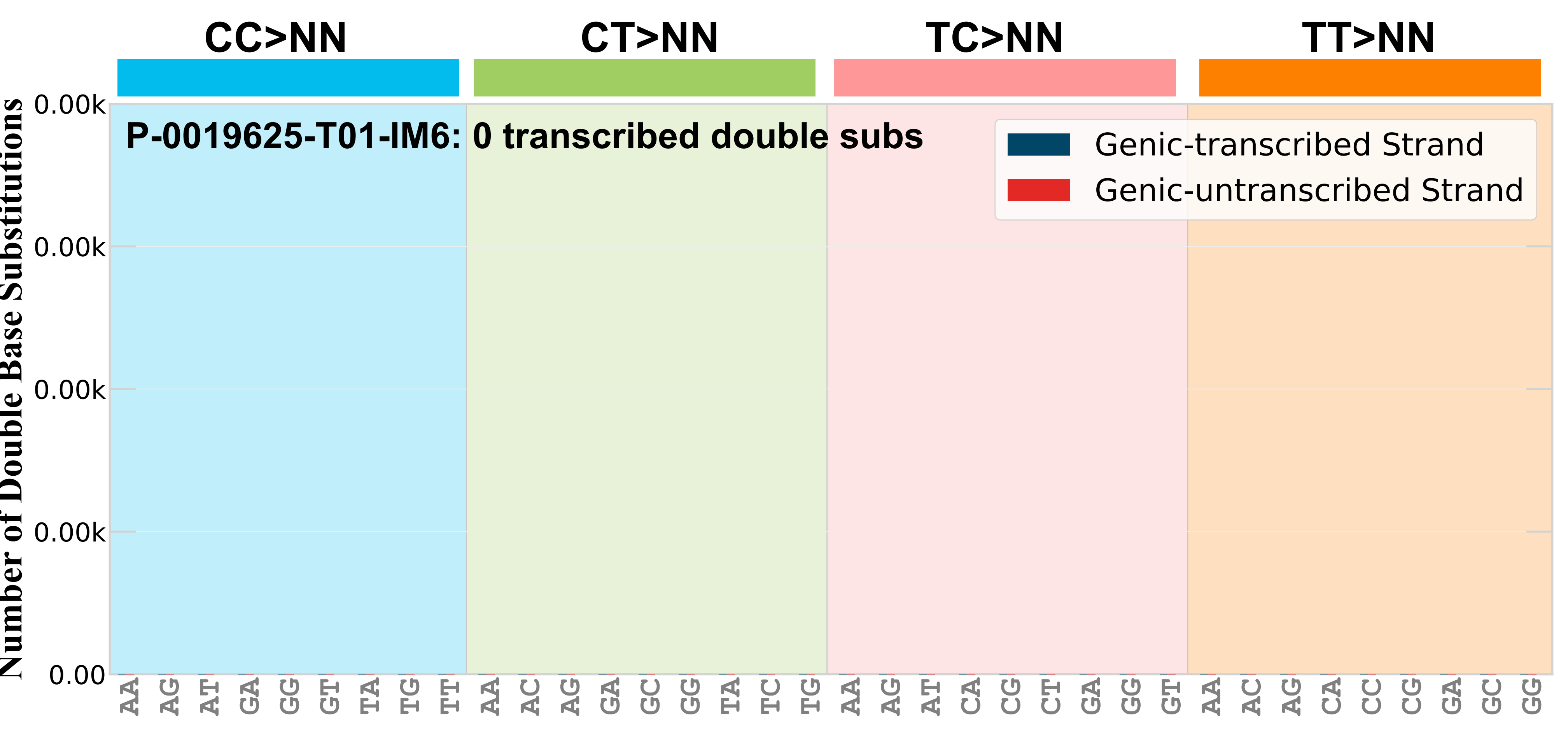


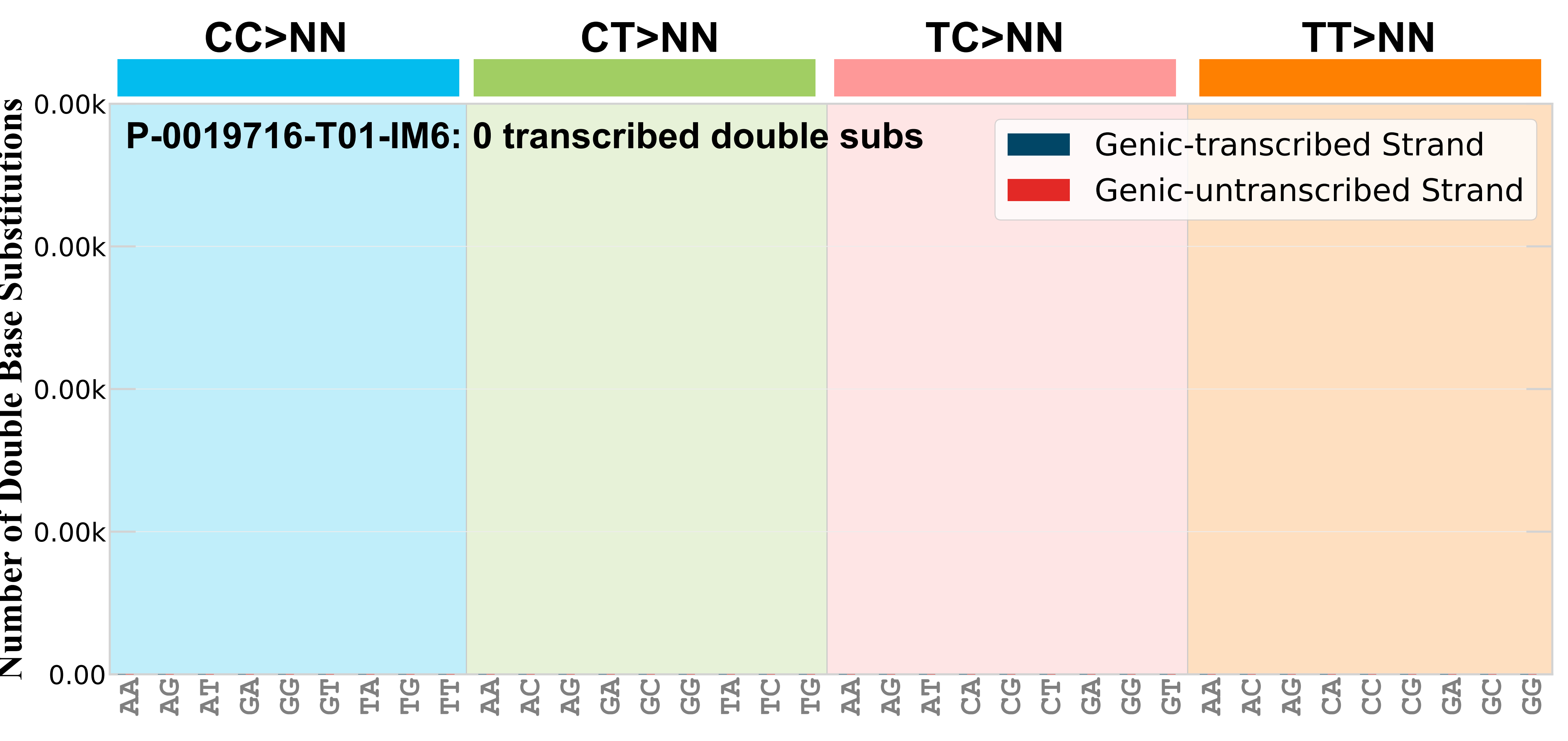
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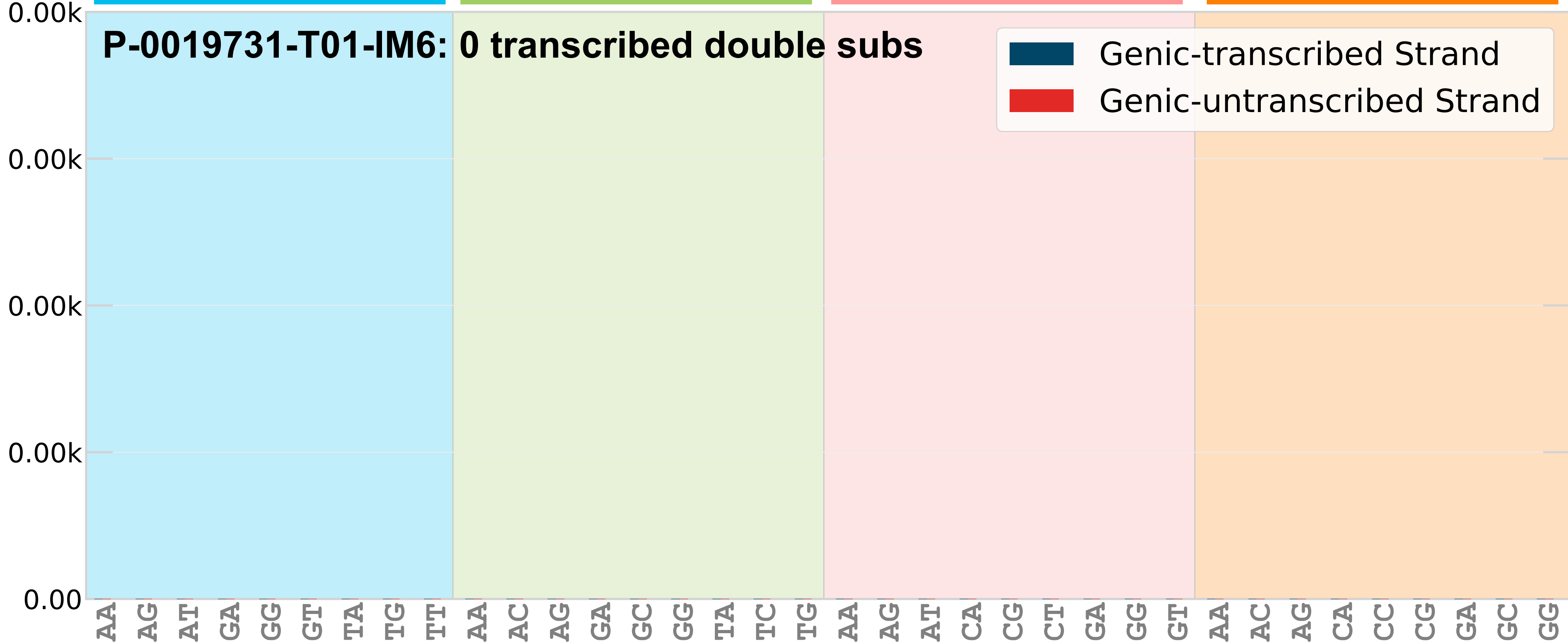
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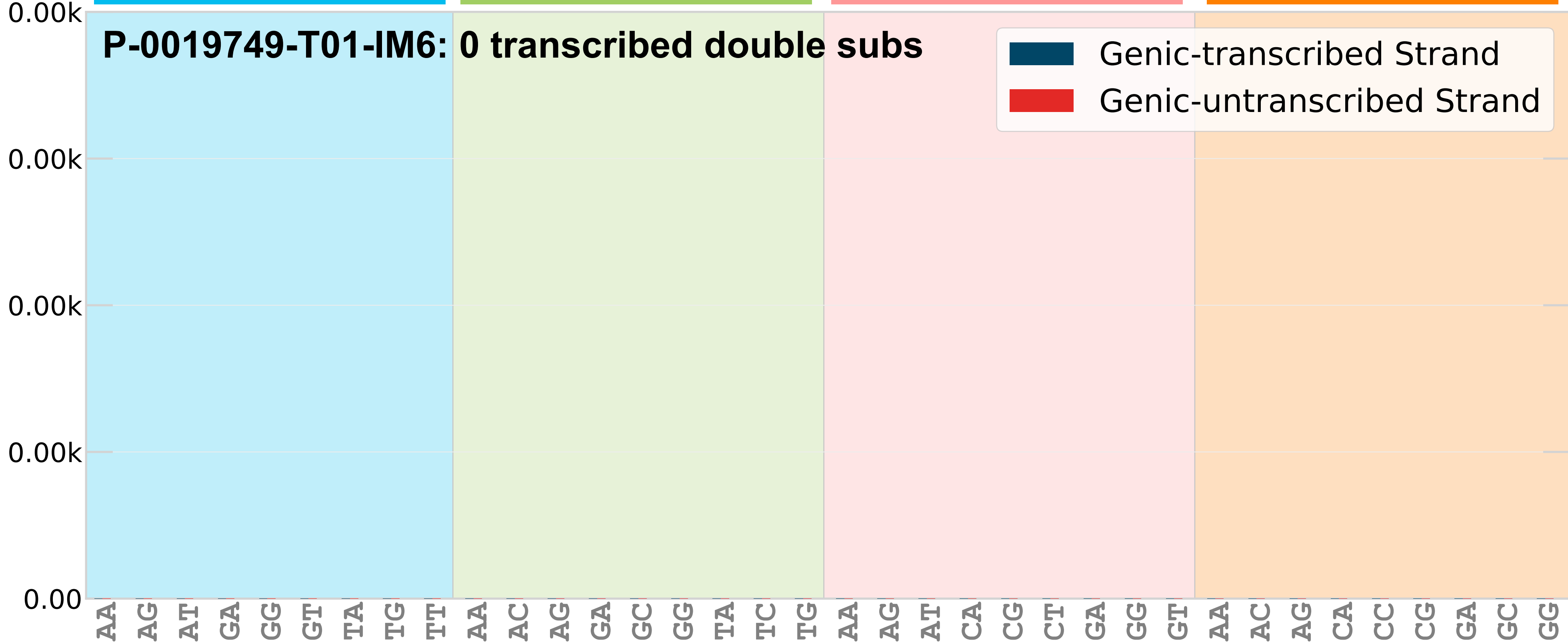




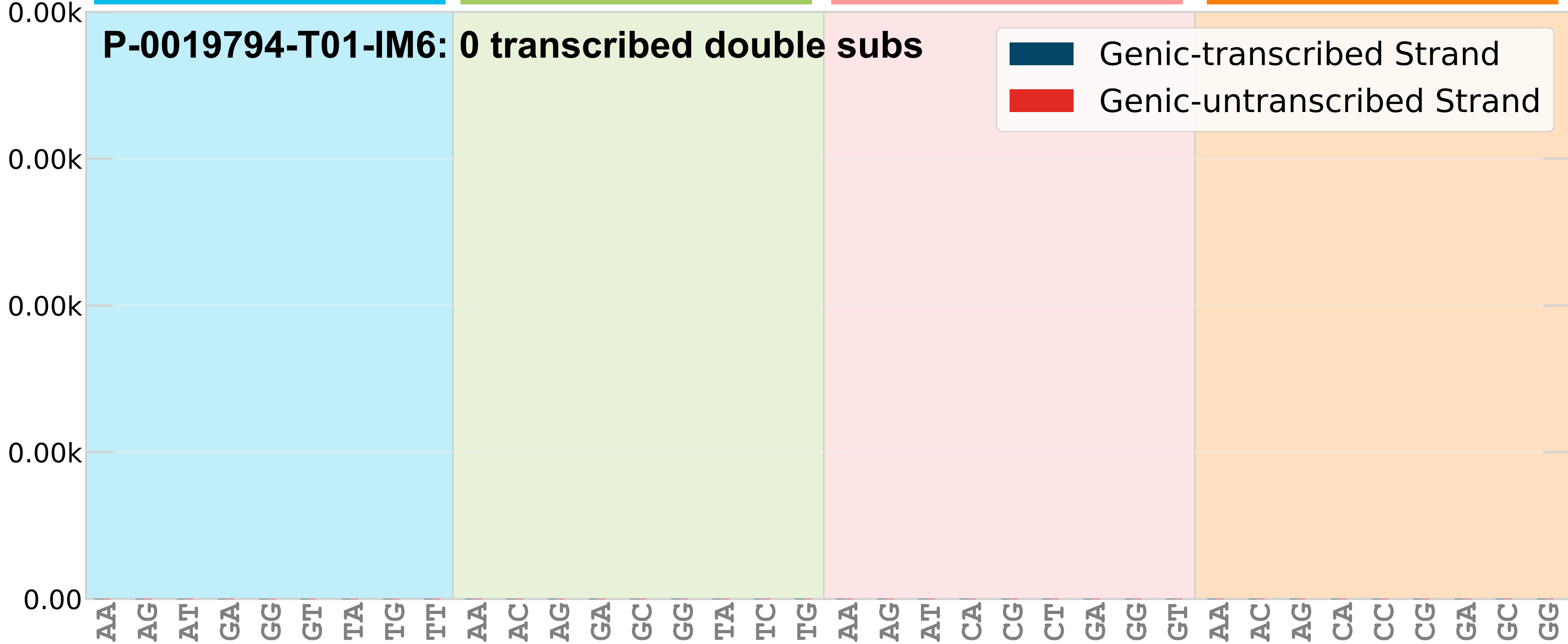
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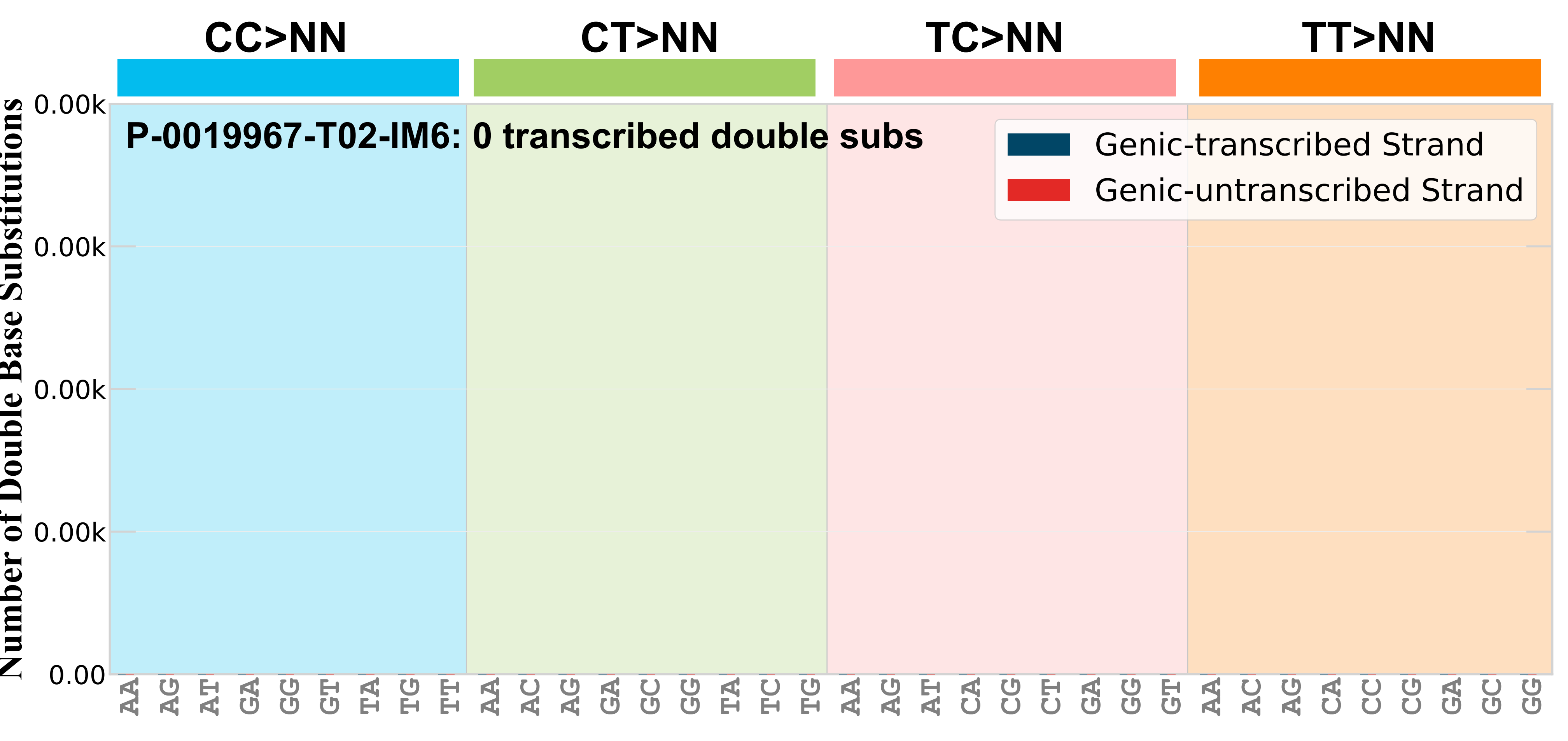


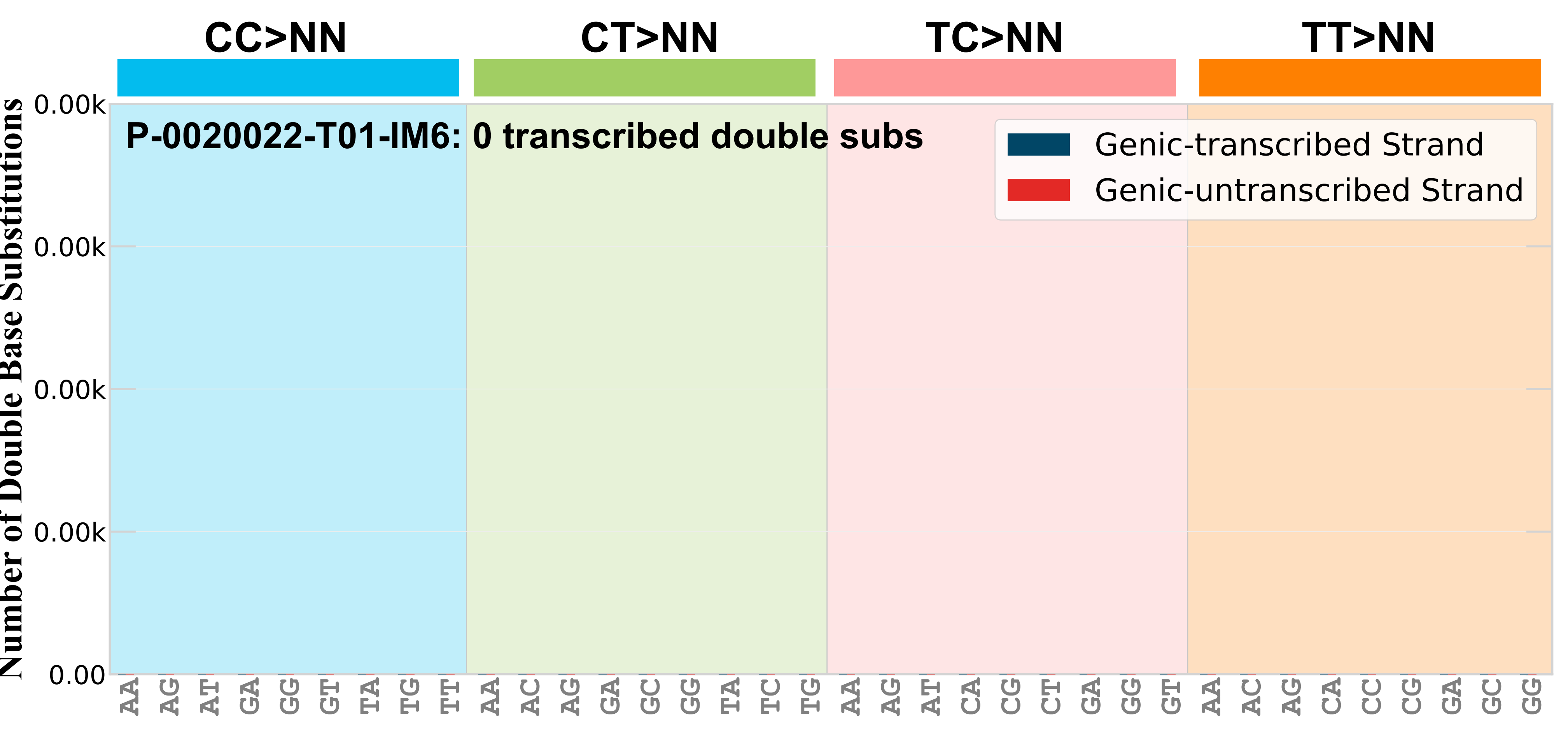
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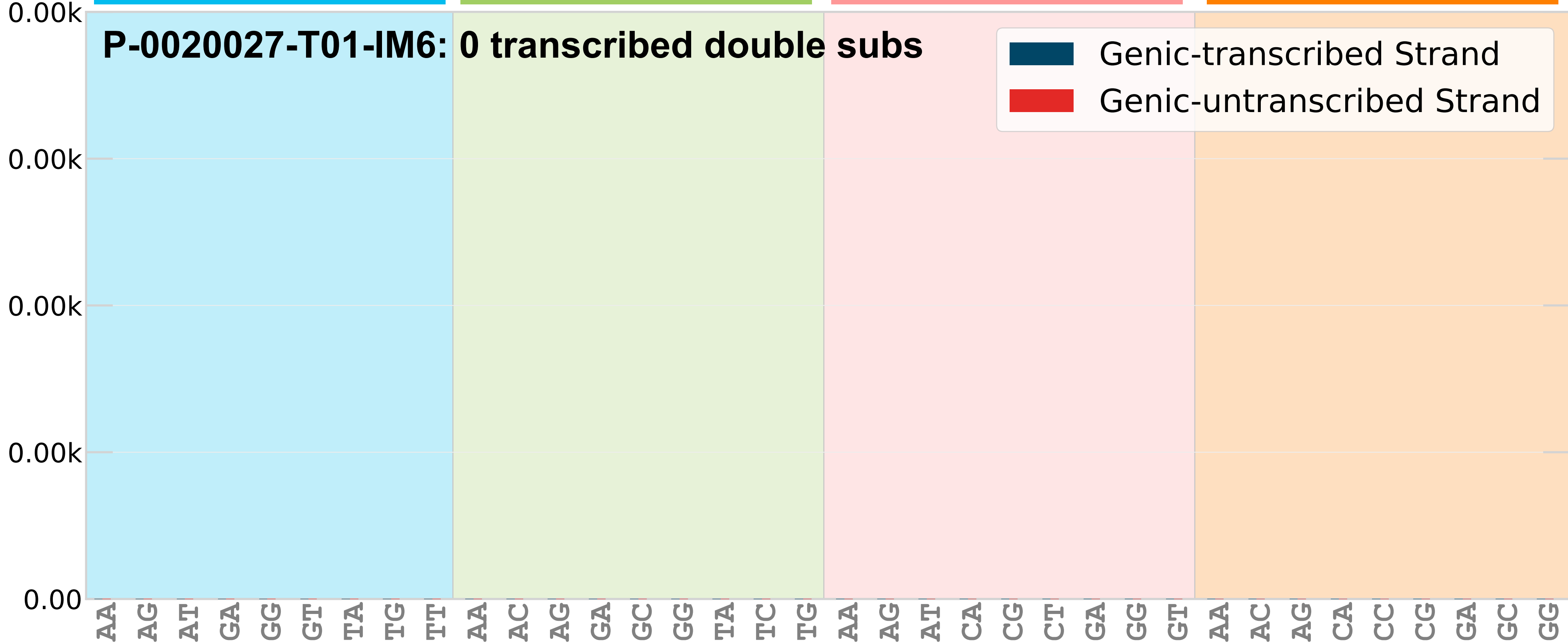
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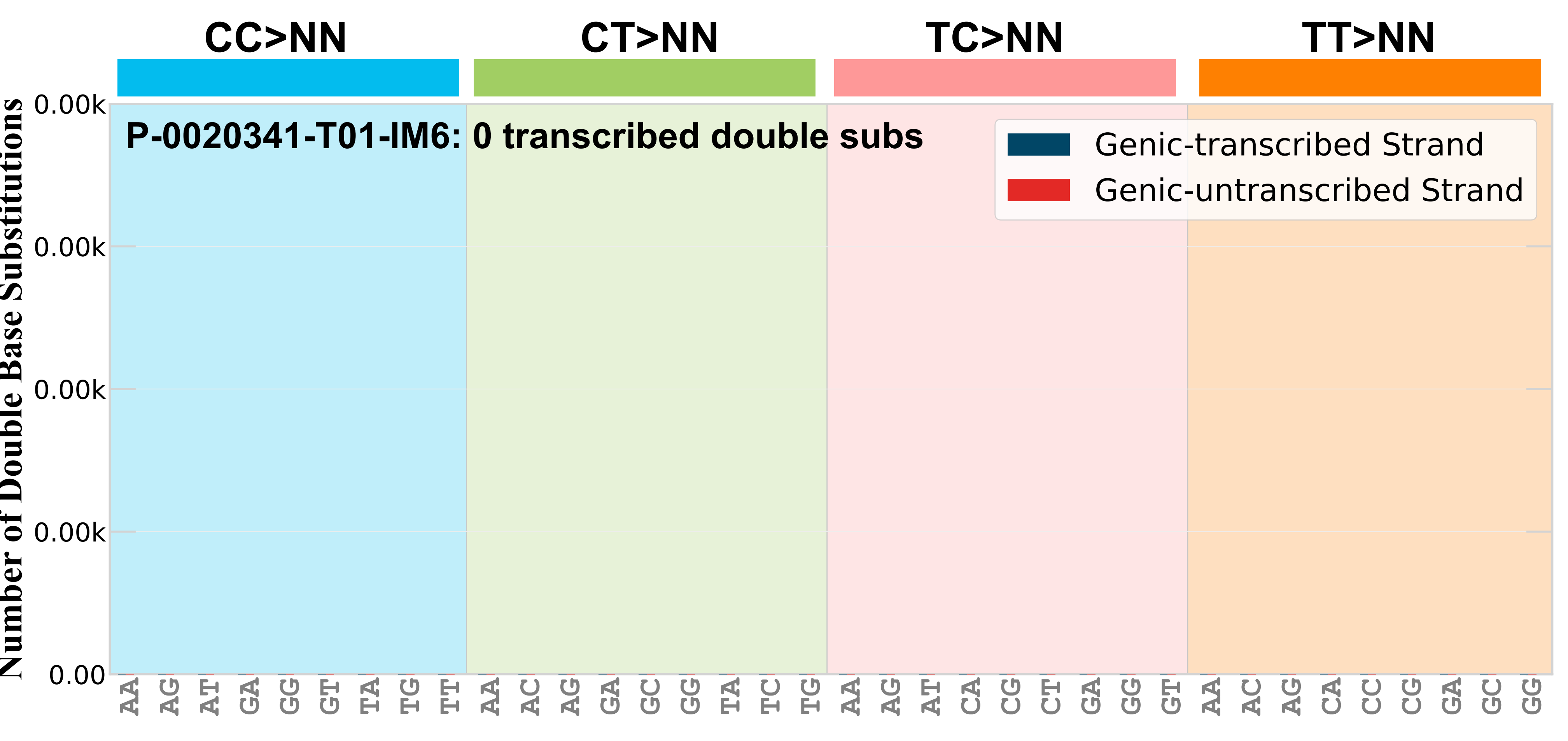




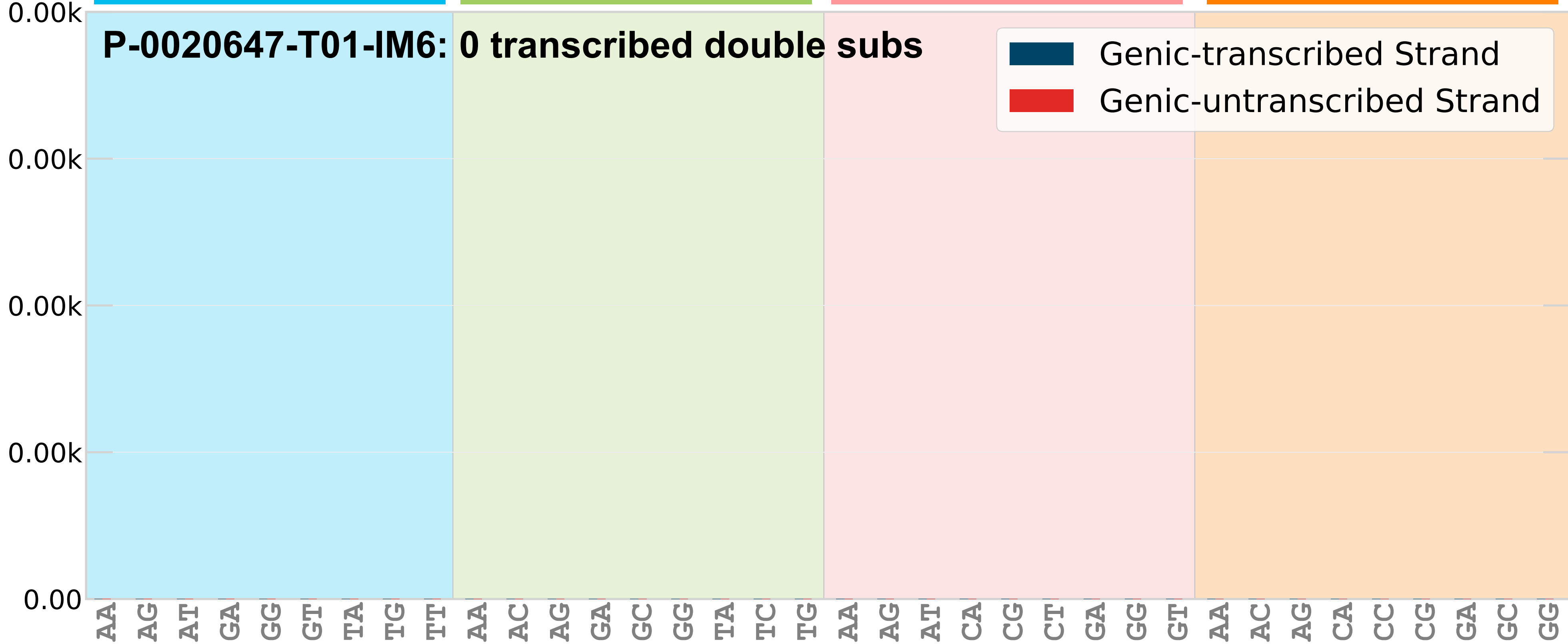


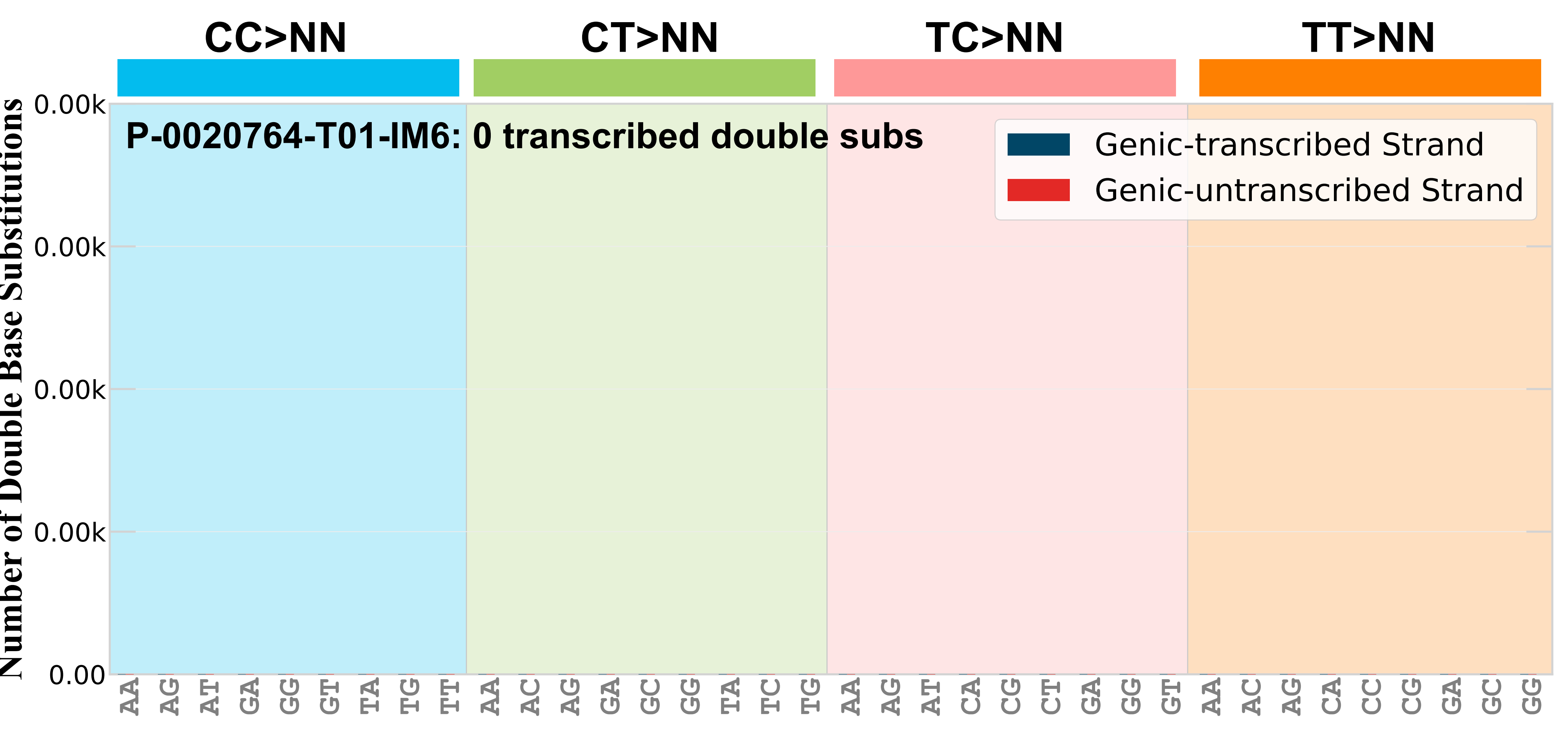
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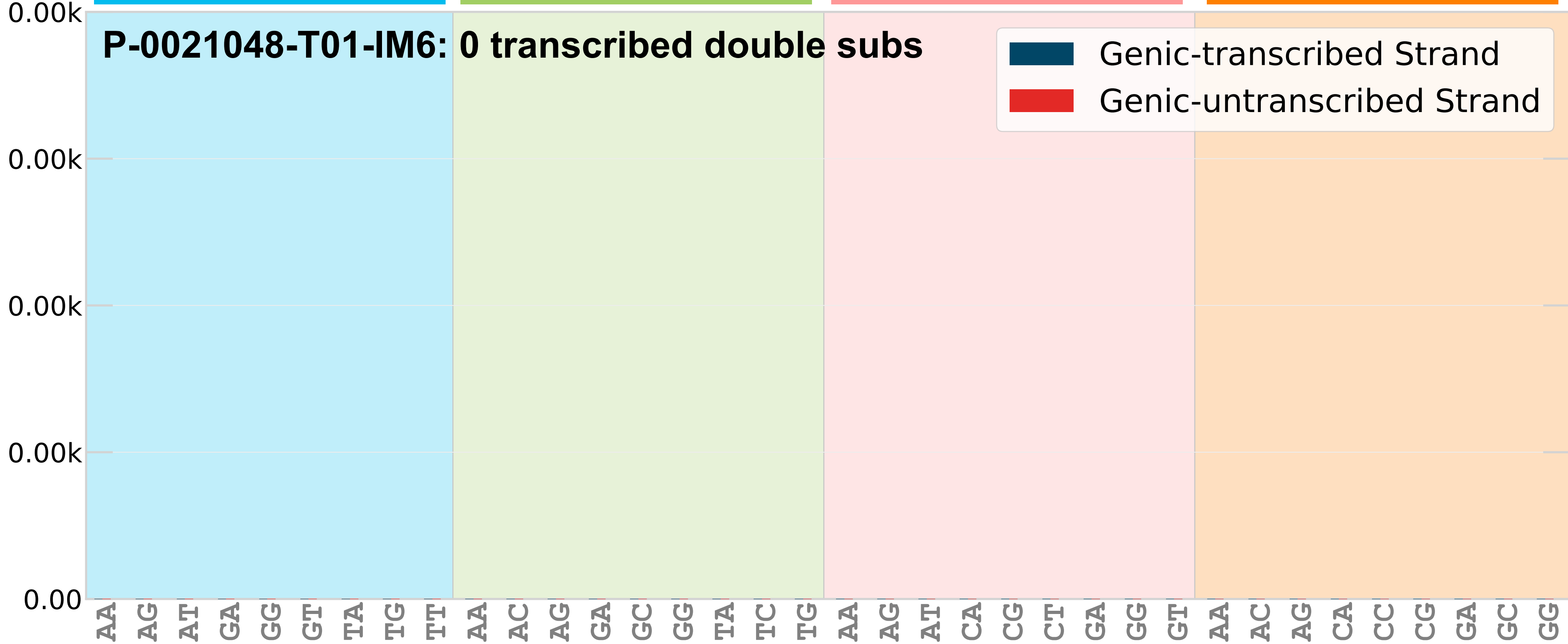


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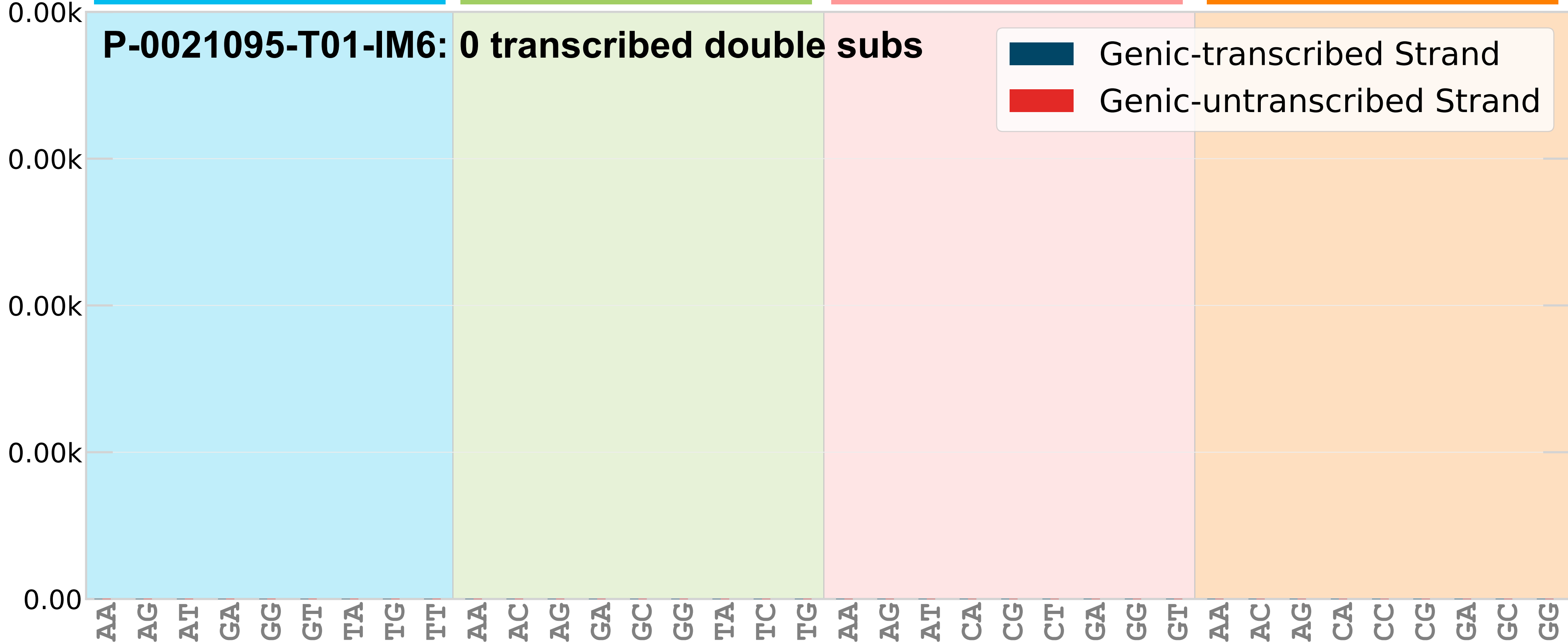


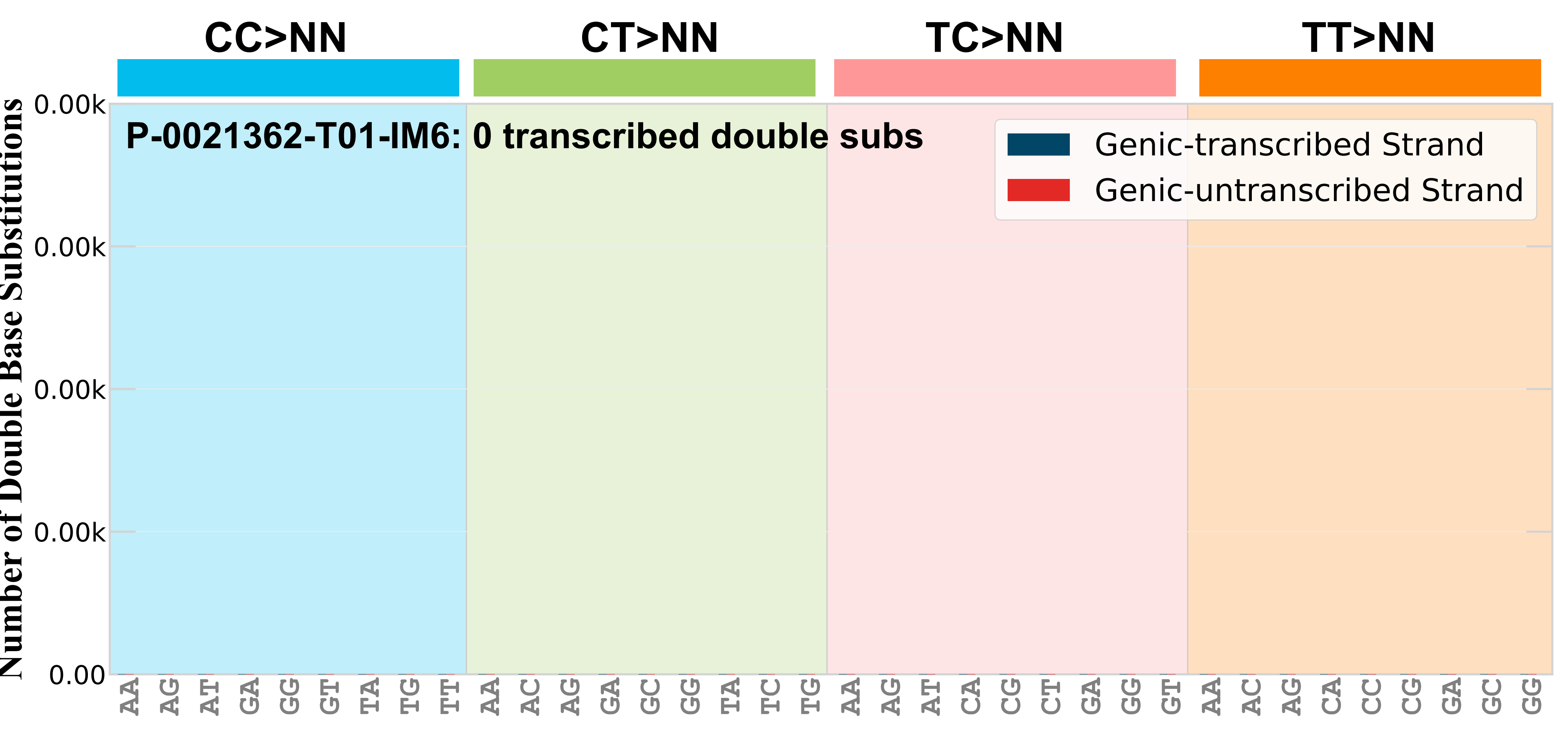


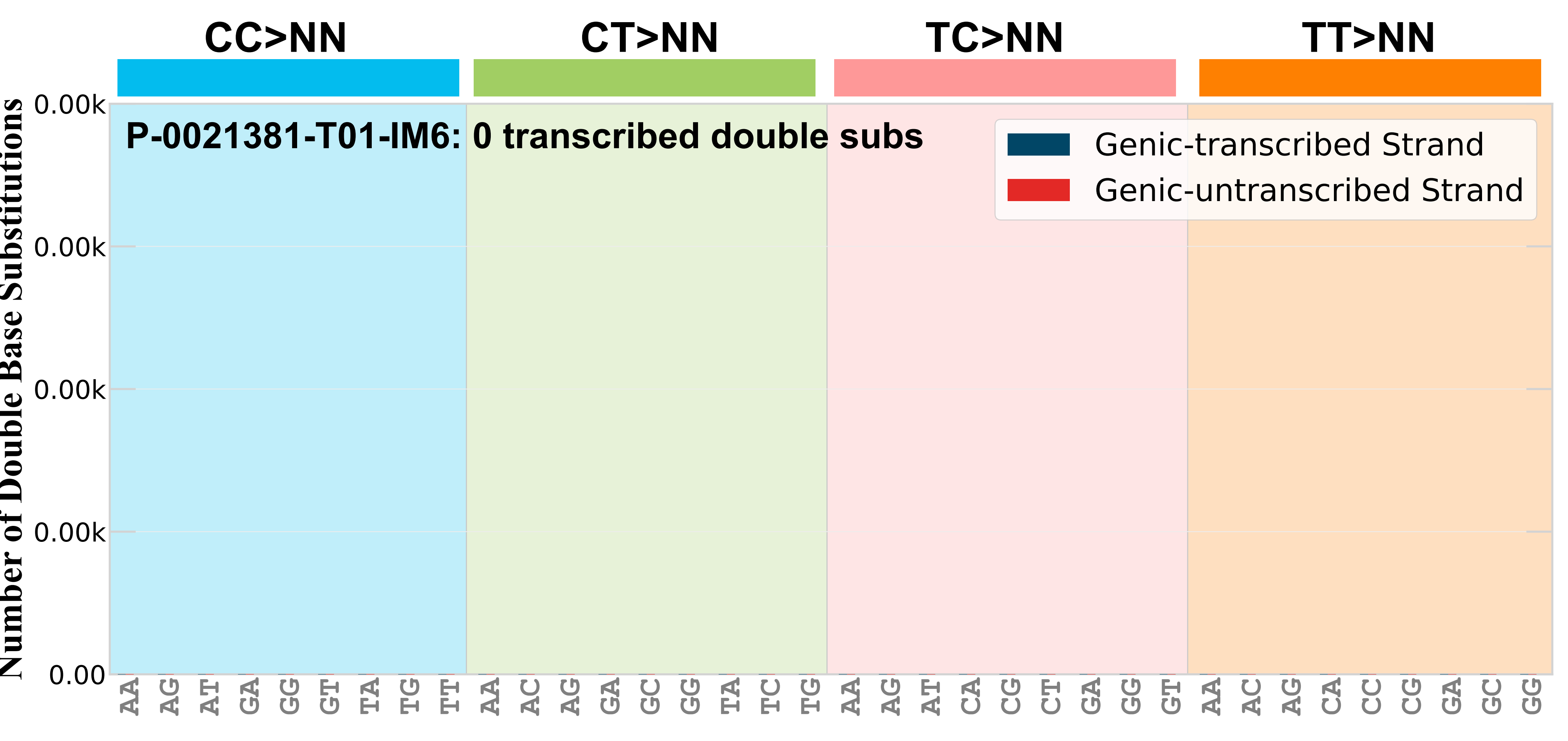
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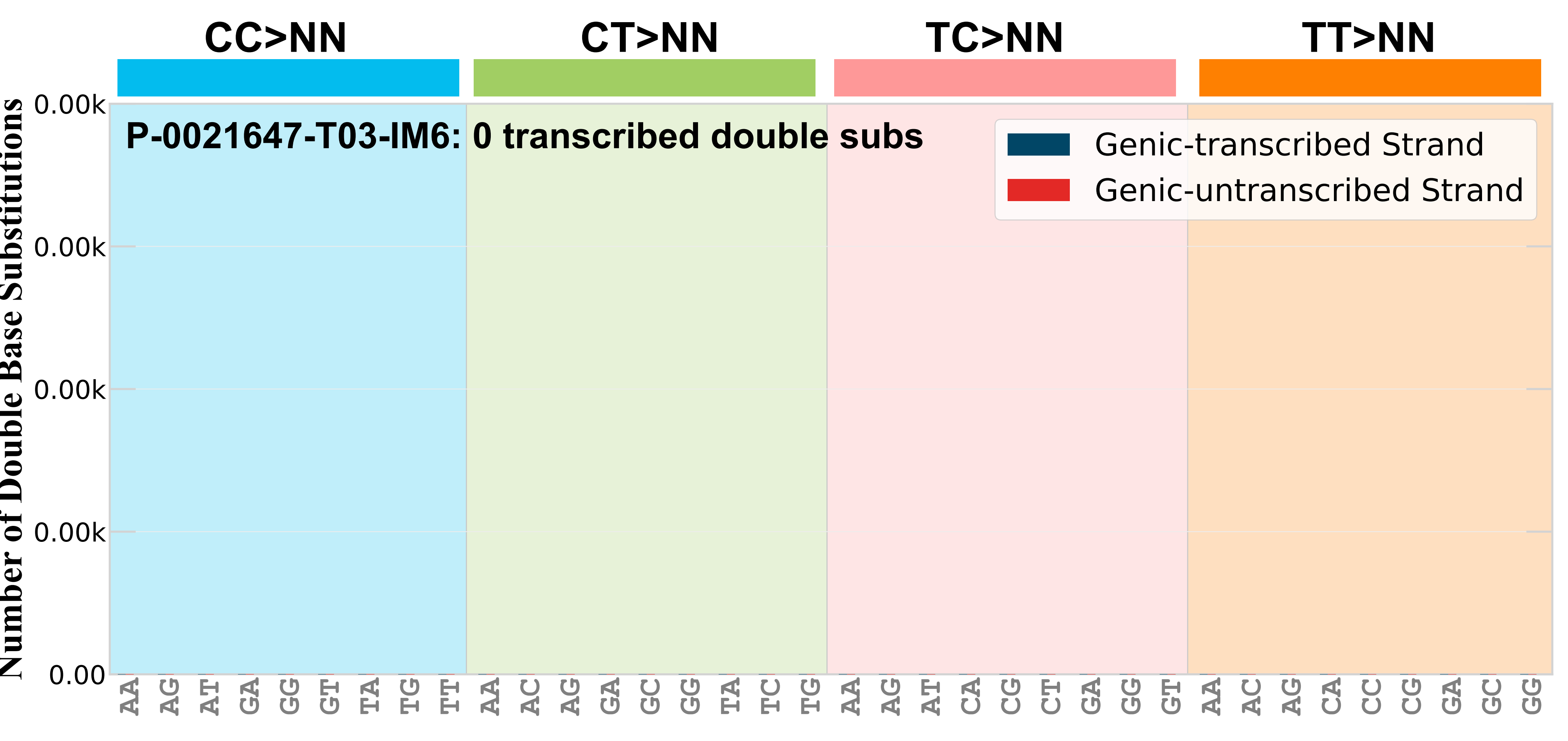


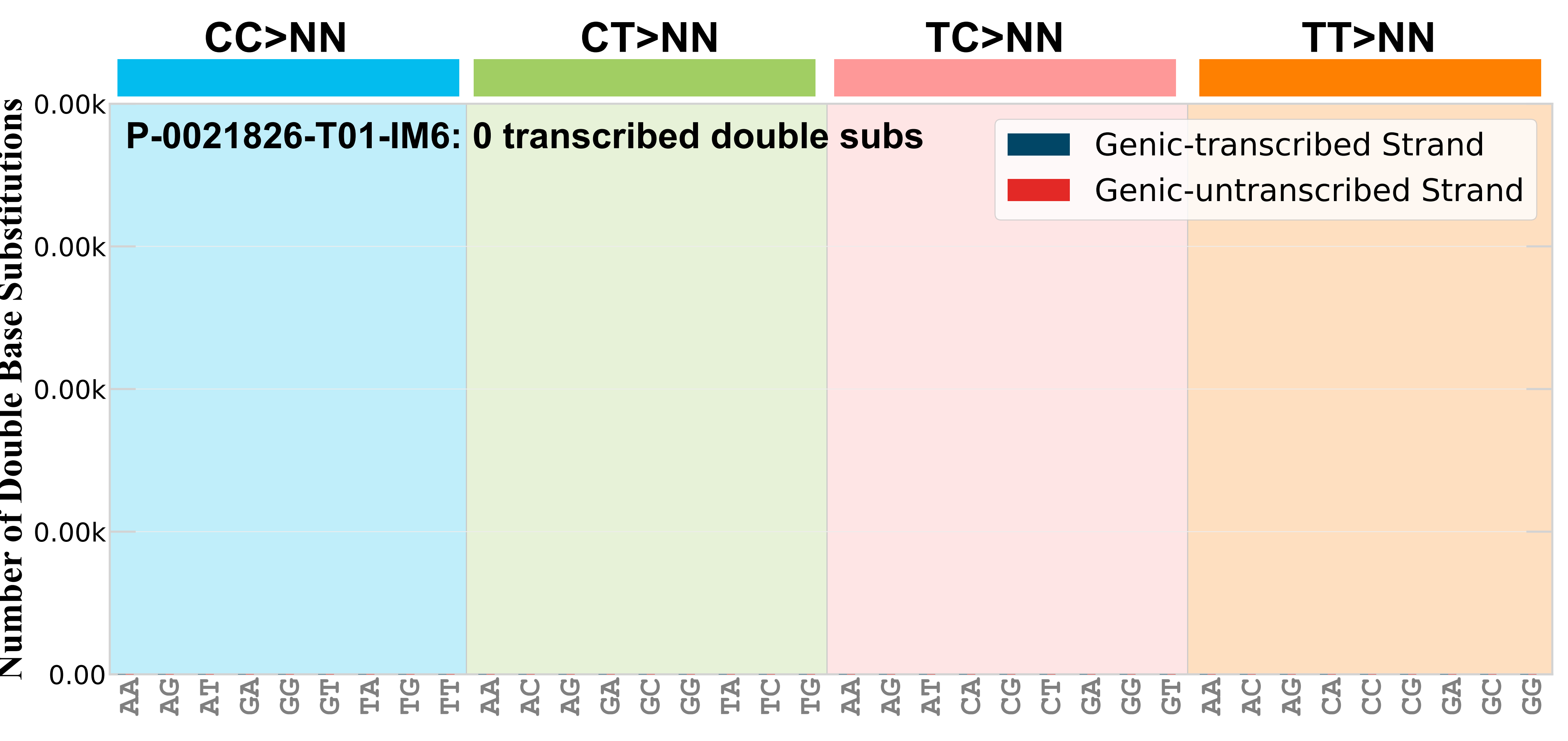
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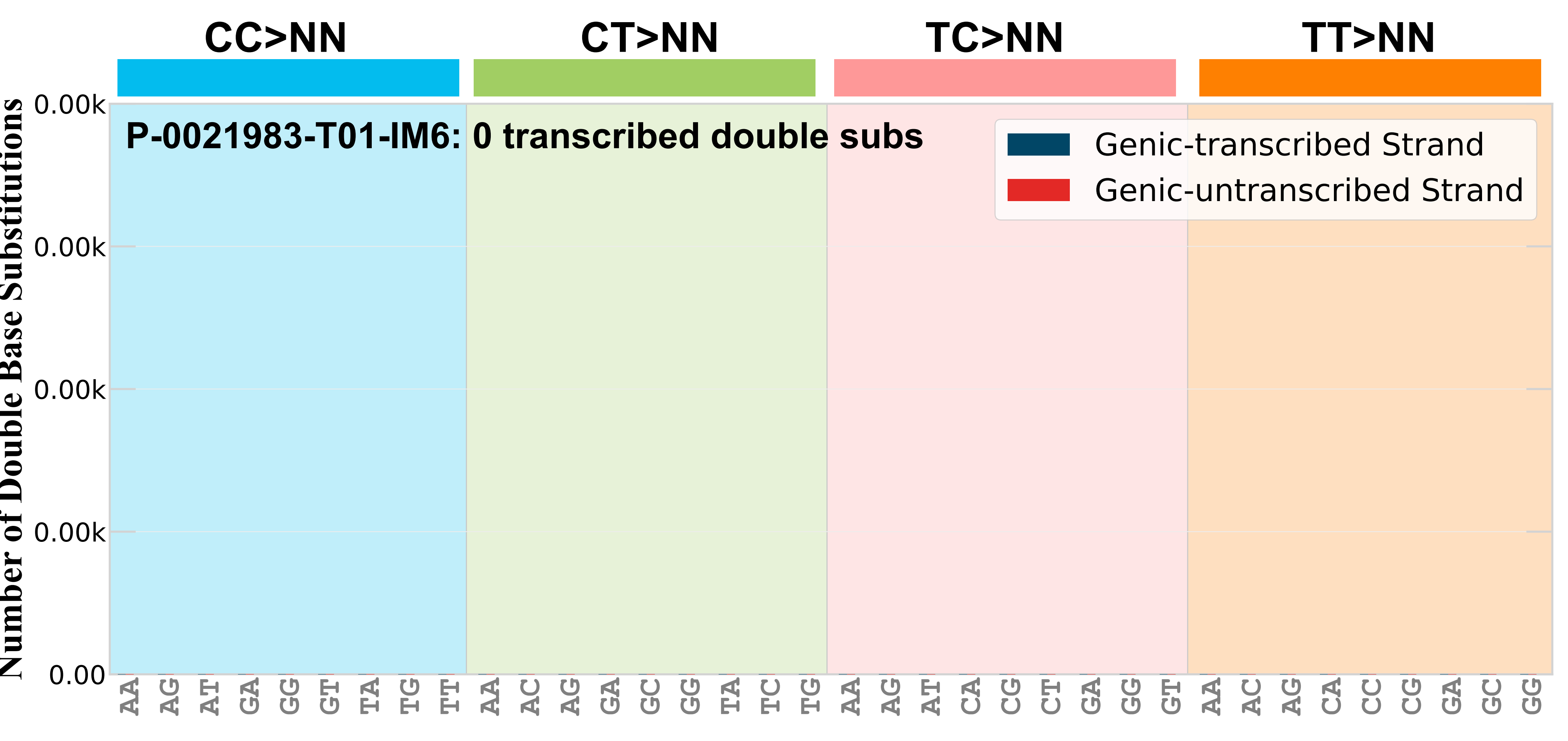


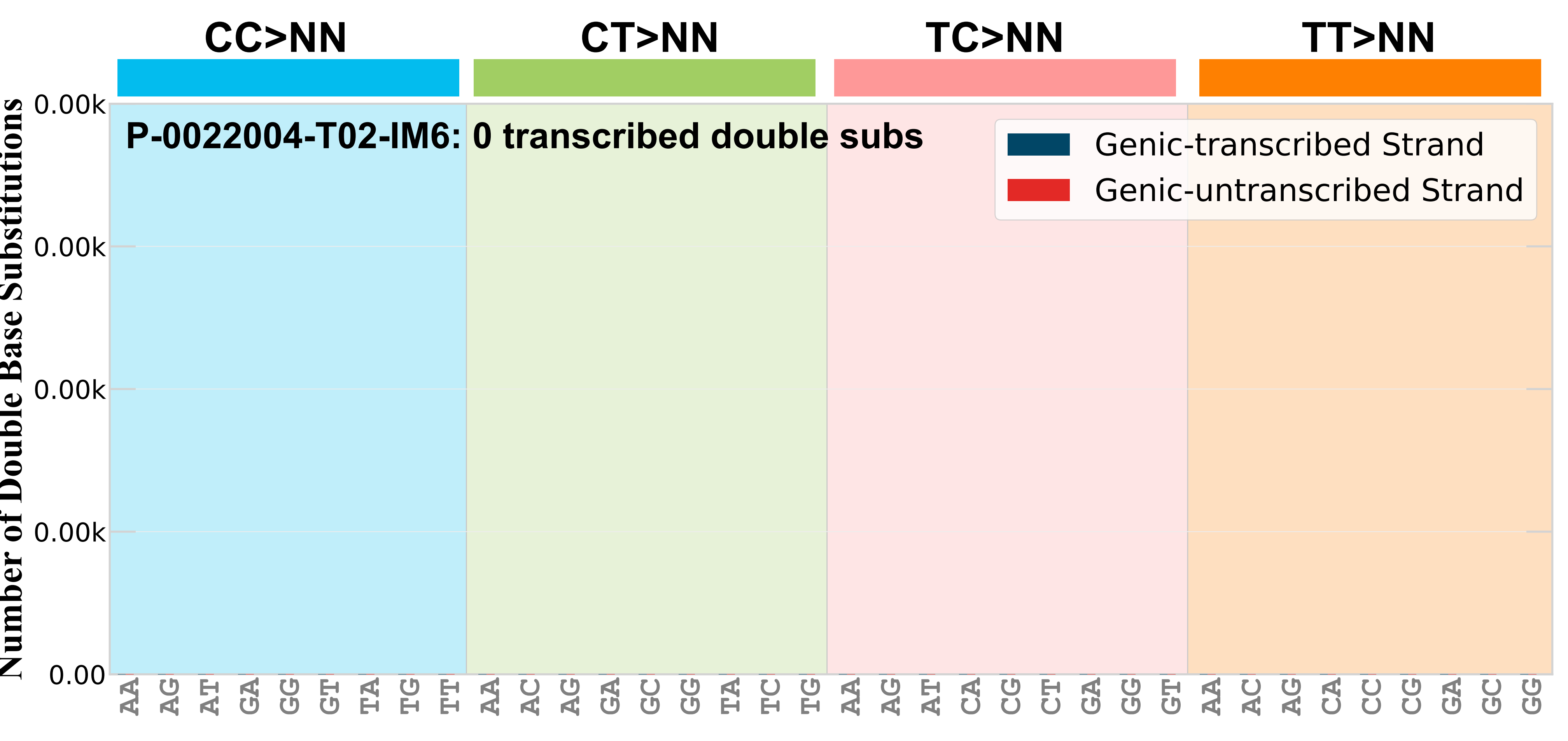




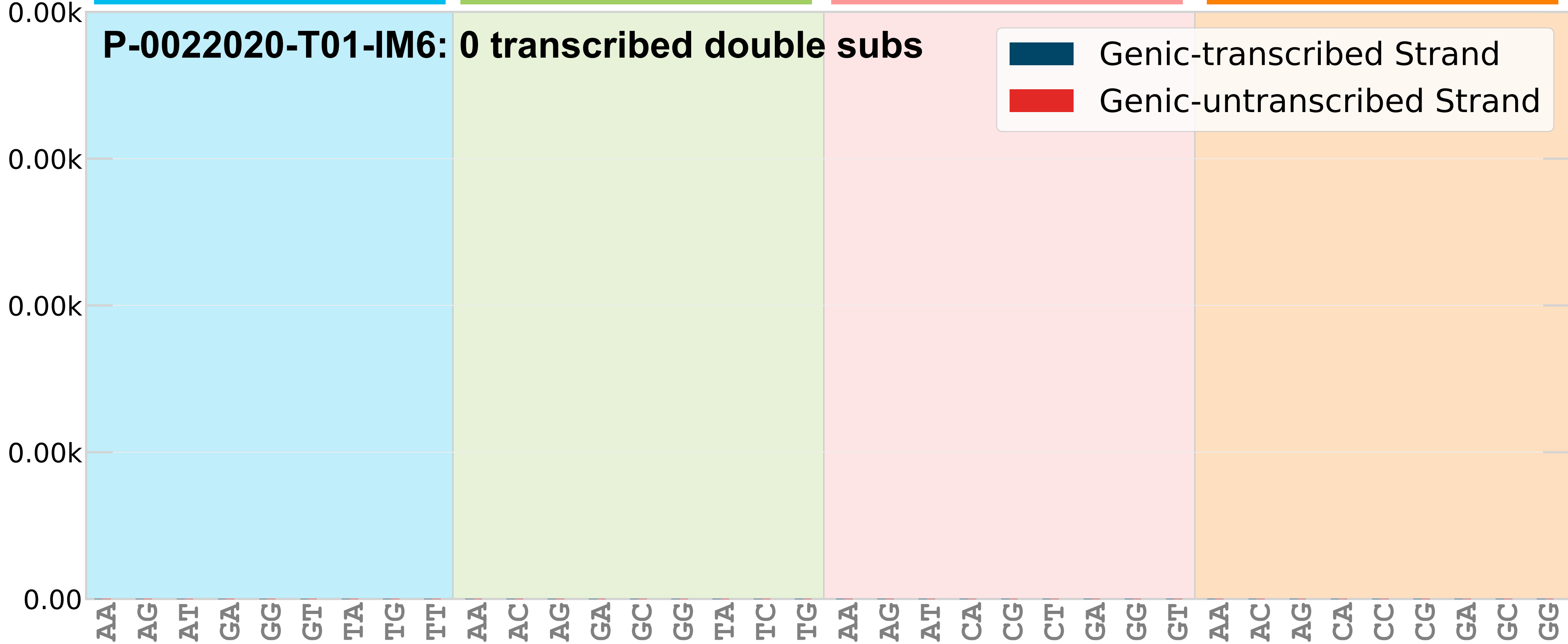


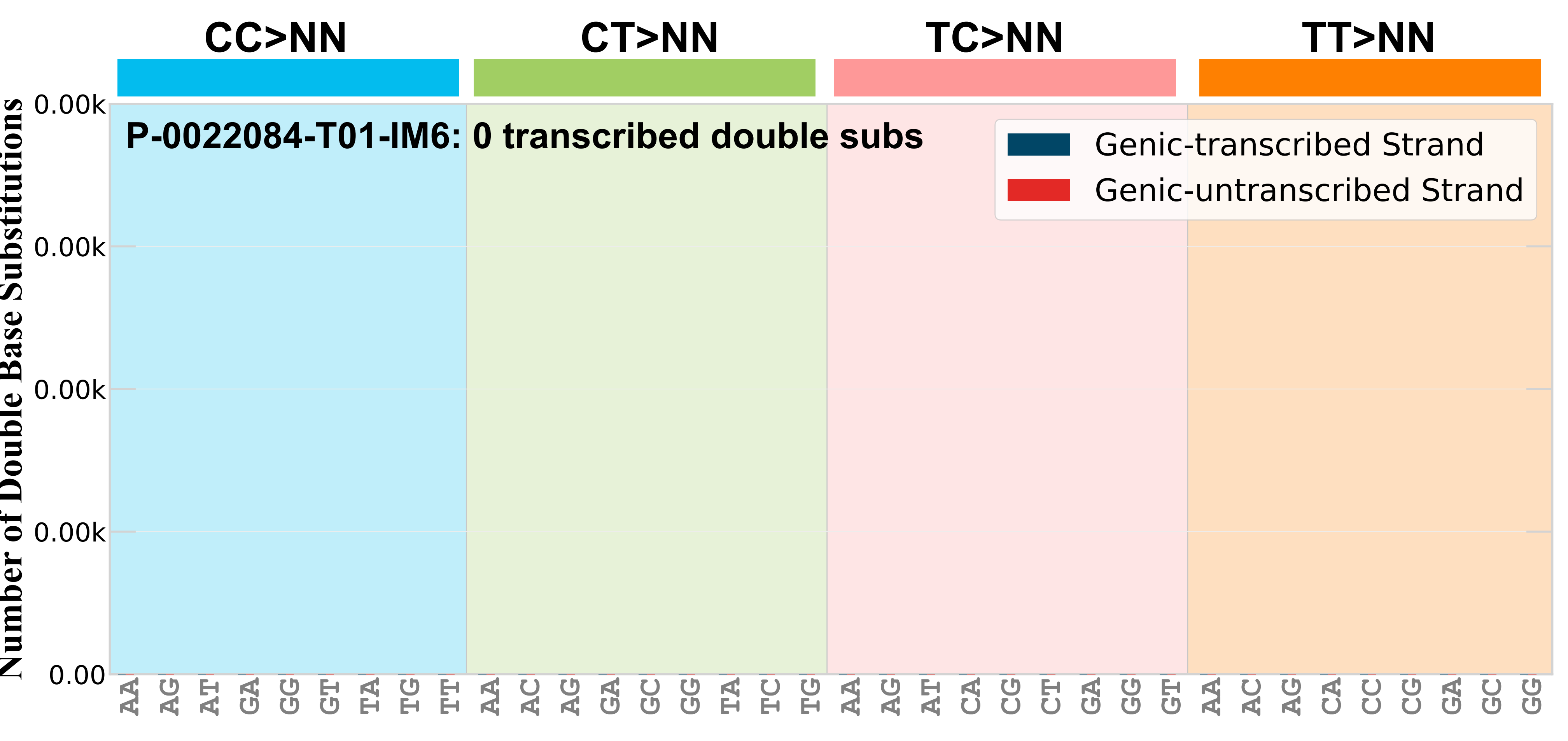




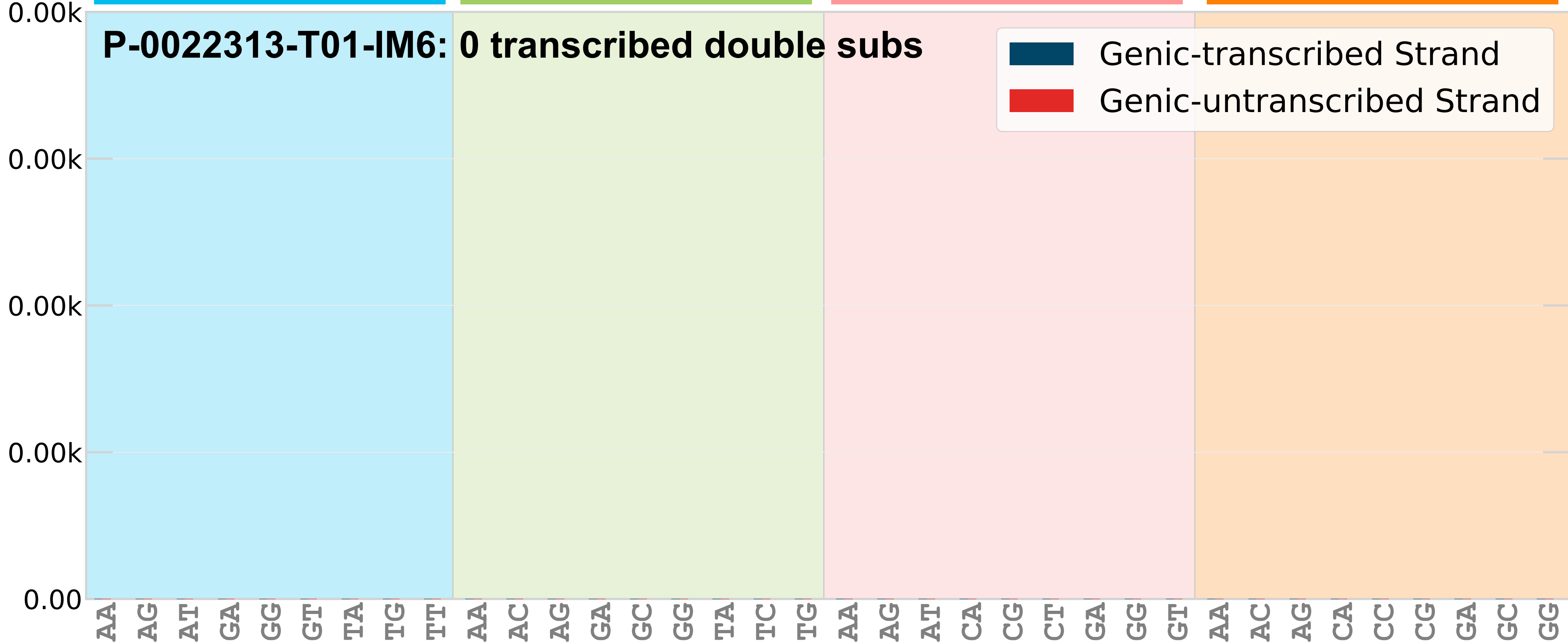


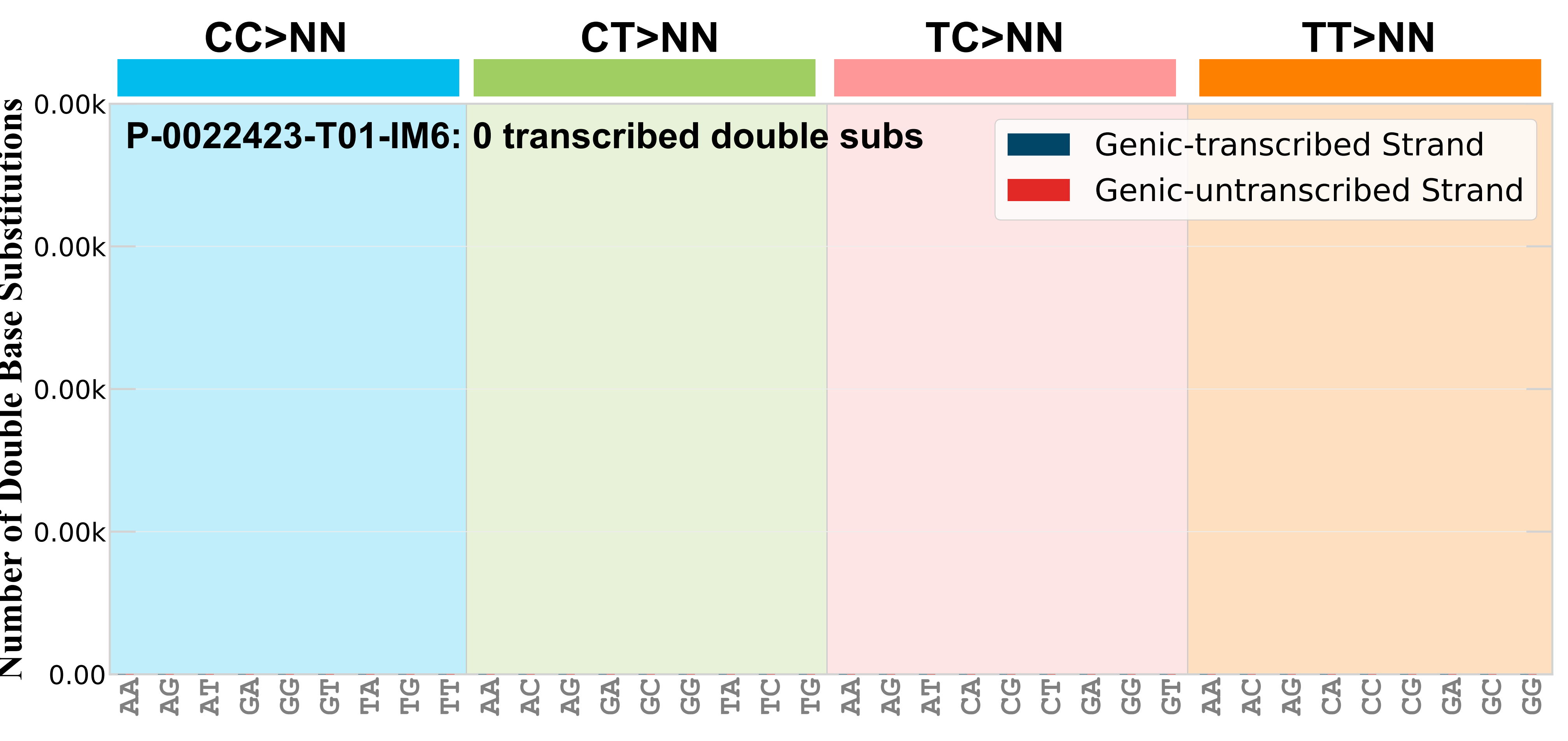
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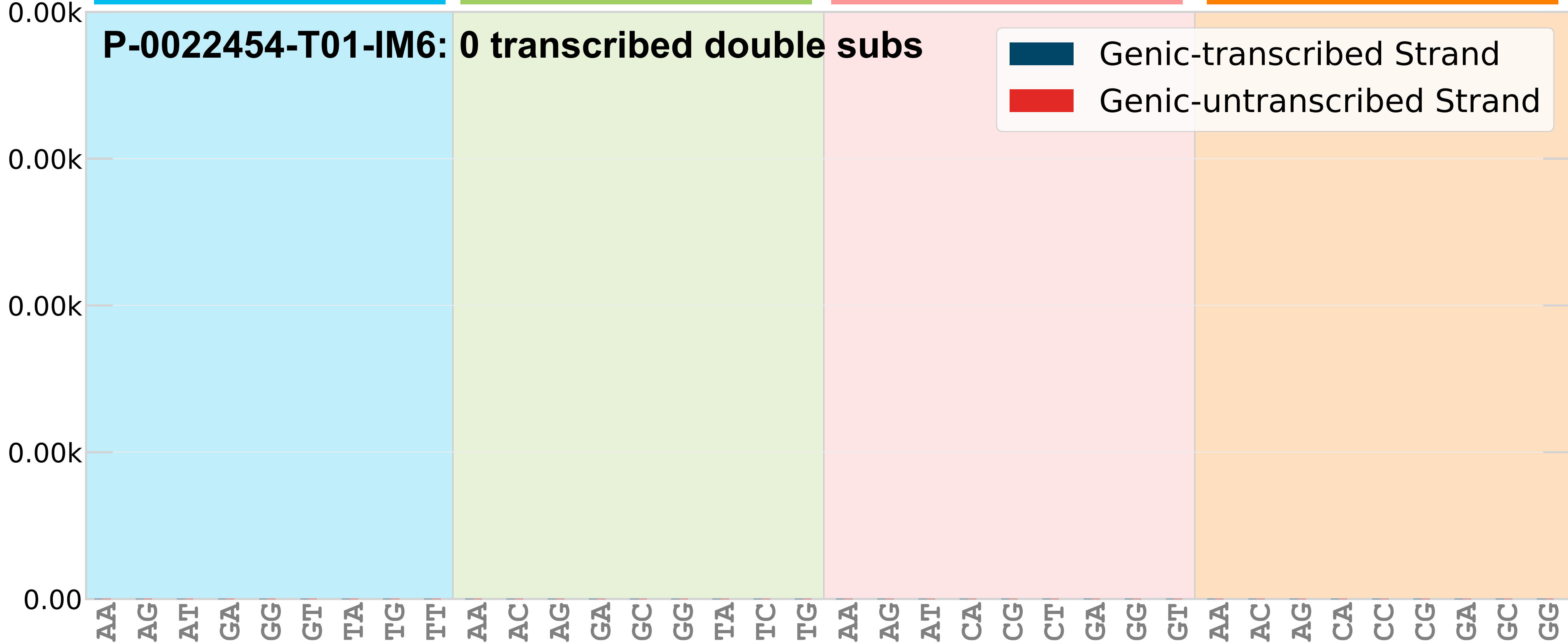


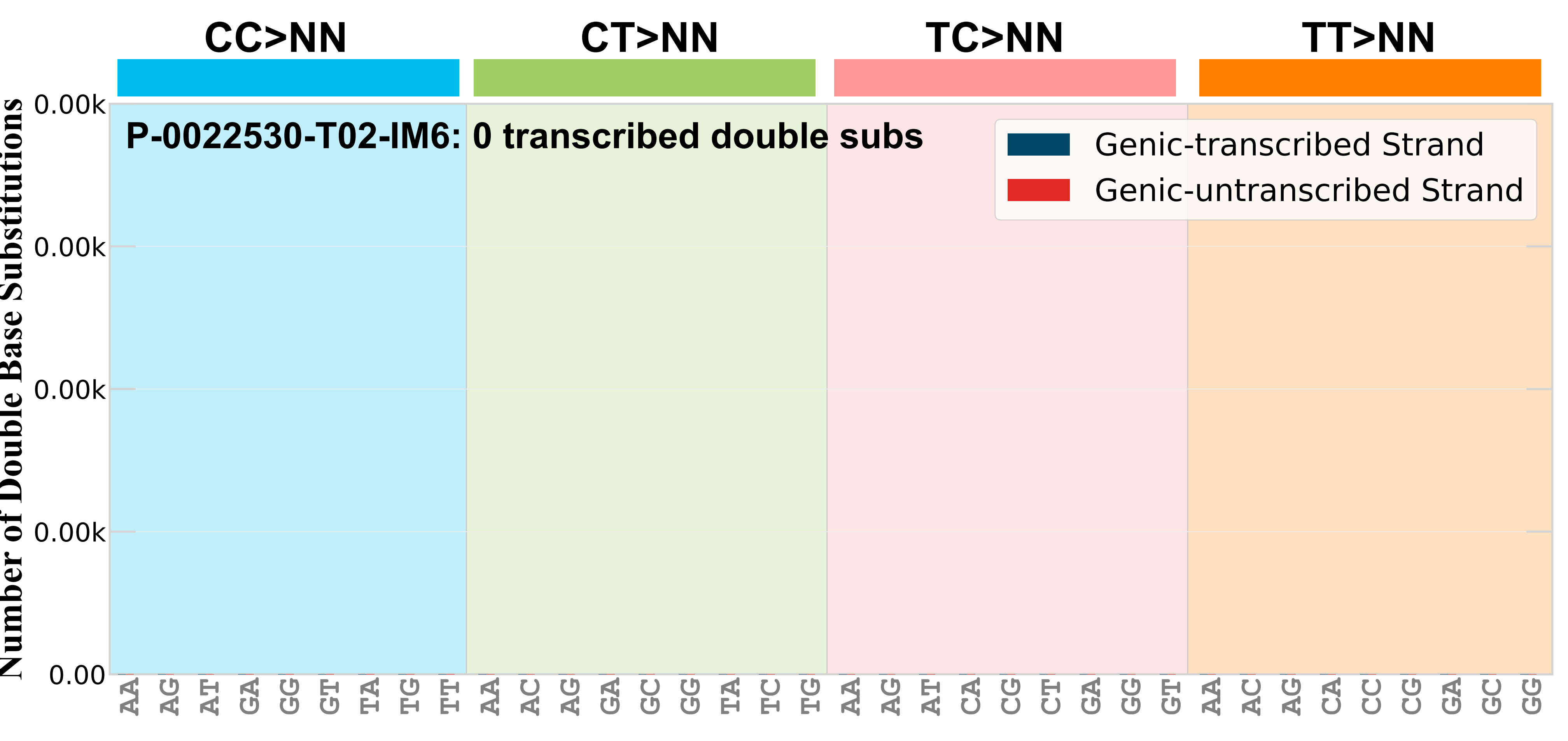
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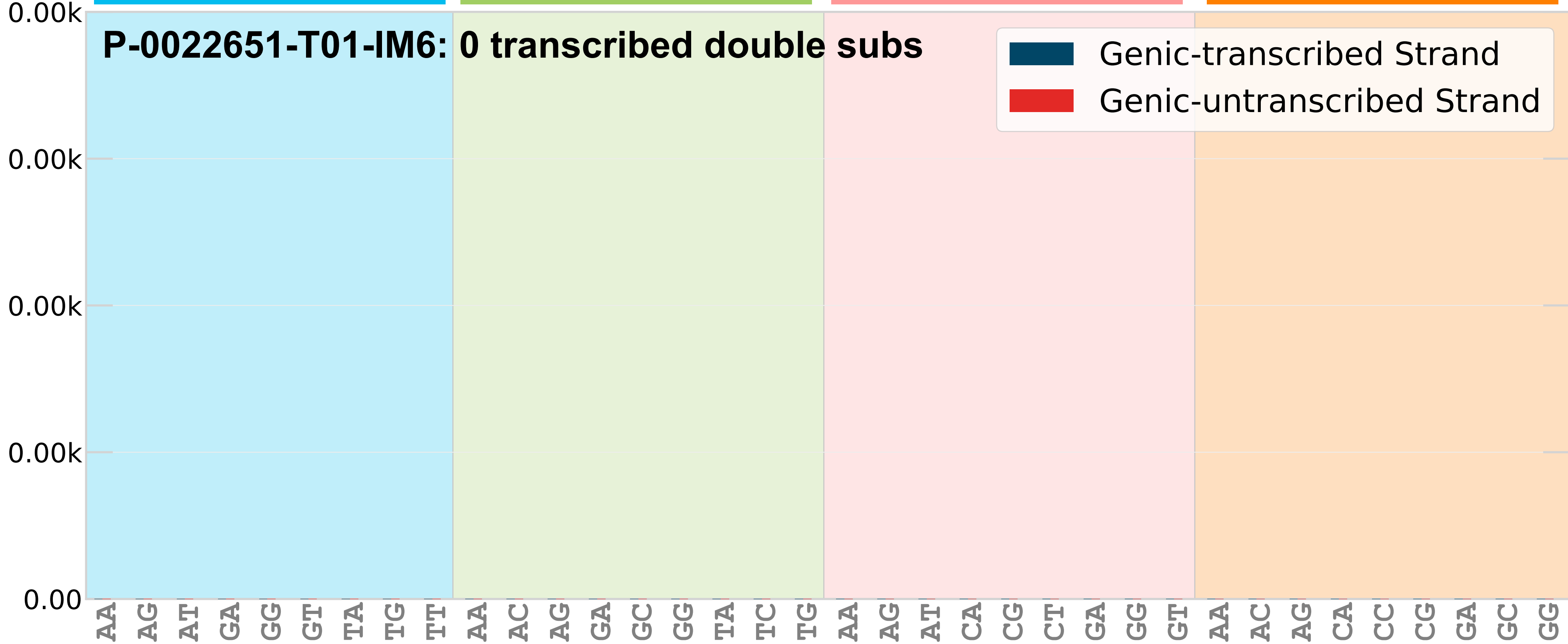


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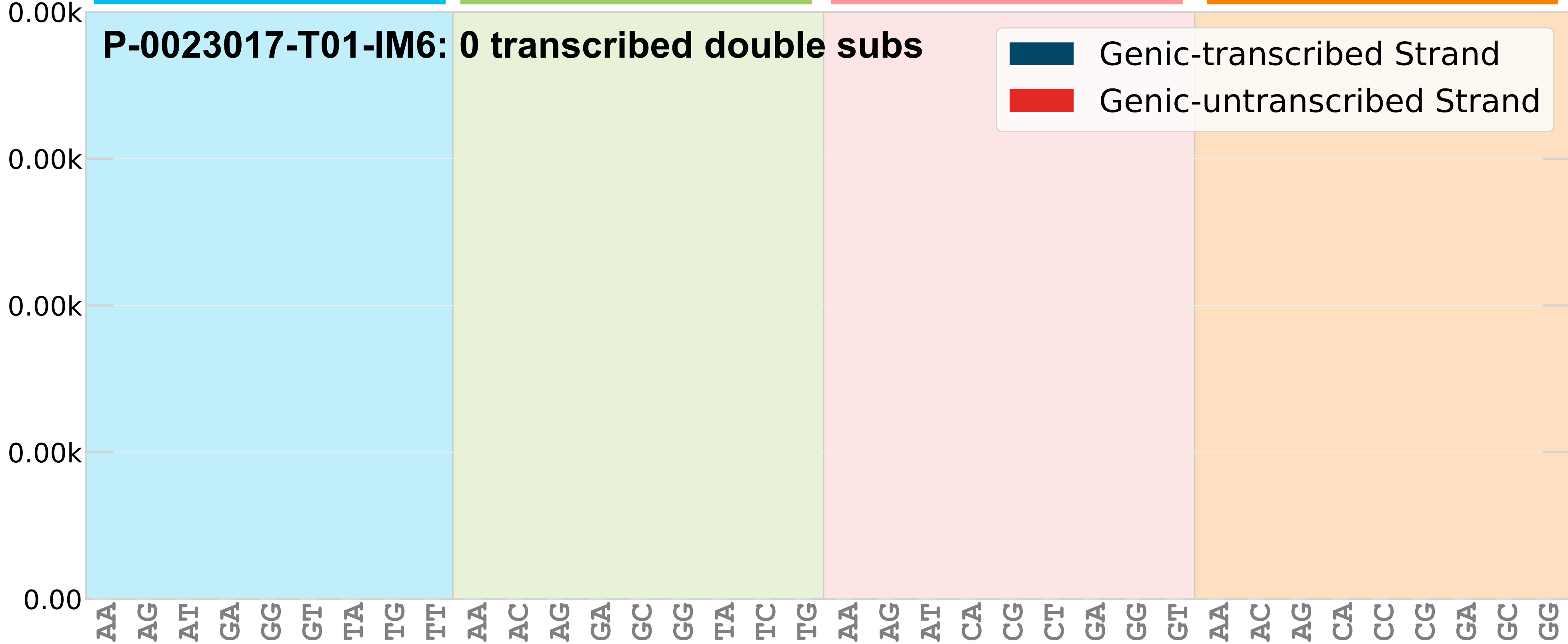


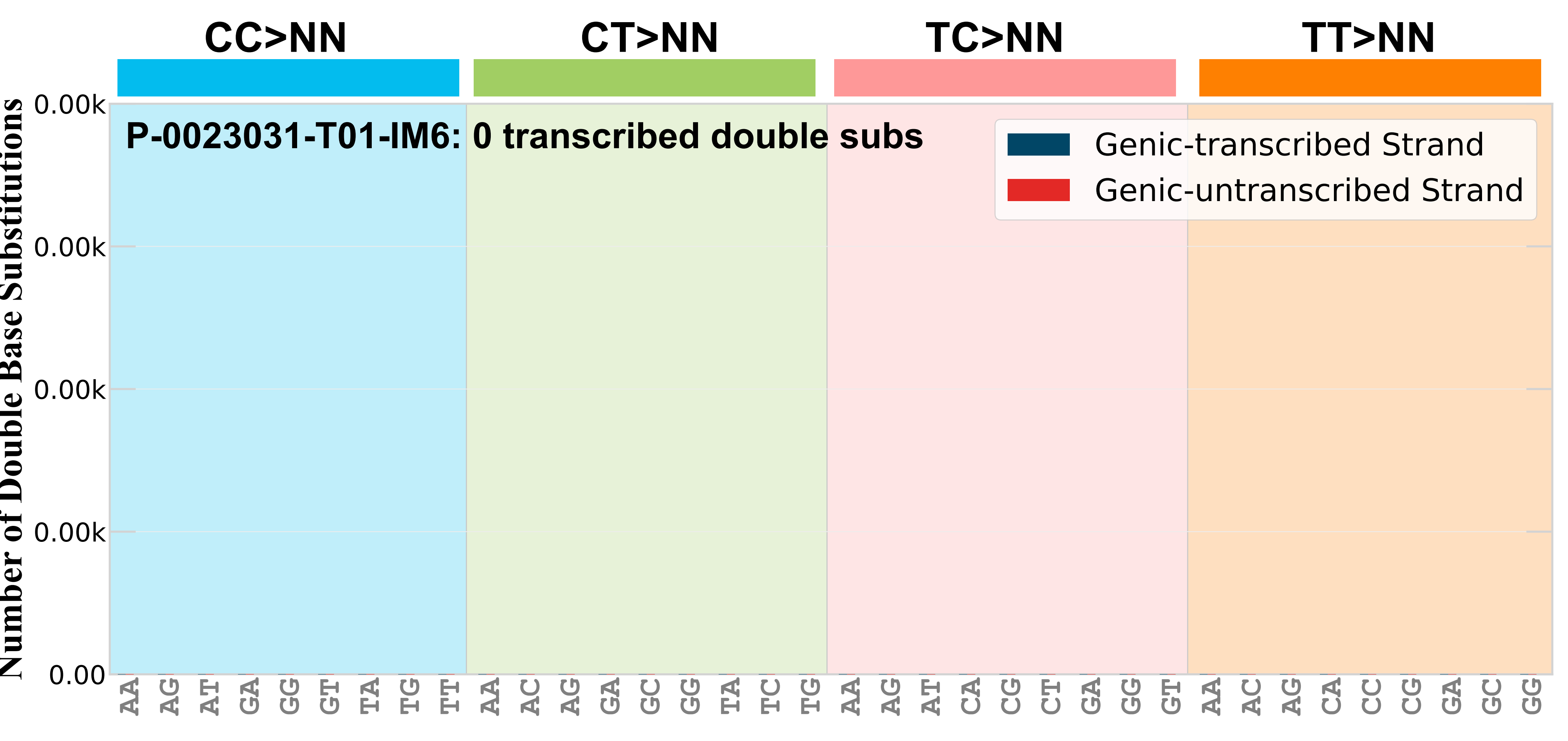


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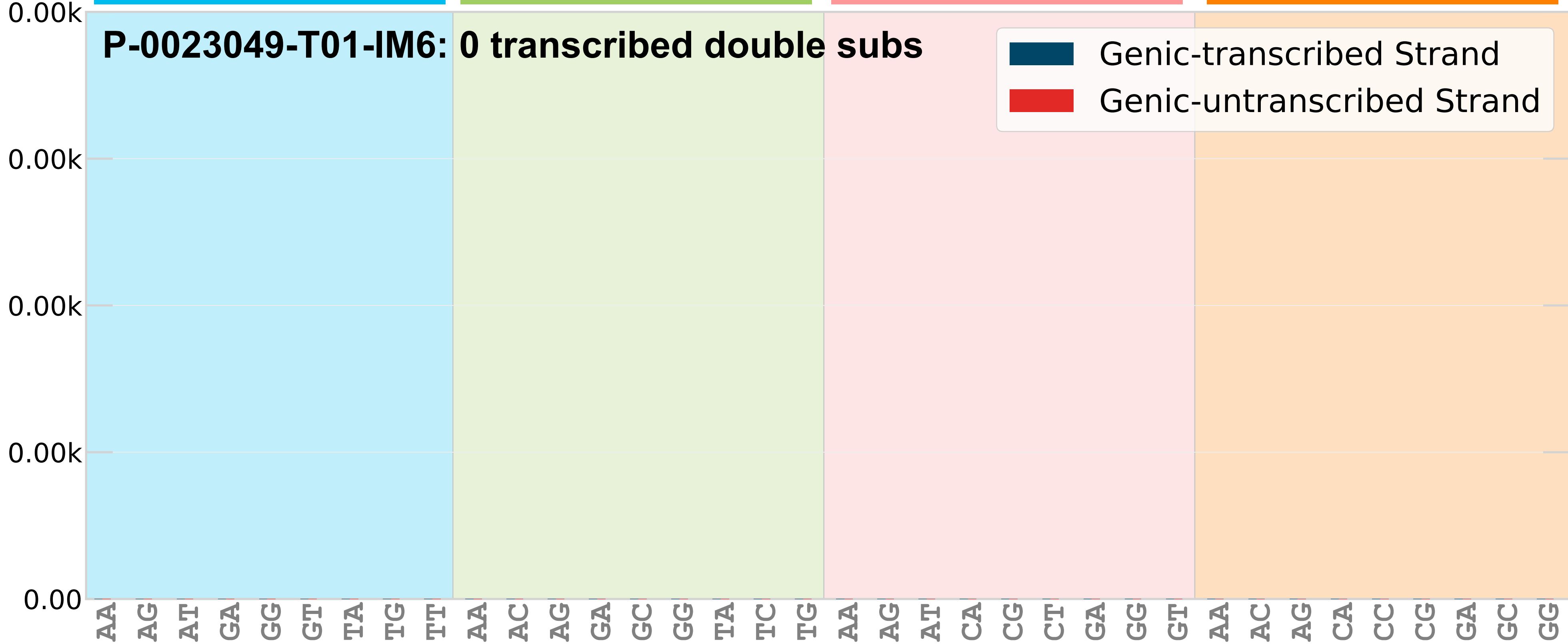


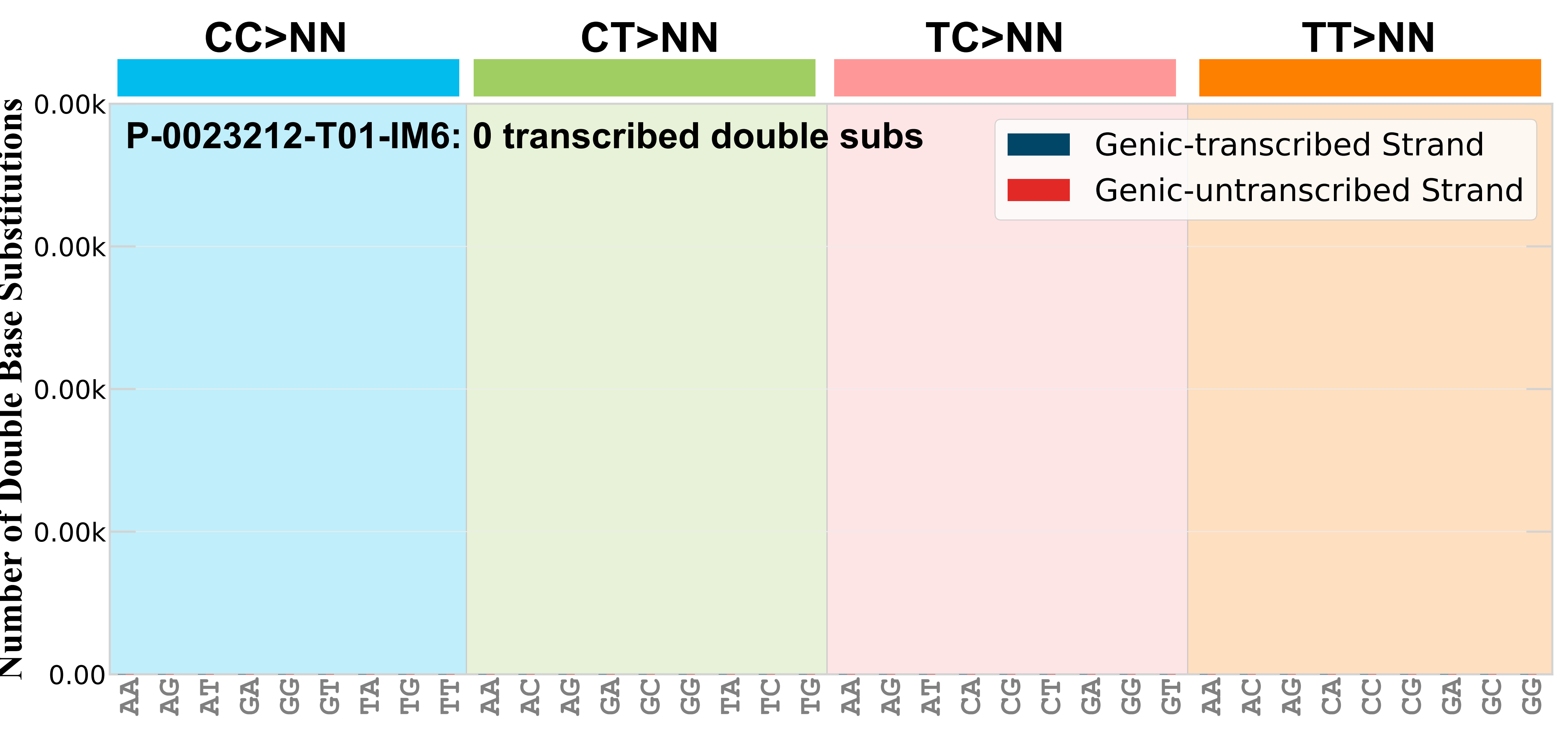
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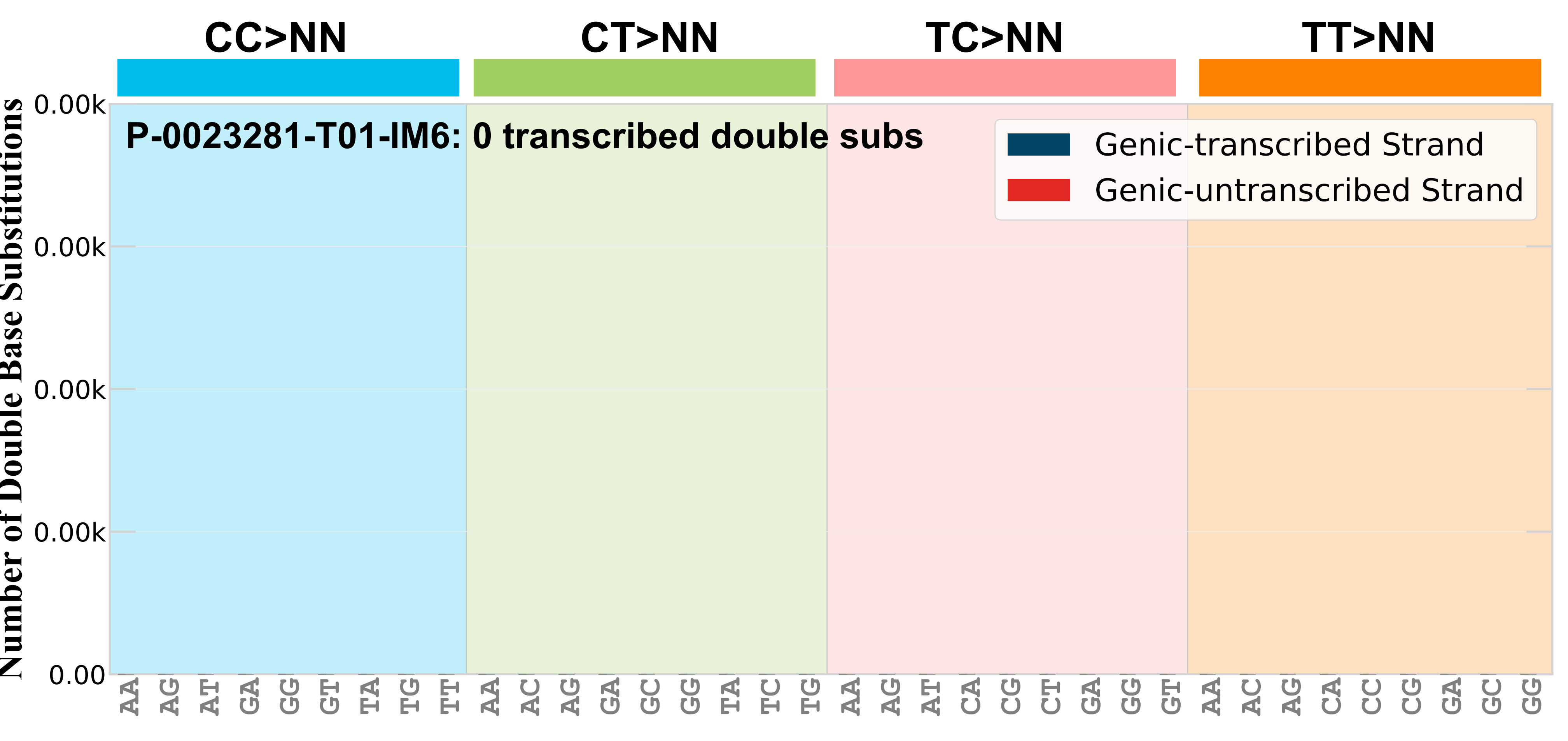




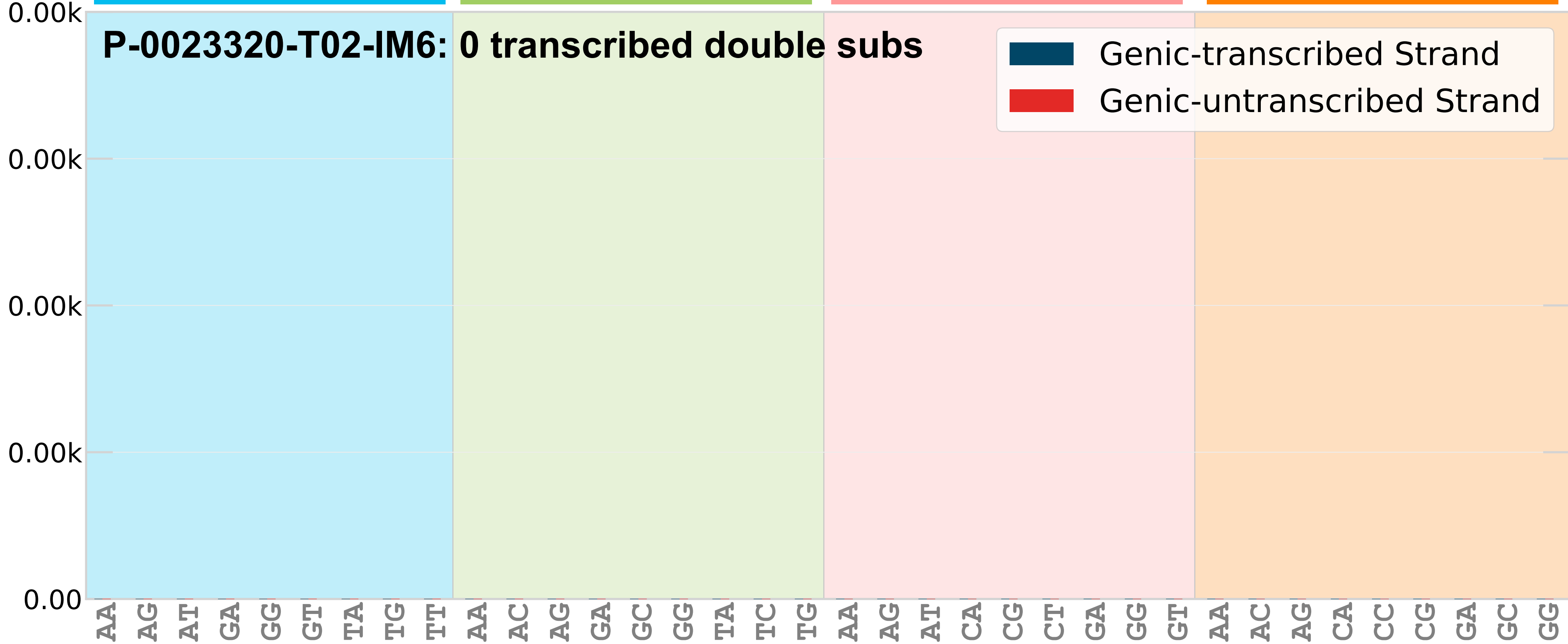
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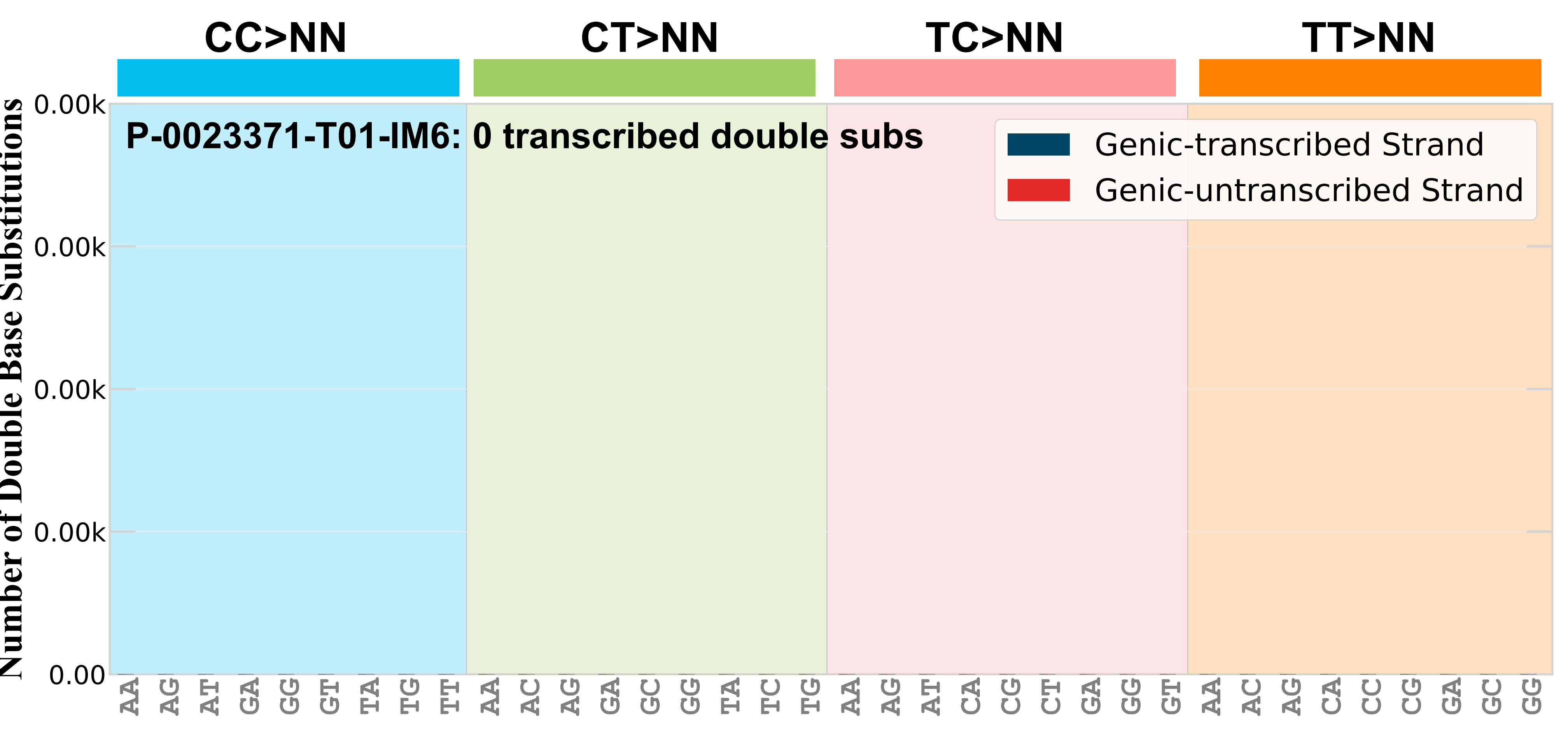


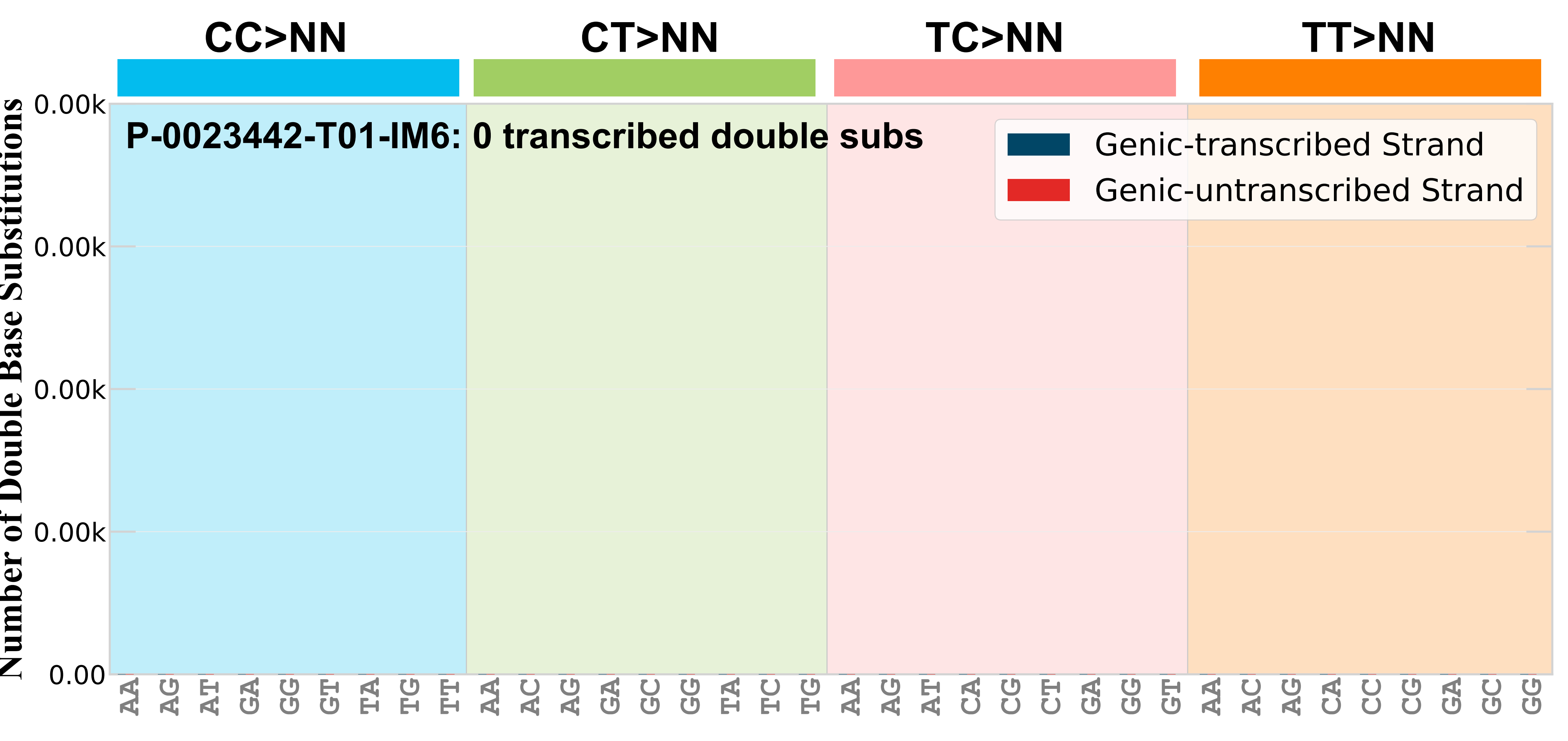


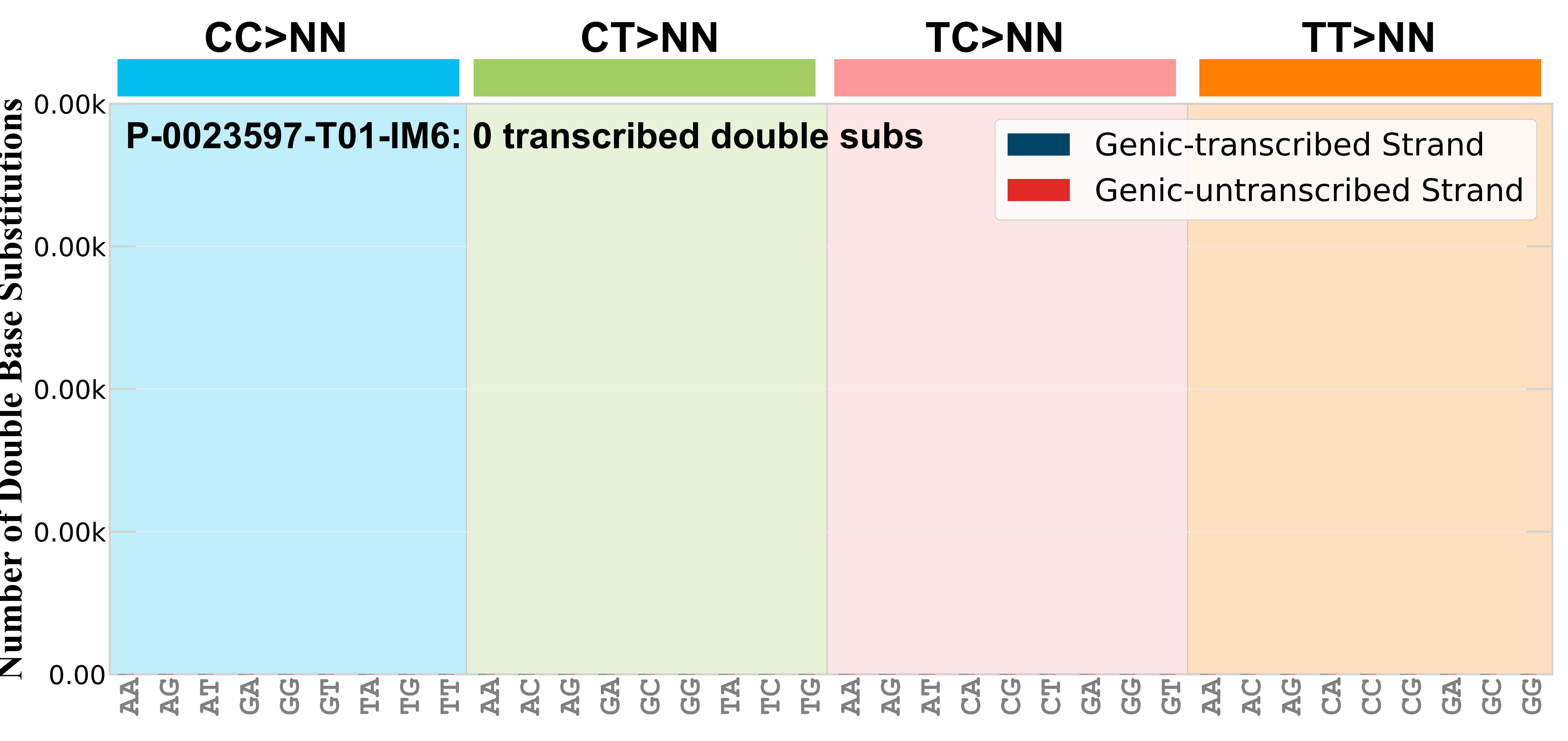


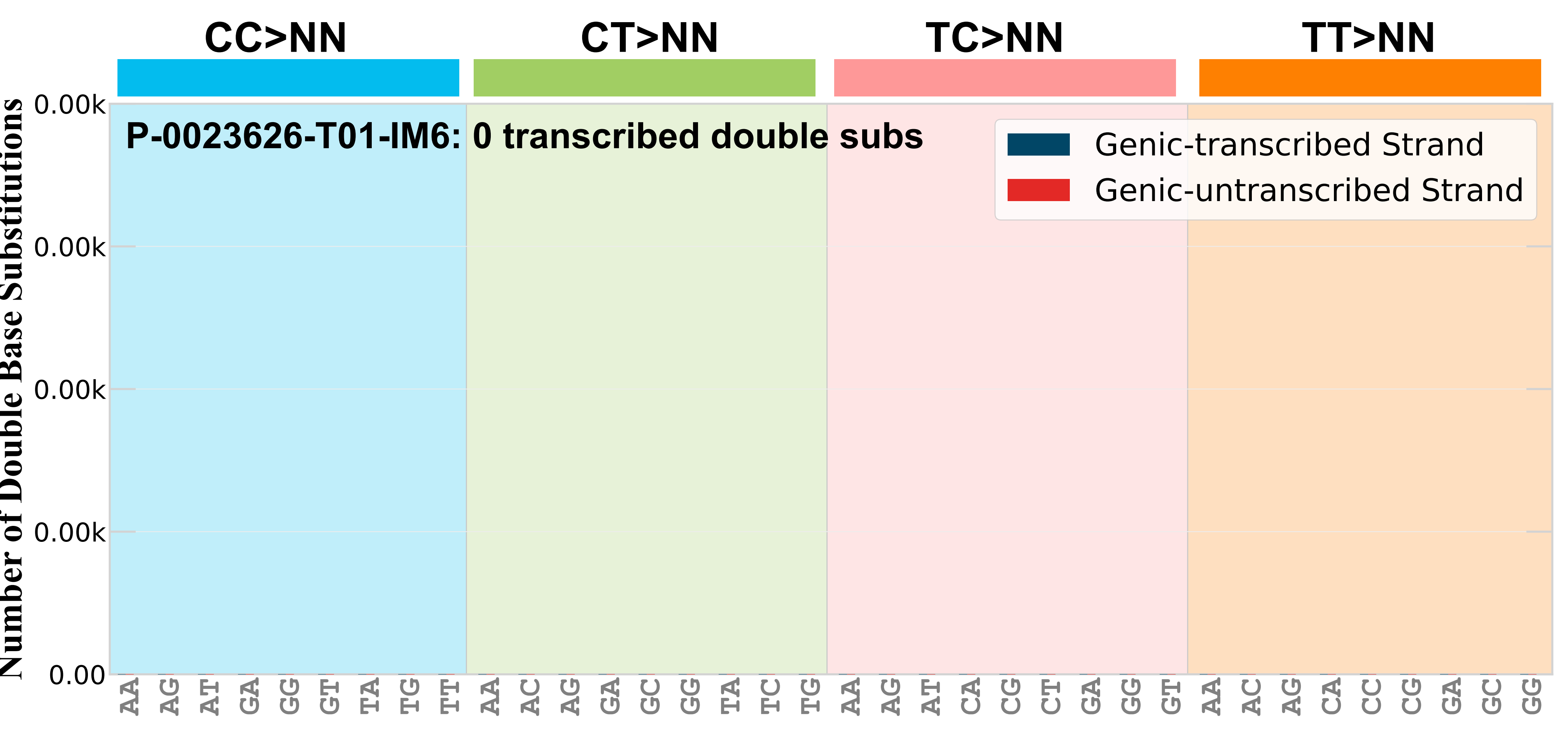
TT>NN











Number of Double Base Substitutions

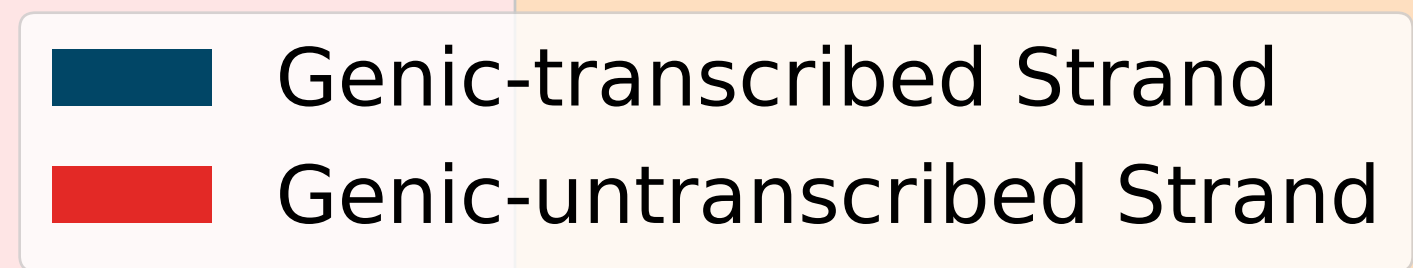
CC>NN

CT>NN

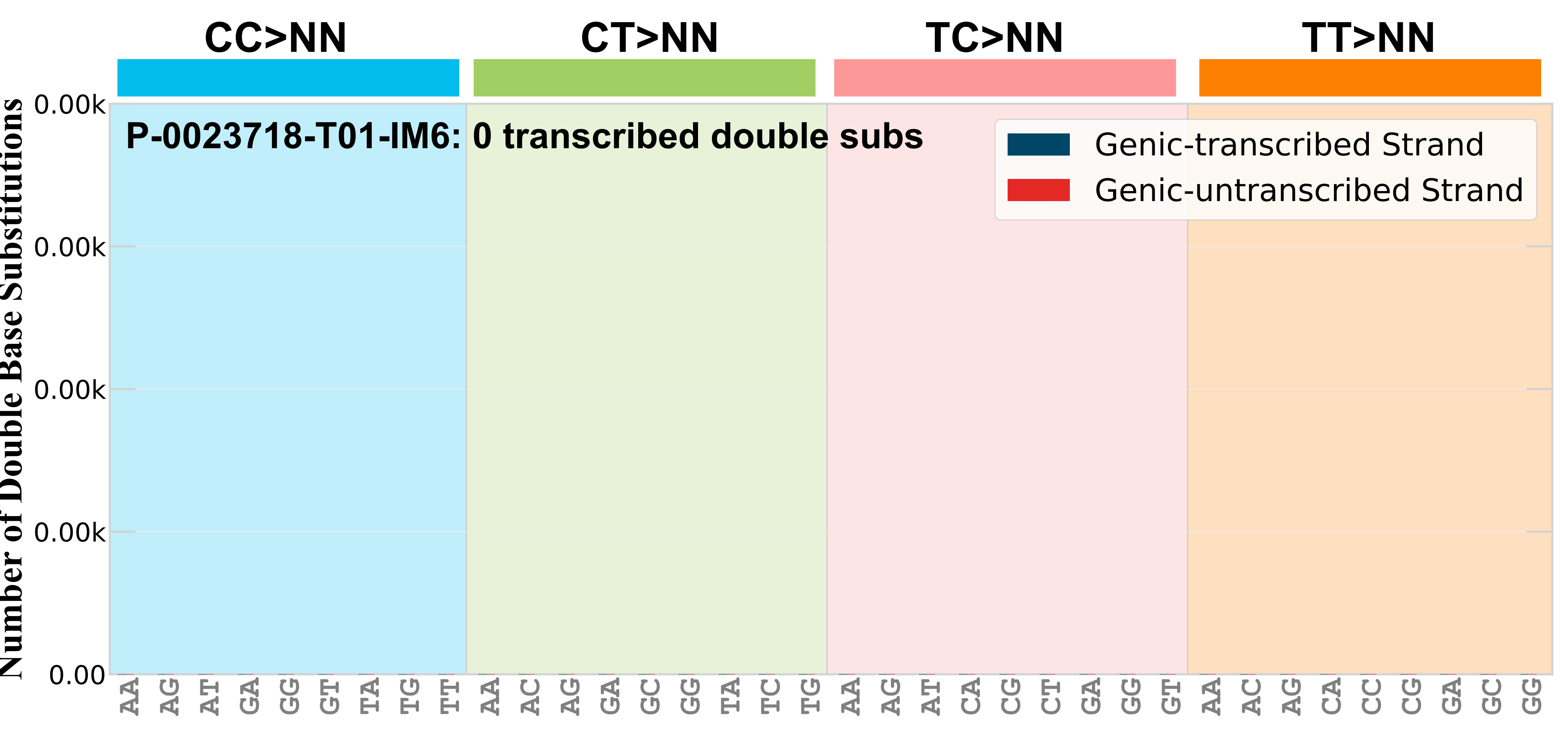
TC>NN

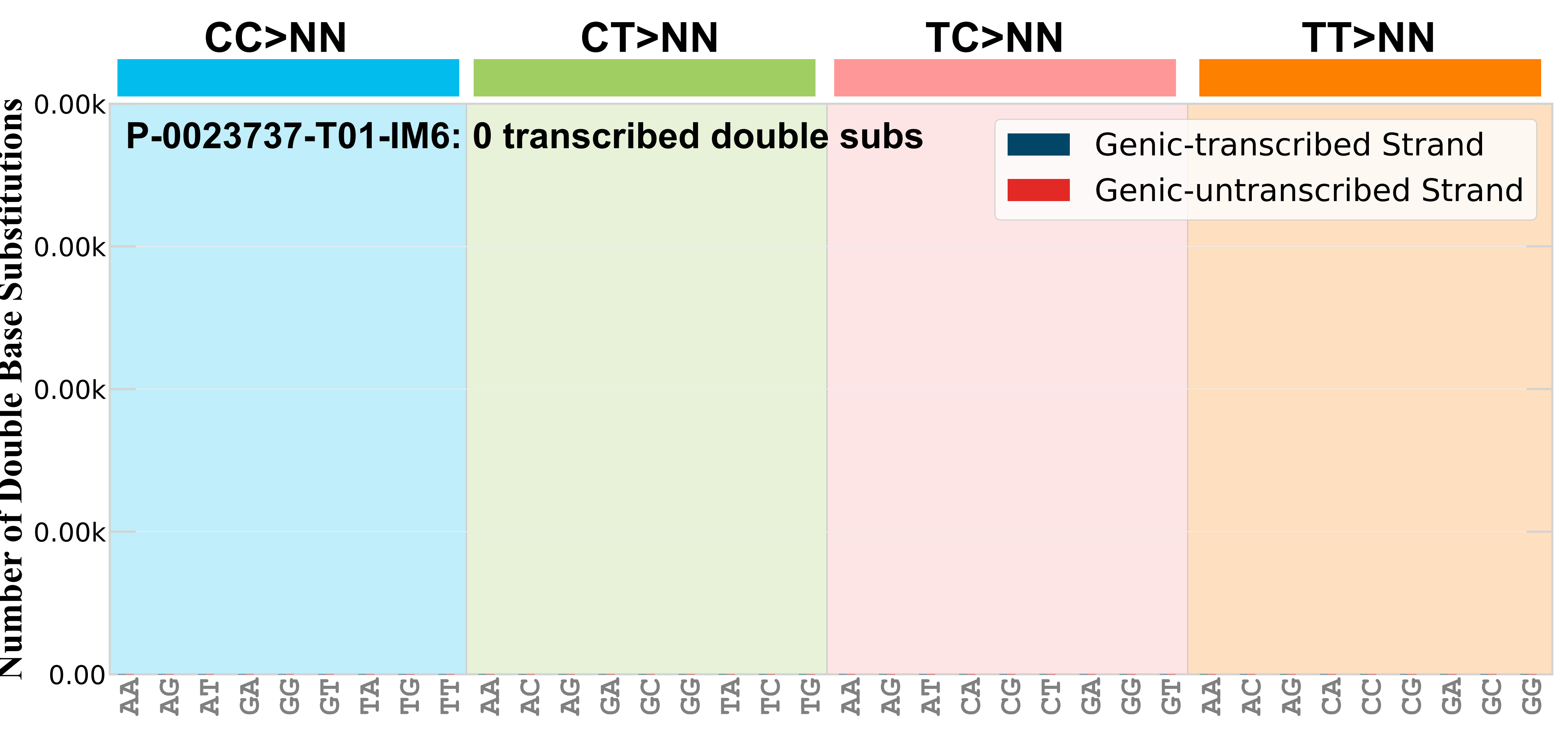
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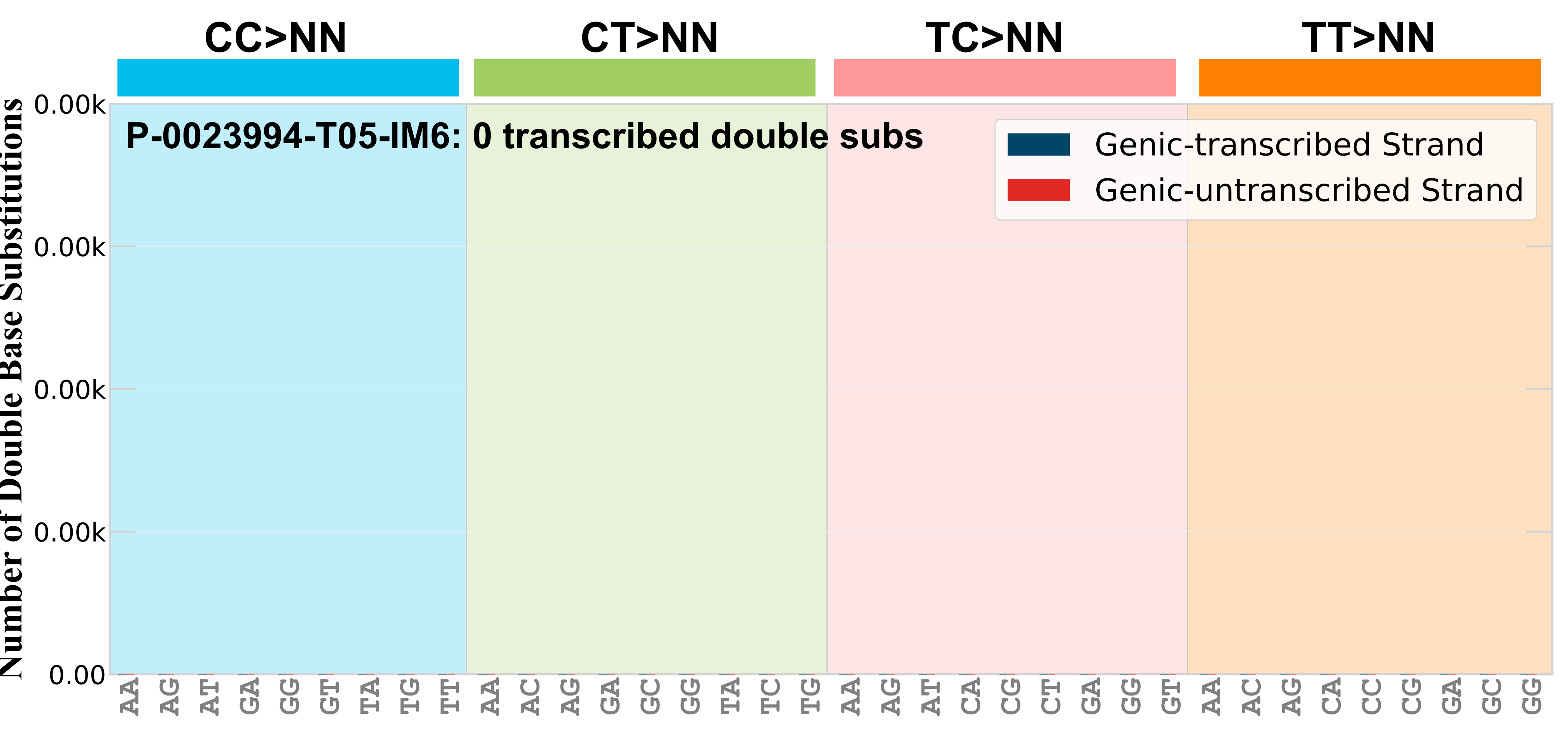
P-0023702-T01-IM6: 0 transcribed double subs

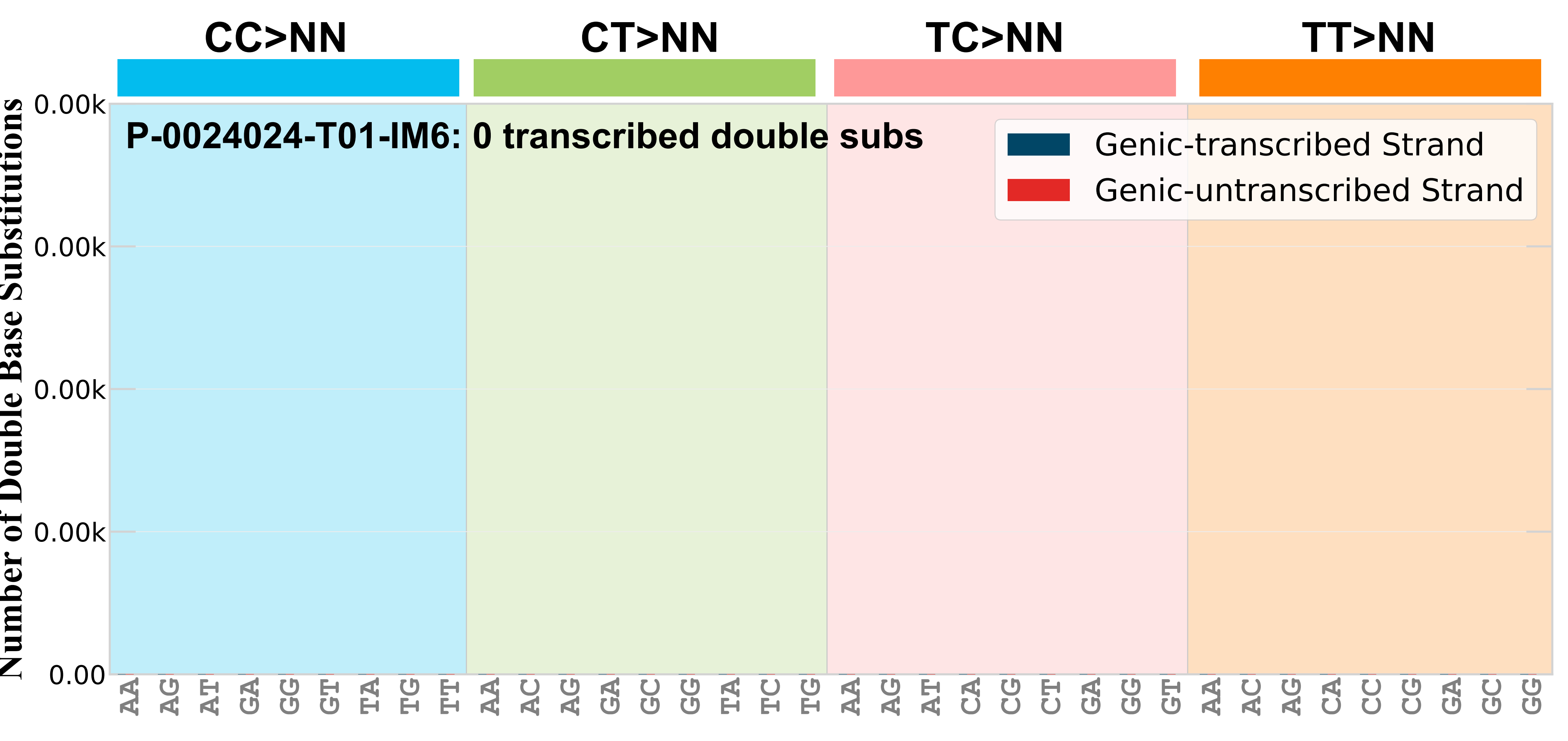


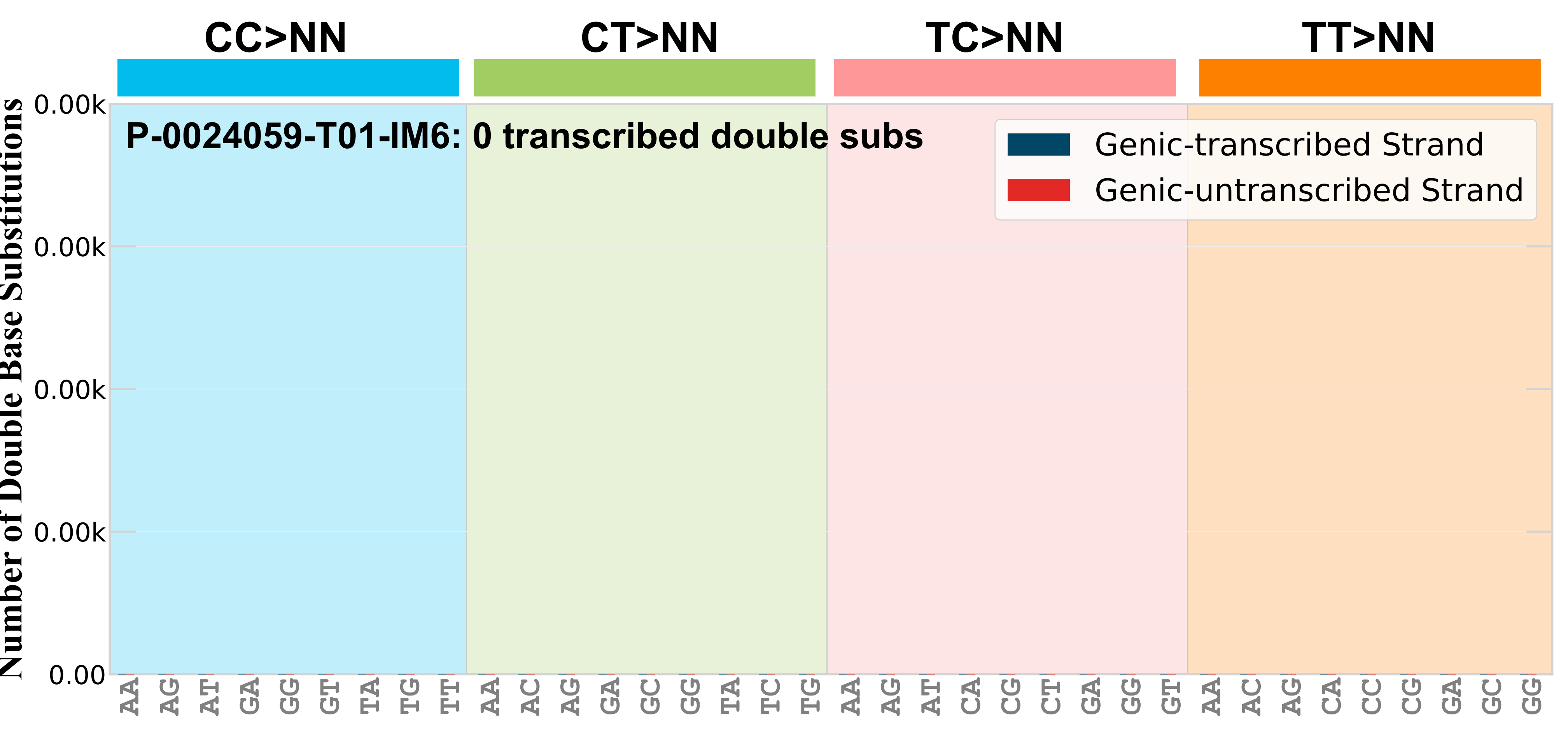
AA AG AT GA GG GT TA TG TT AA AC AG GA GC GG TA TC TG AA AG AT CA CG CT GA GG GT AA AC AG CA CC CG GA GC GG

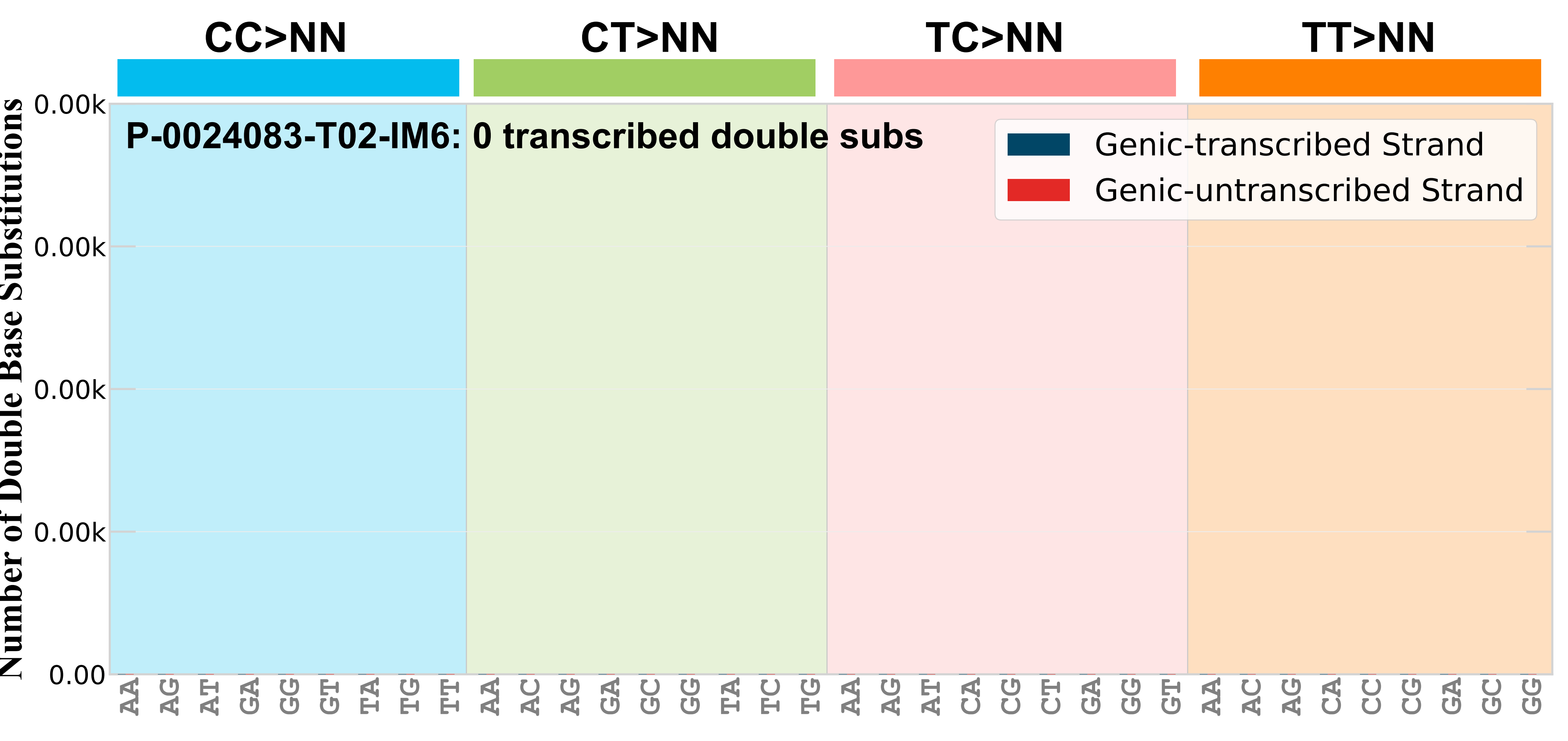


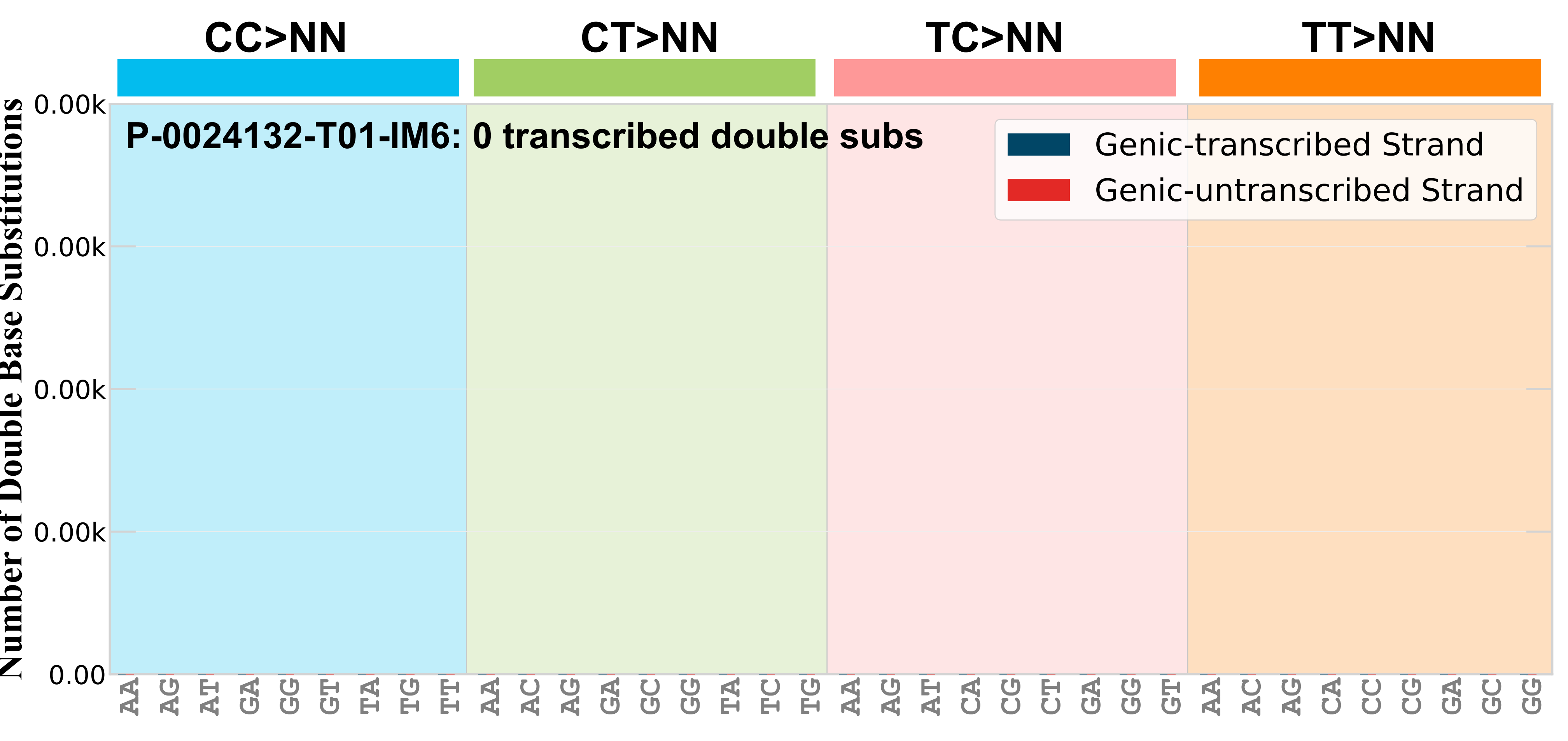




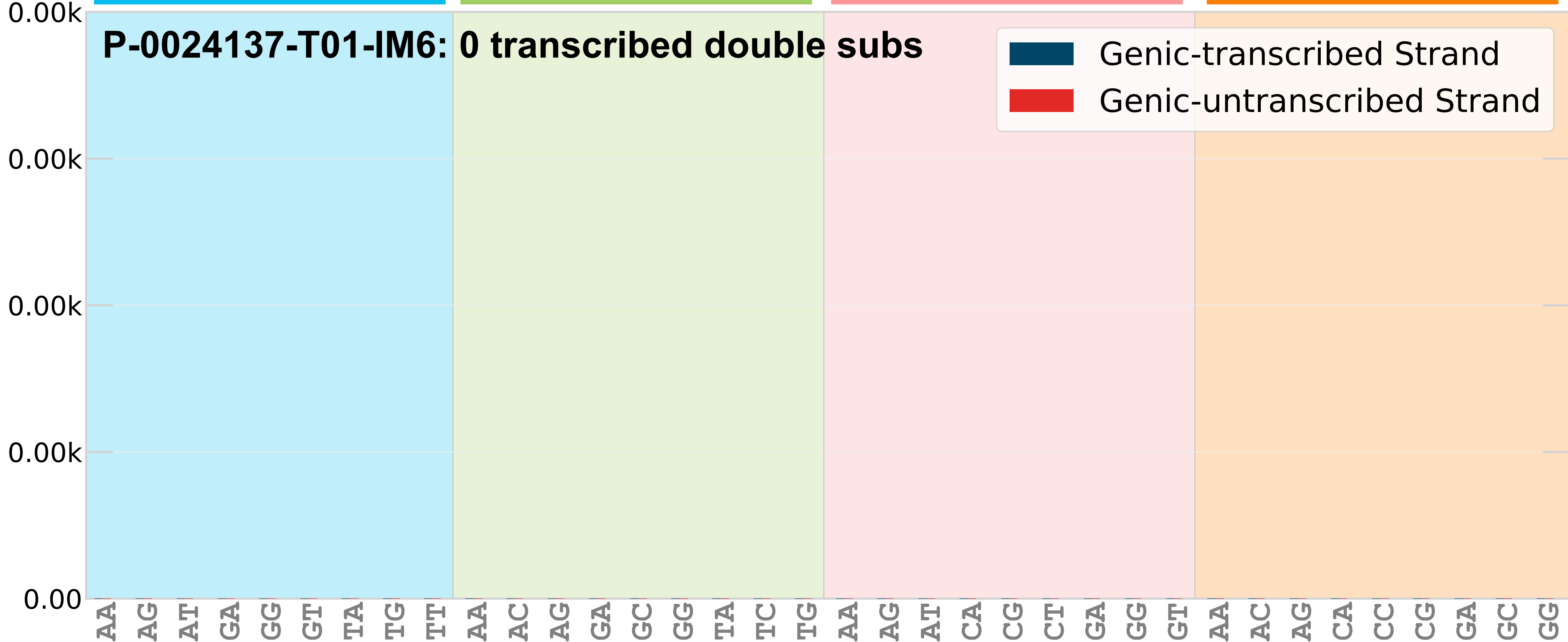




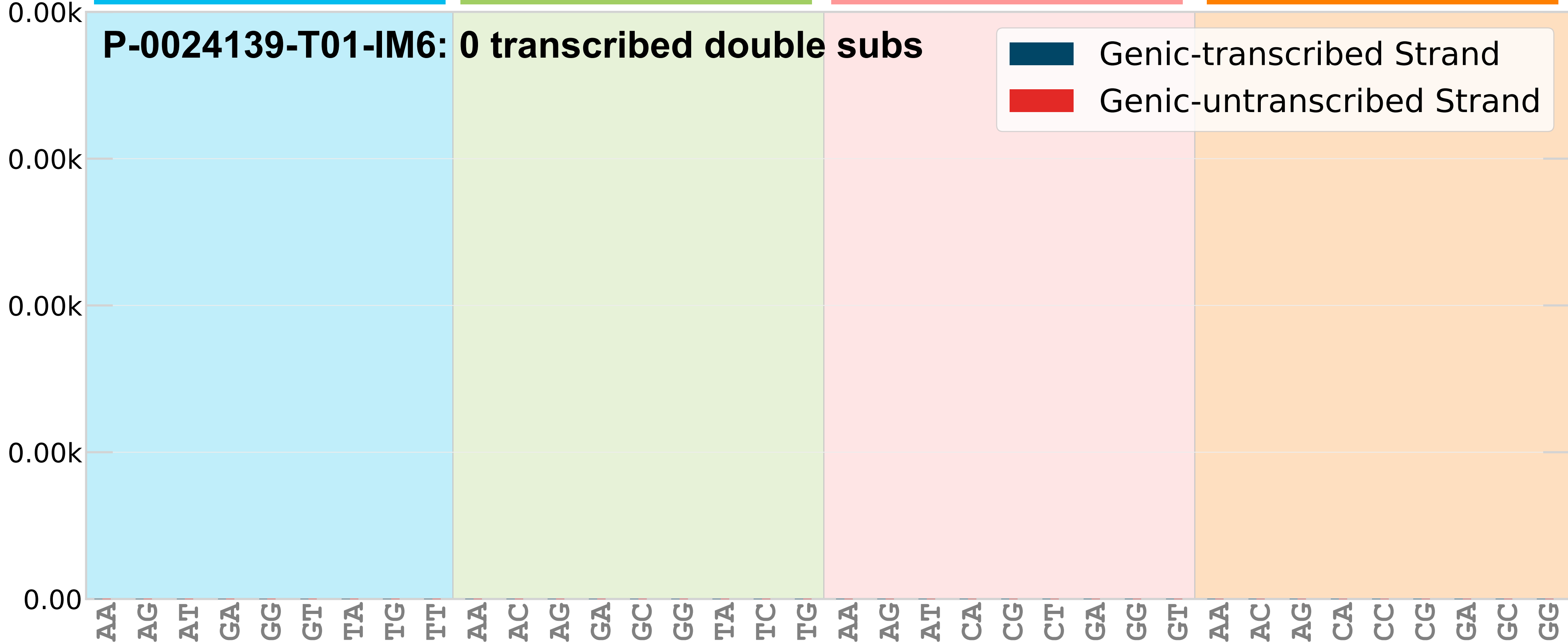


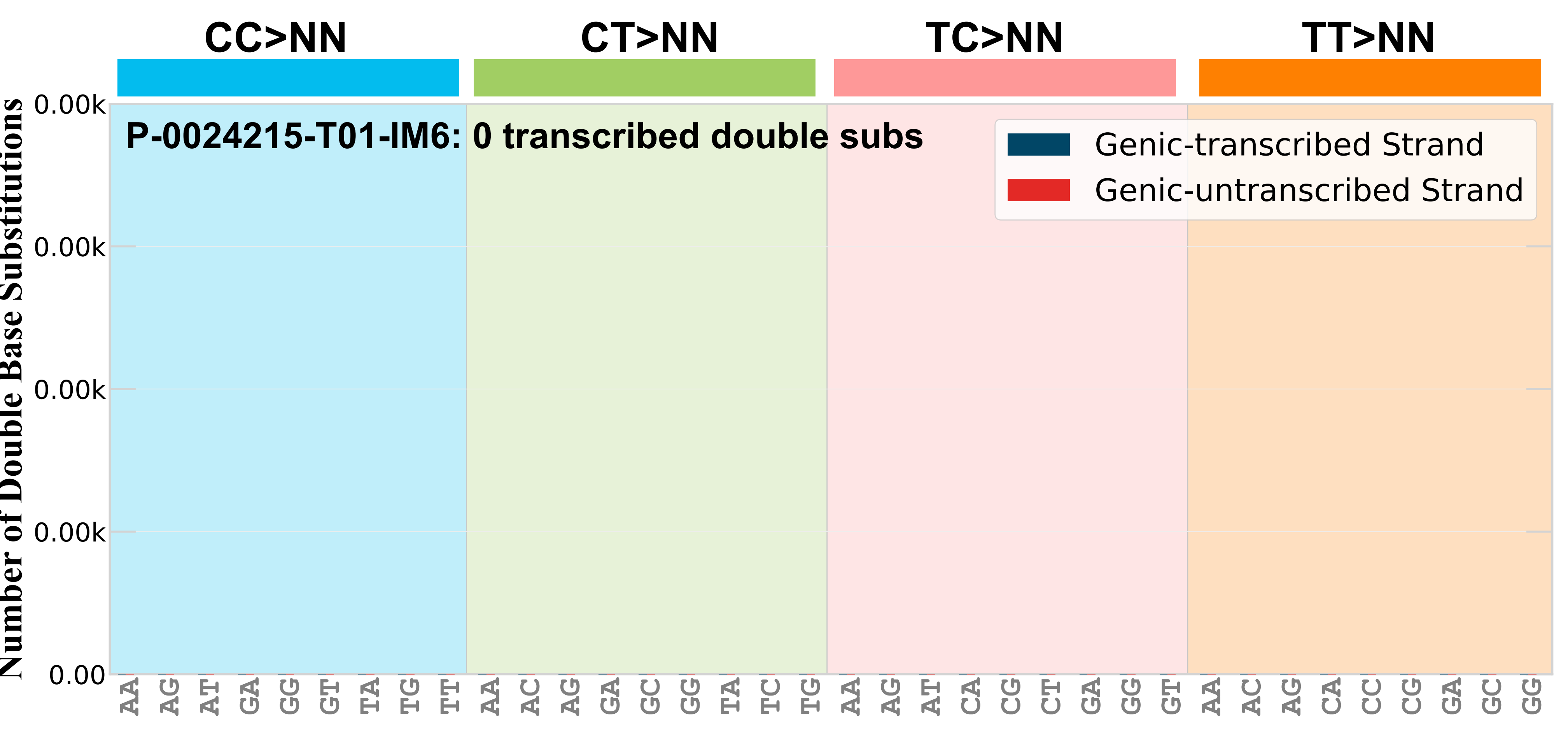


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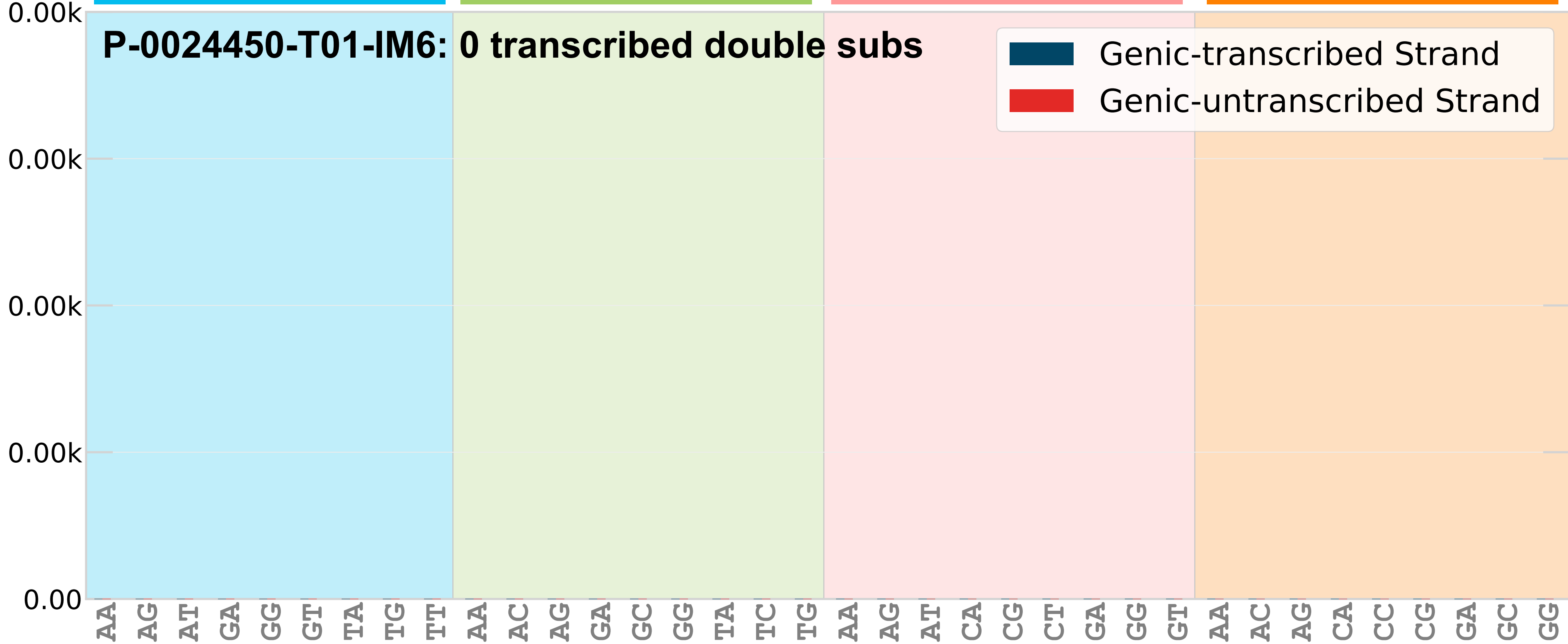


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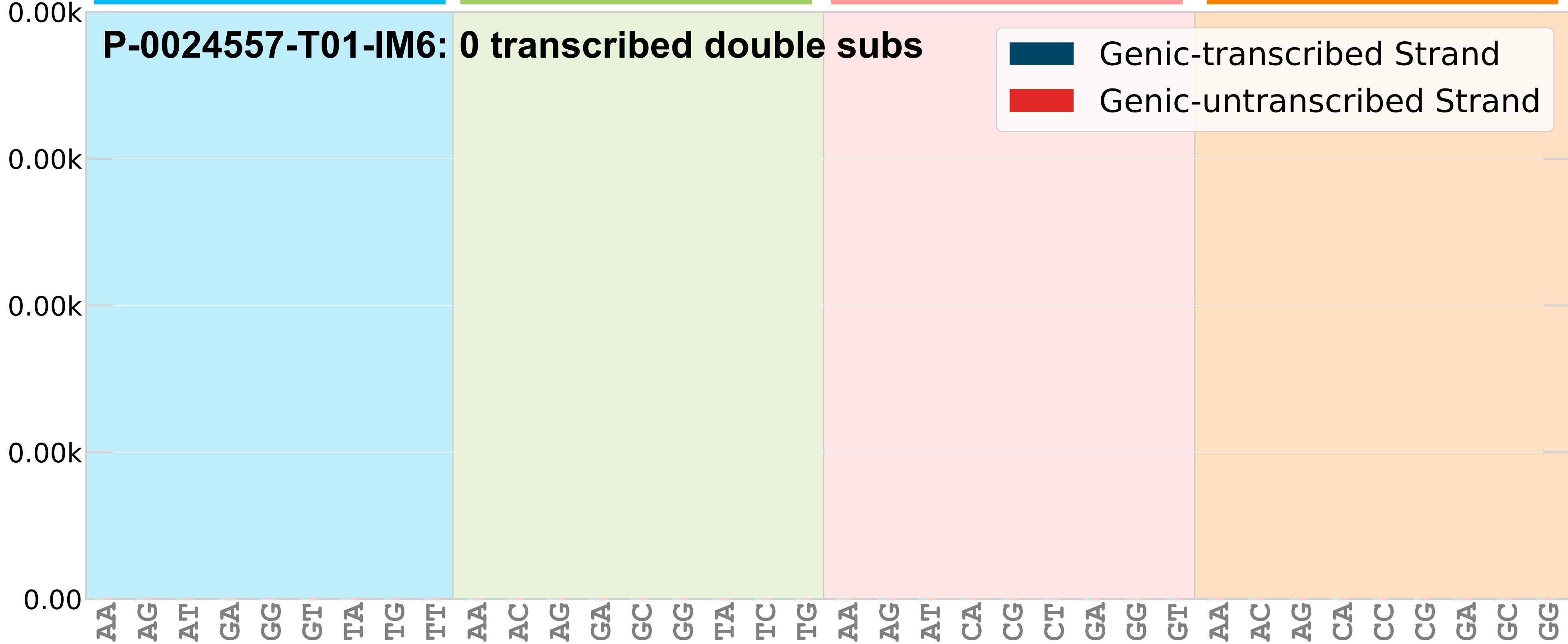


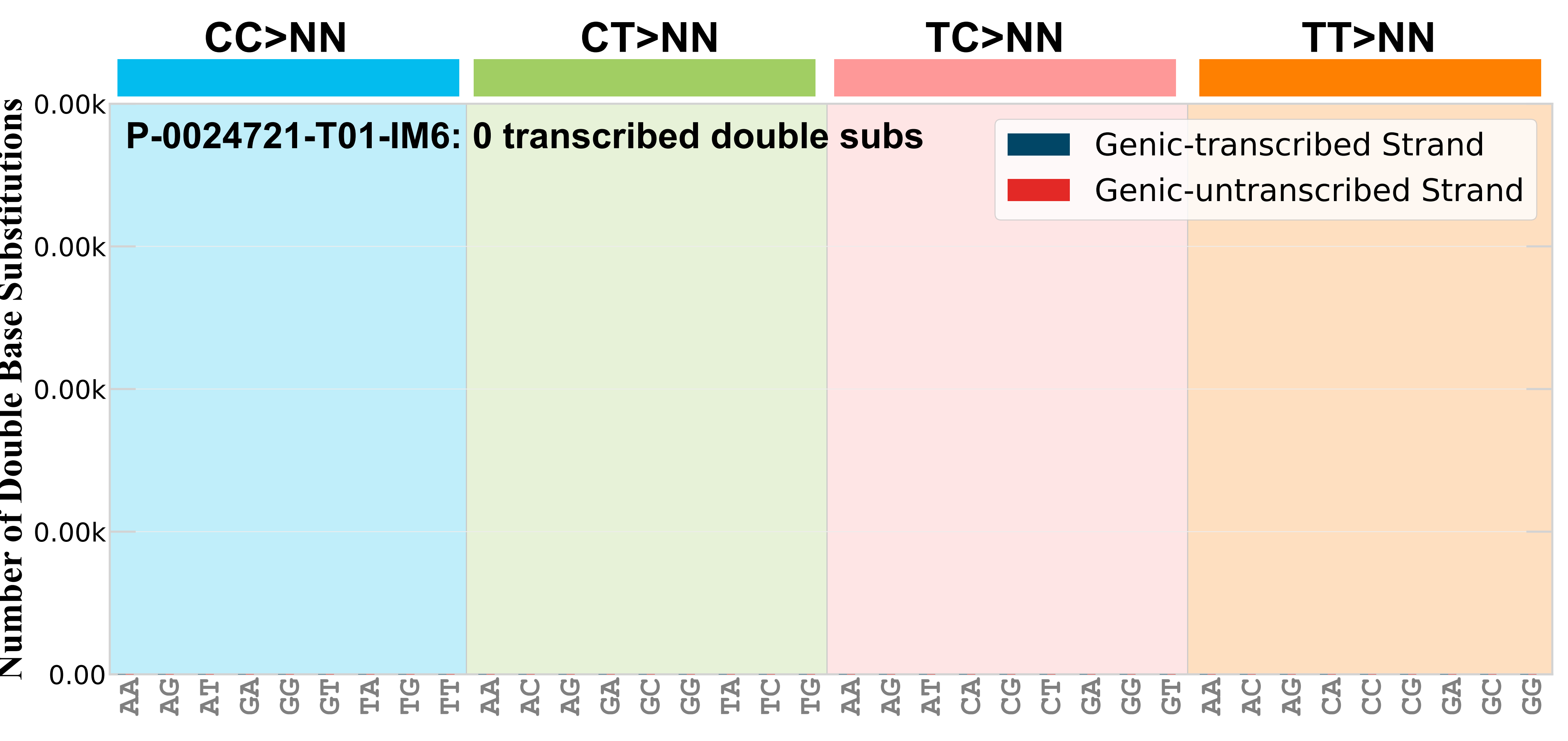


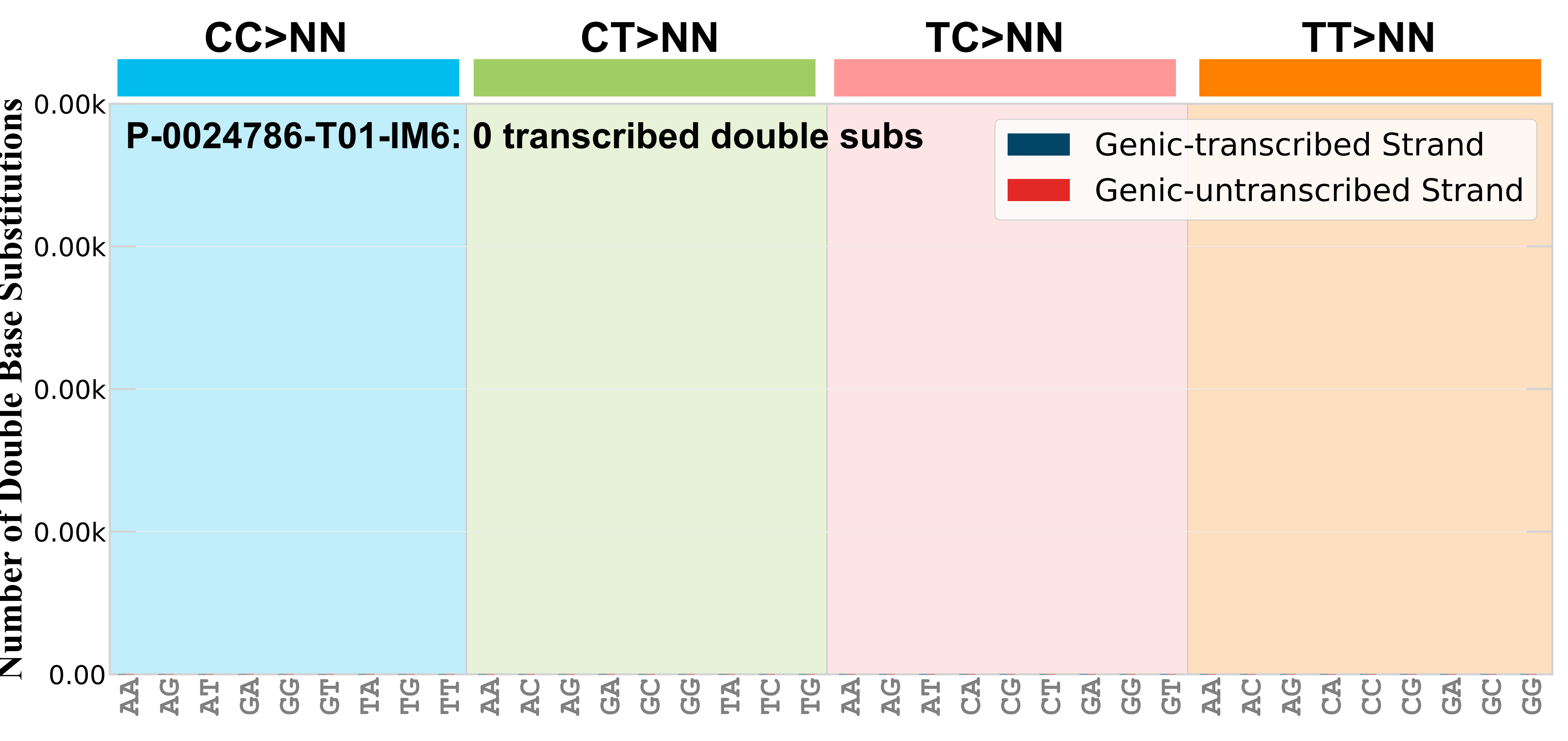
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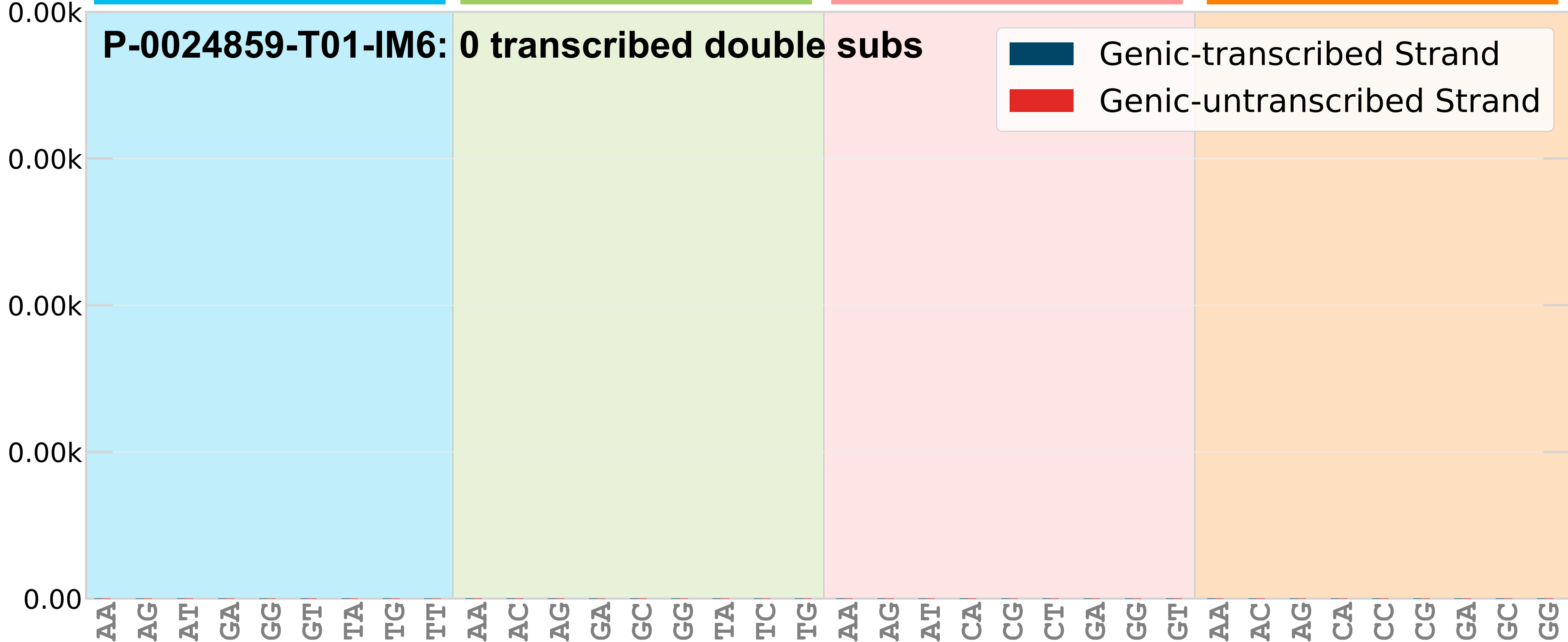
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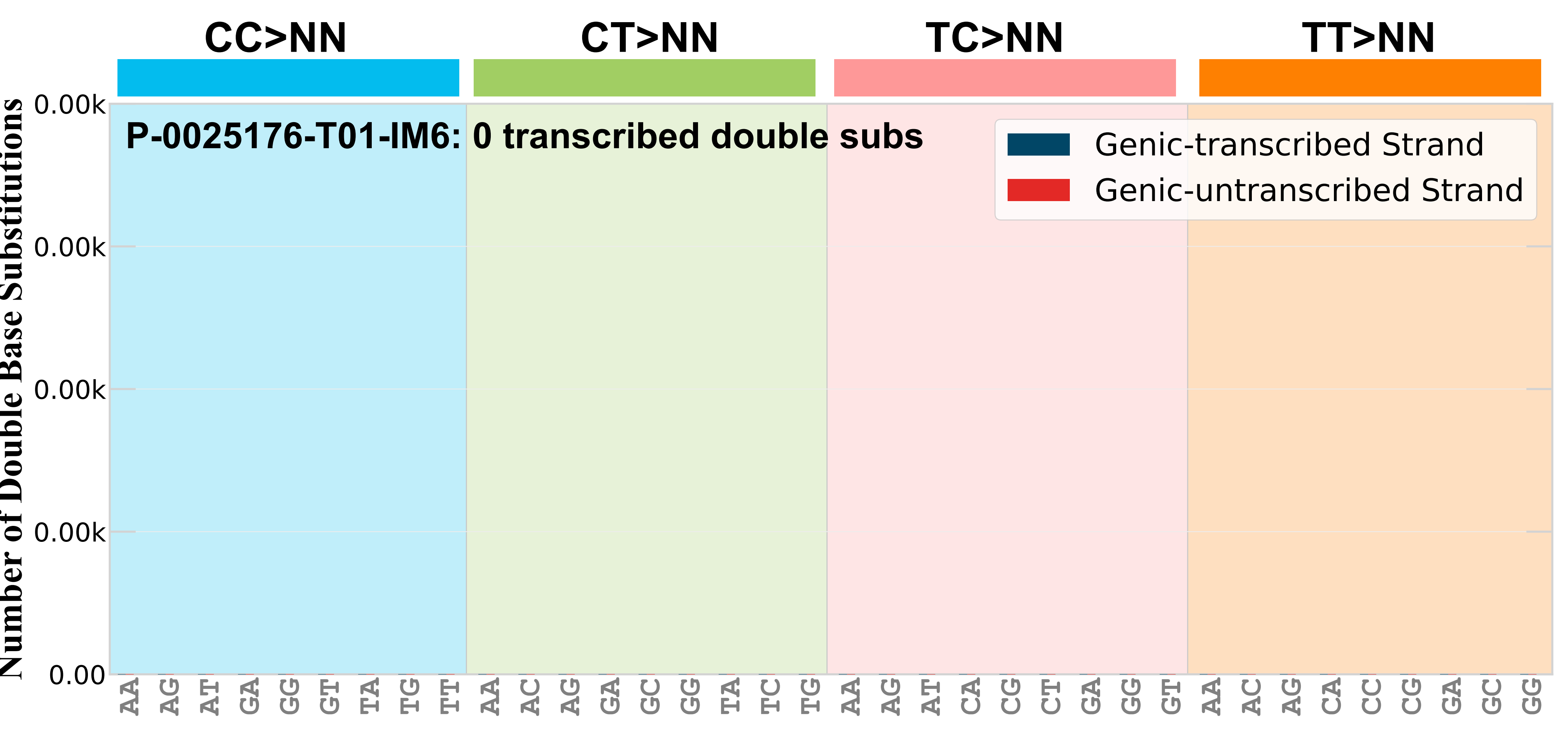


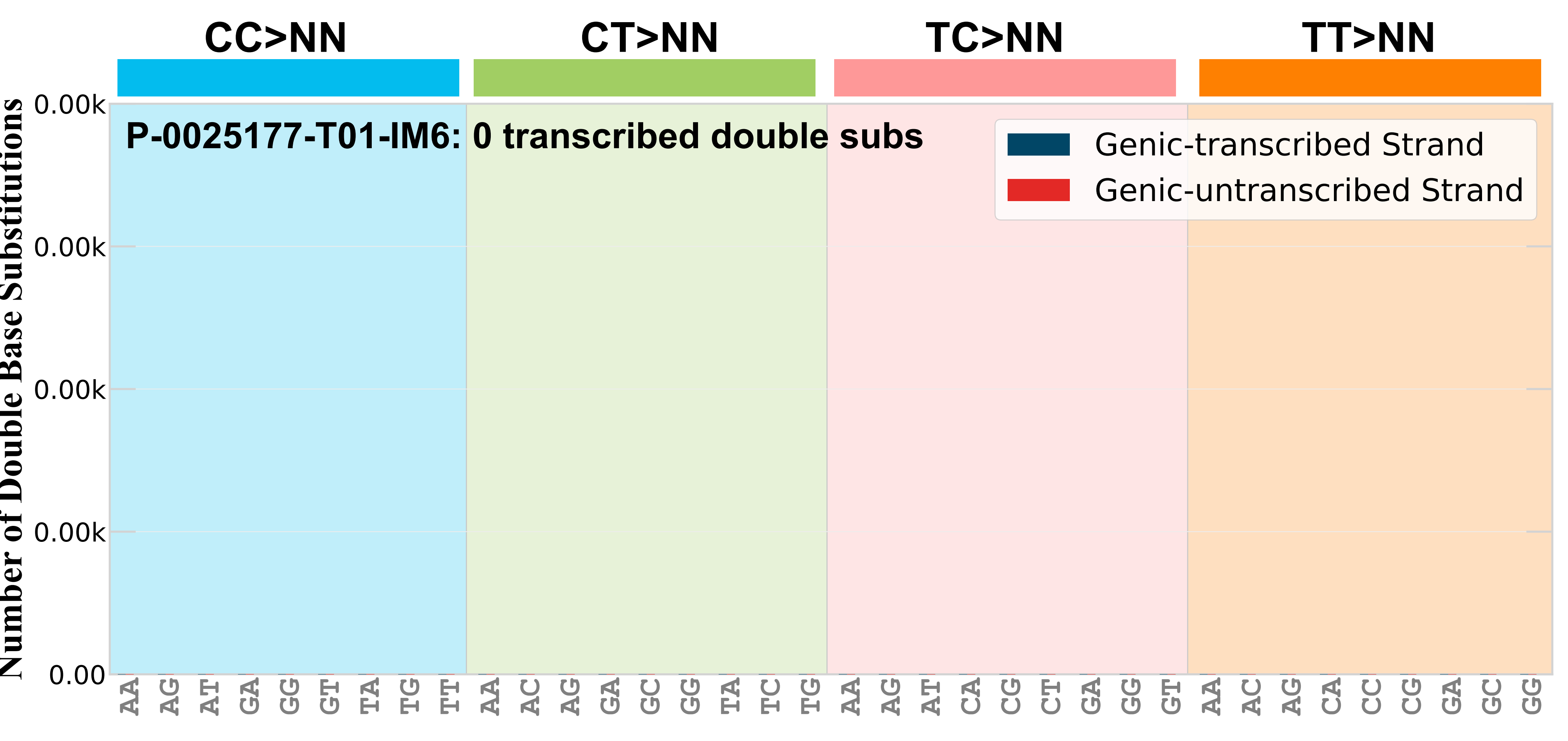




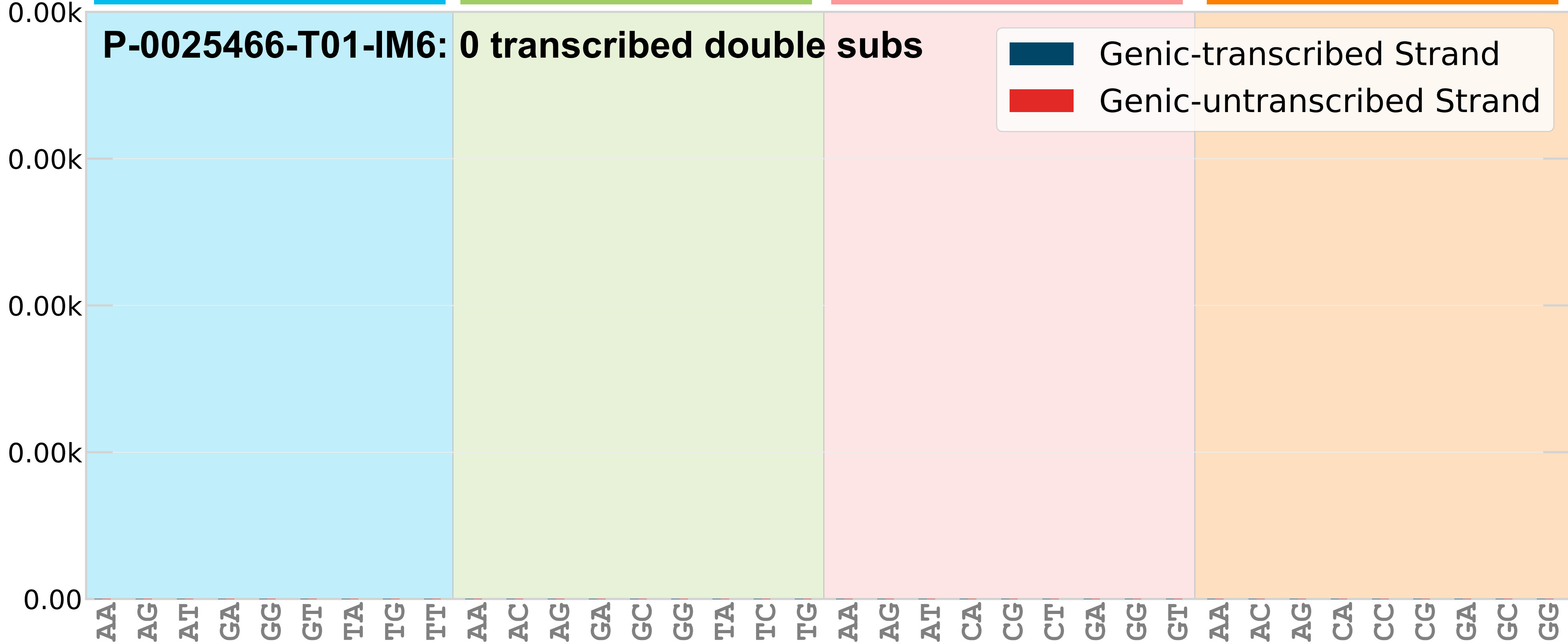
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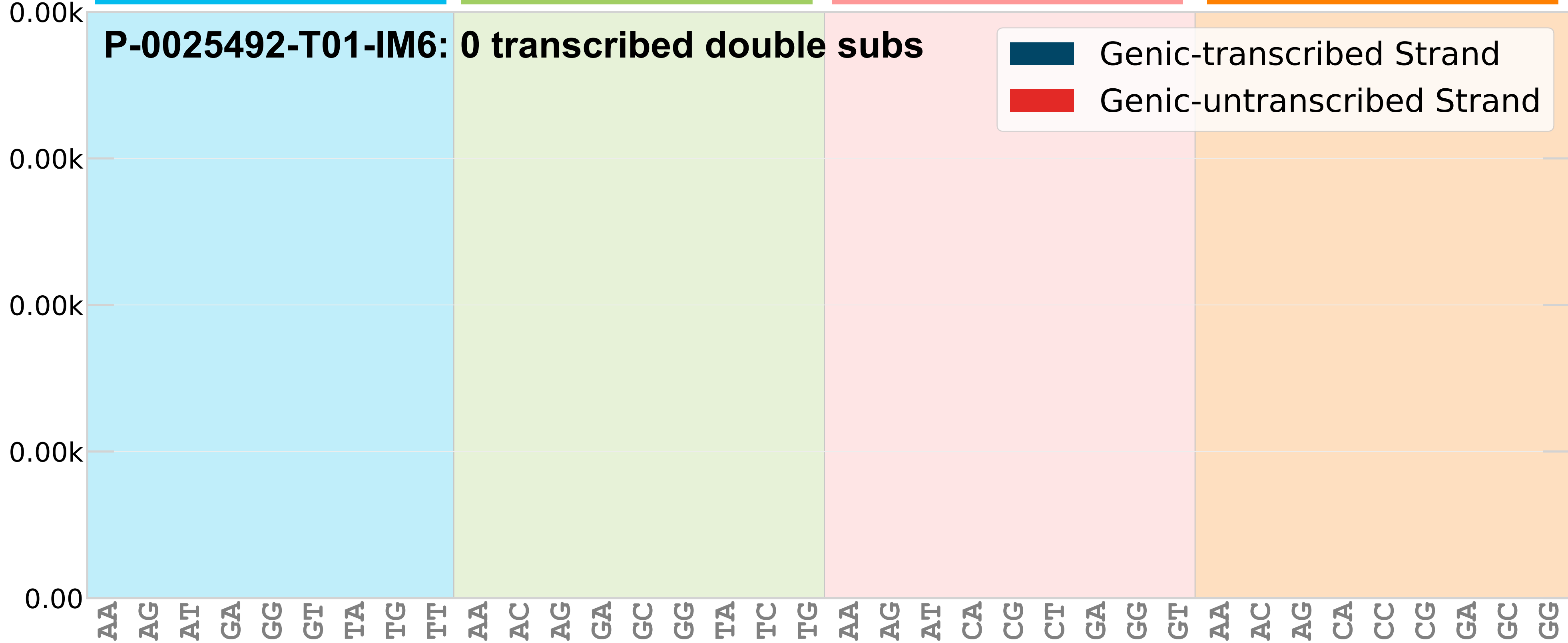


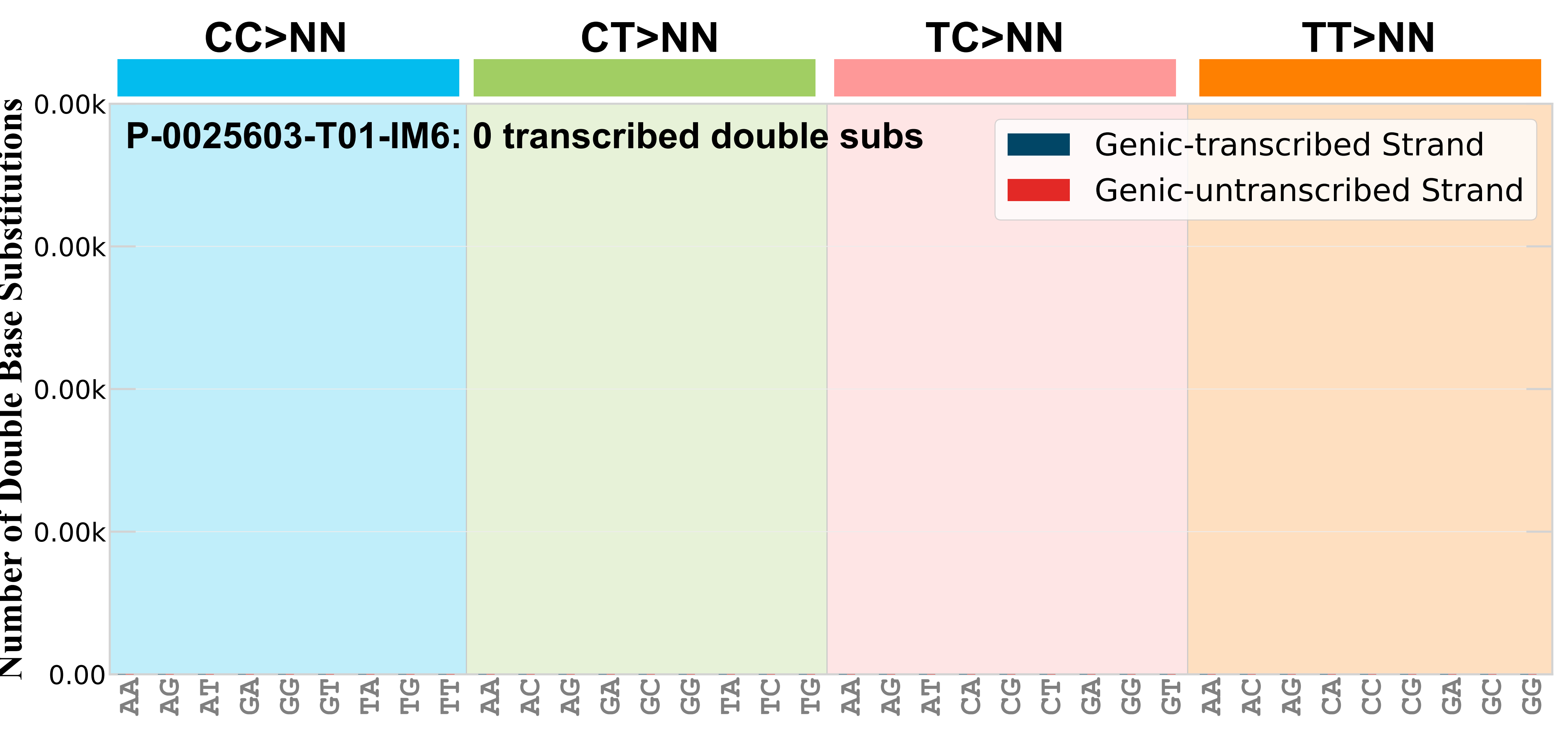


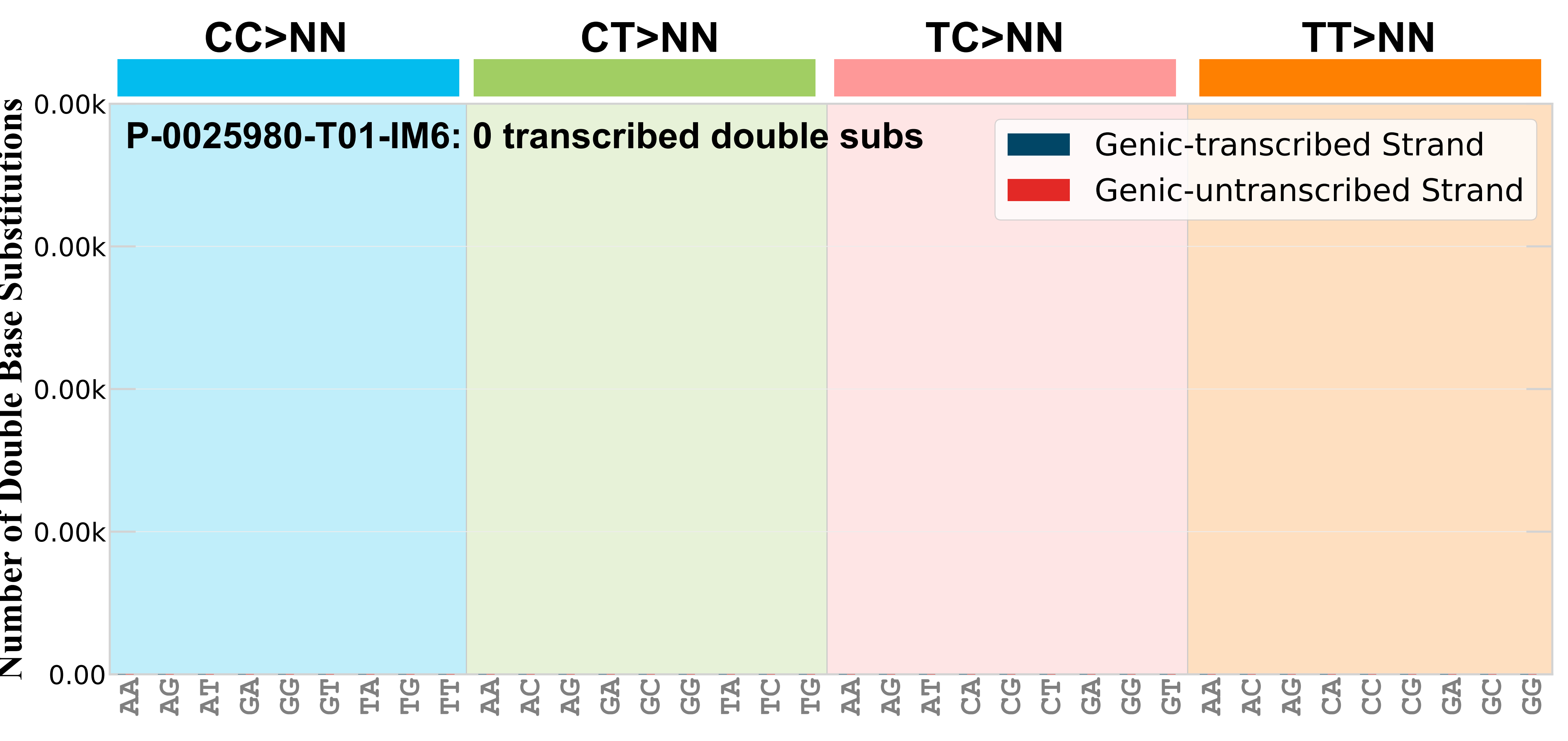
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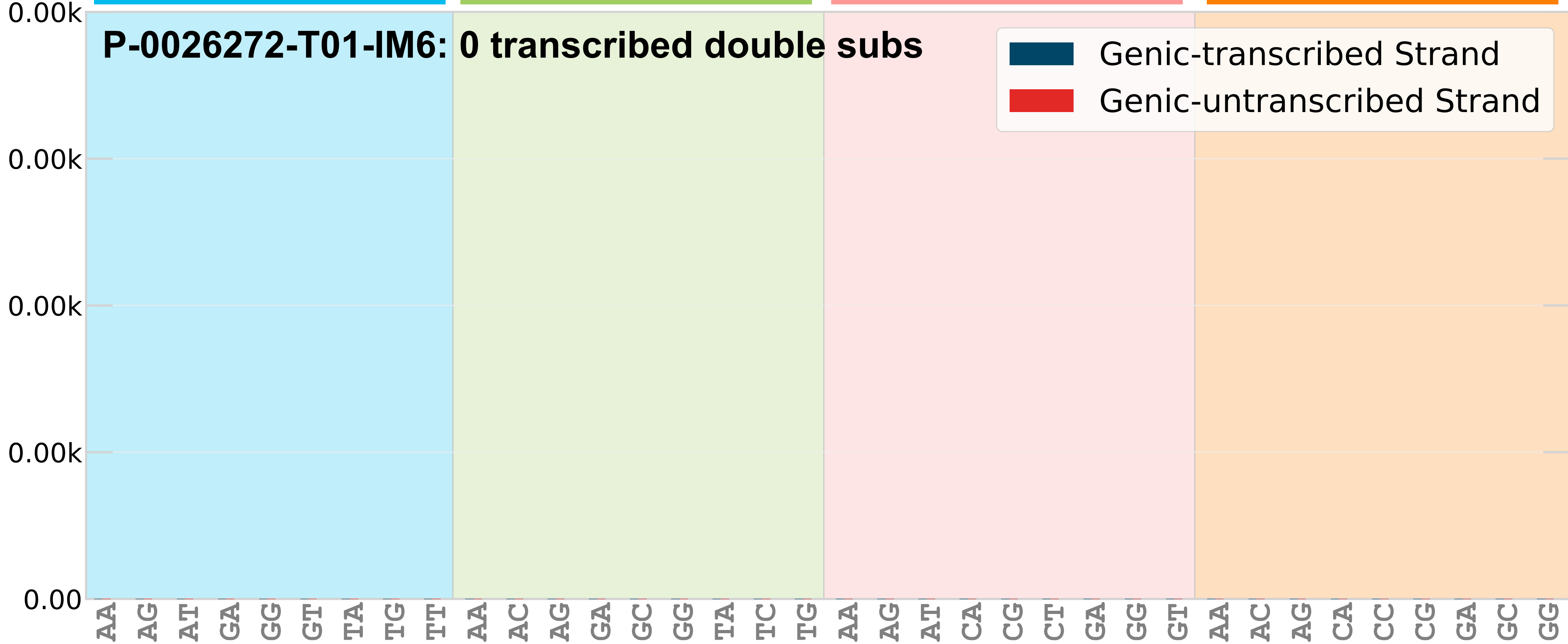
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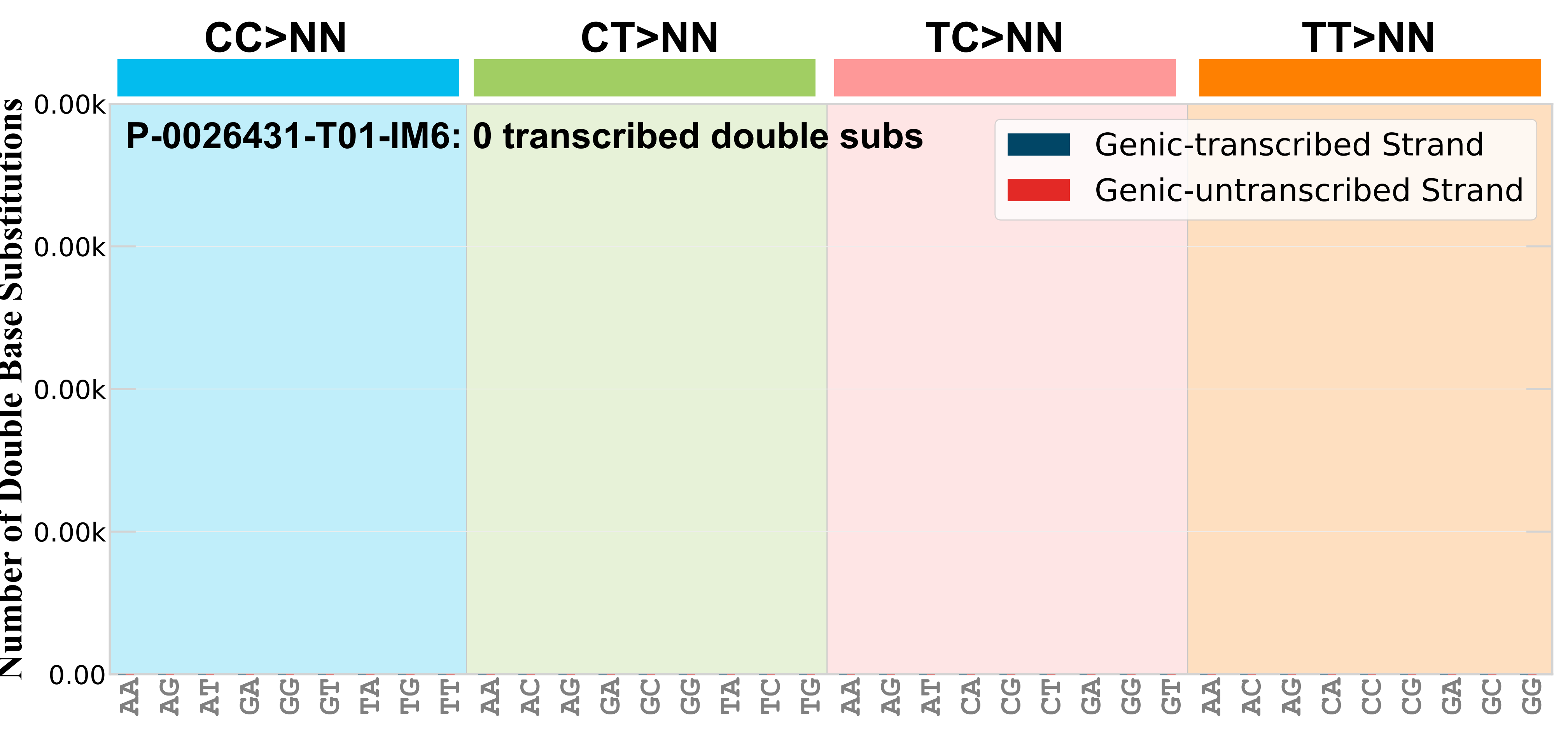




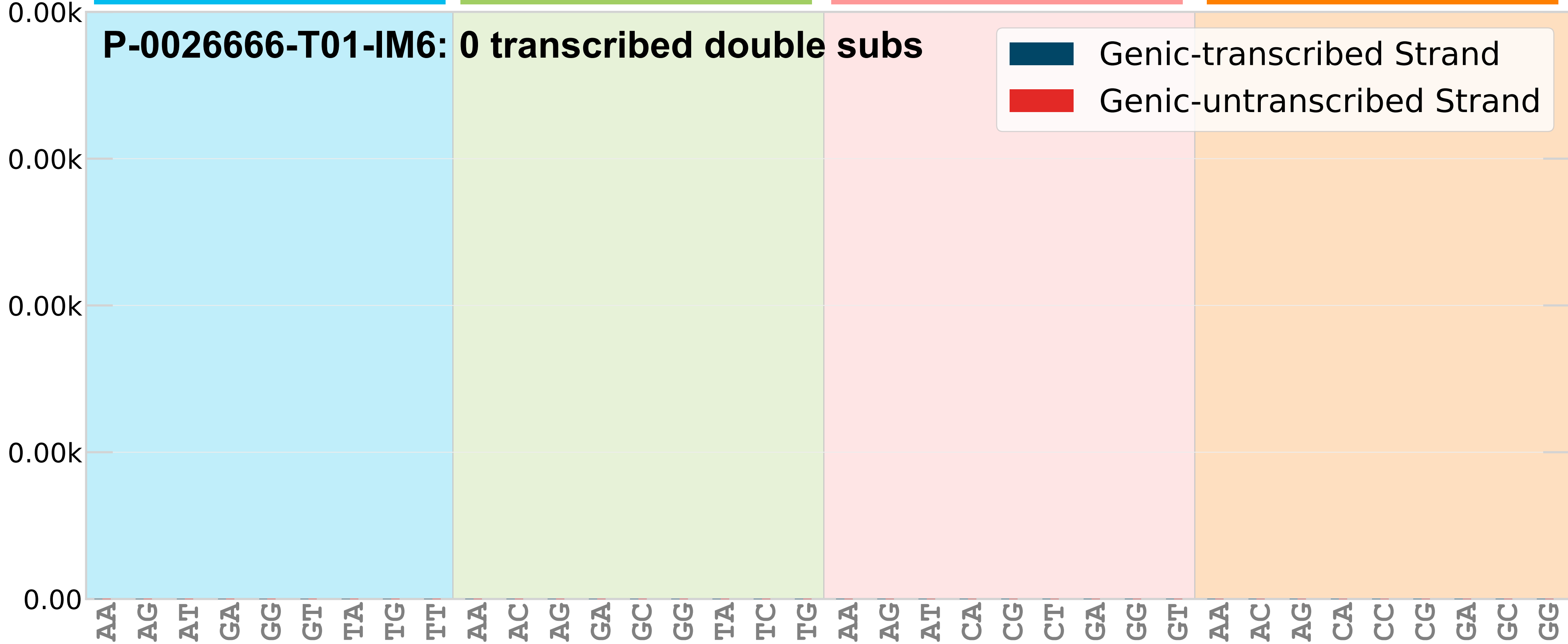


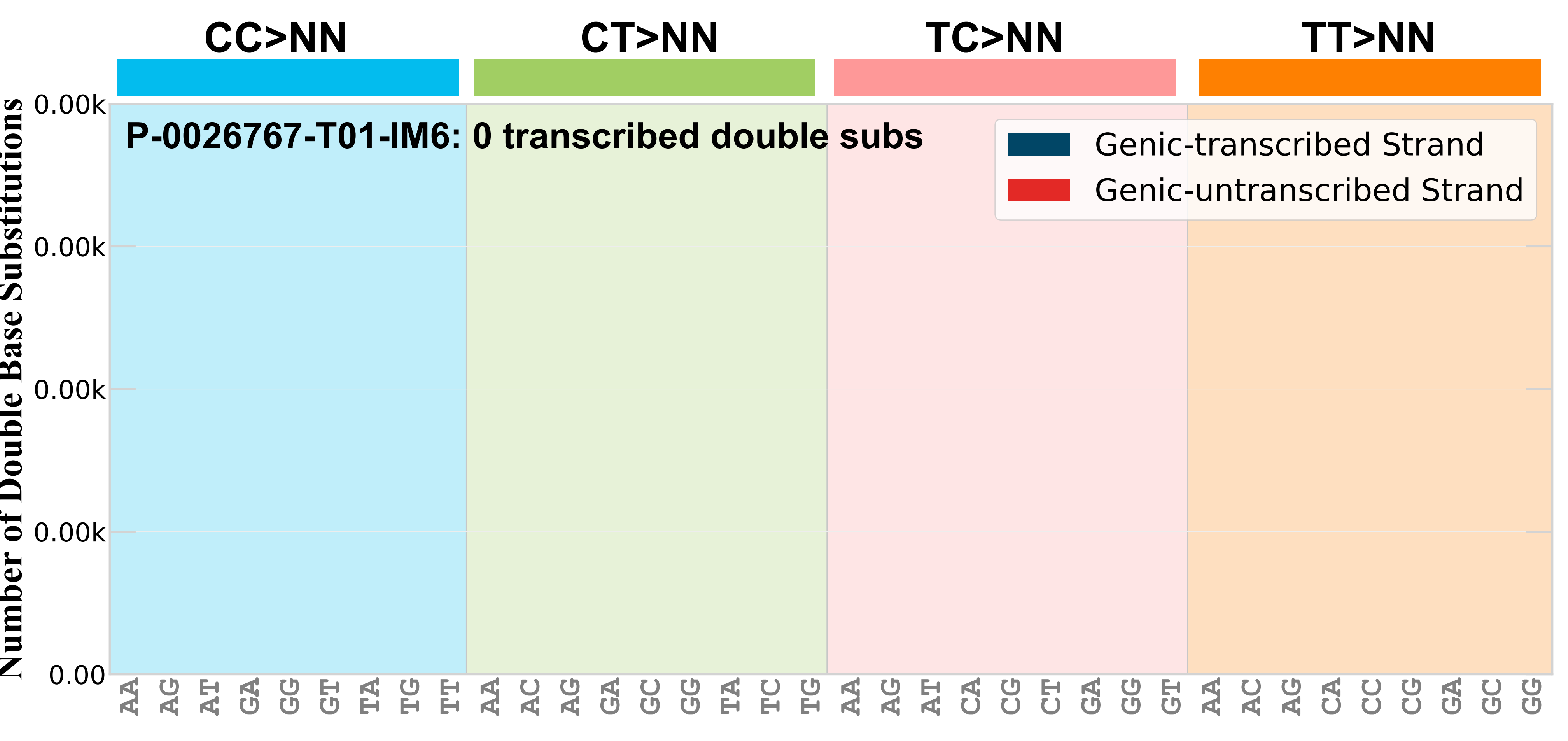
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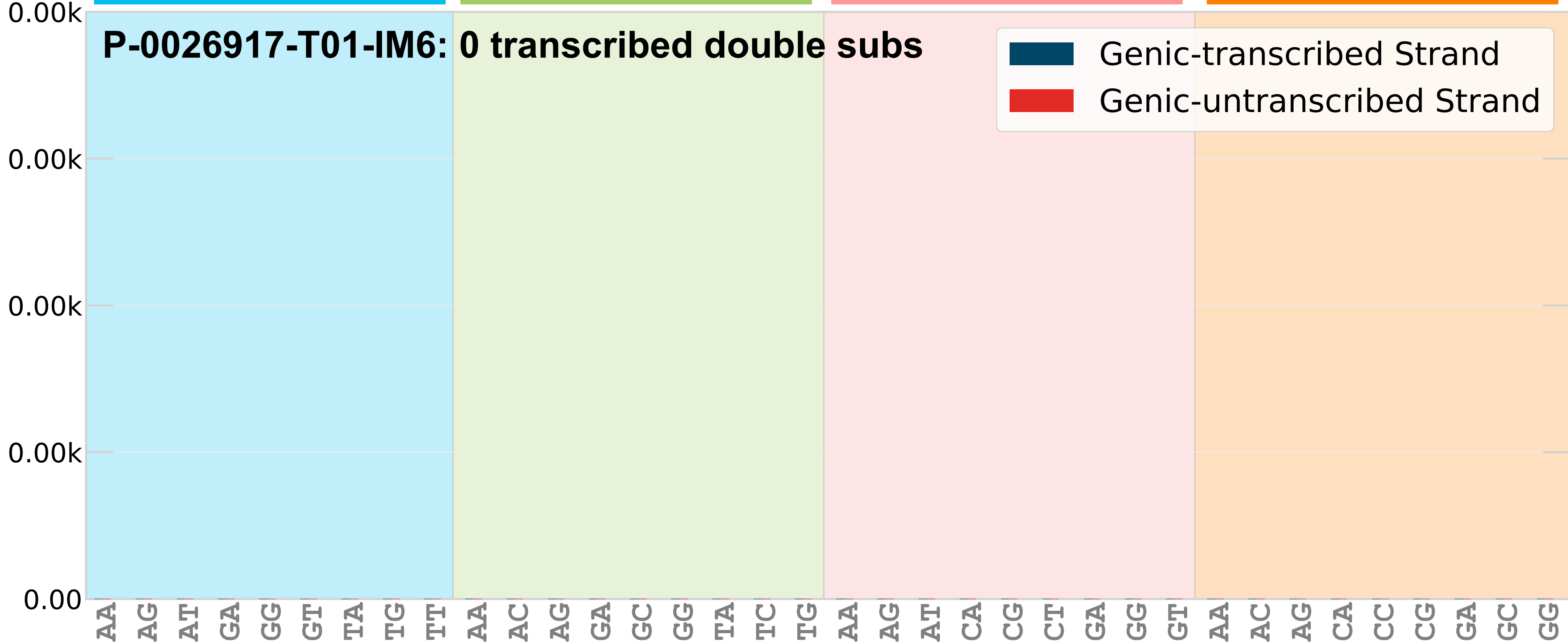


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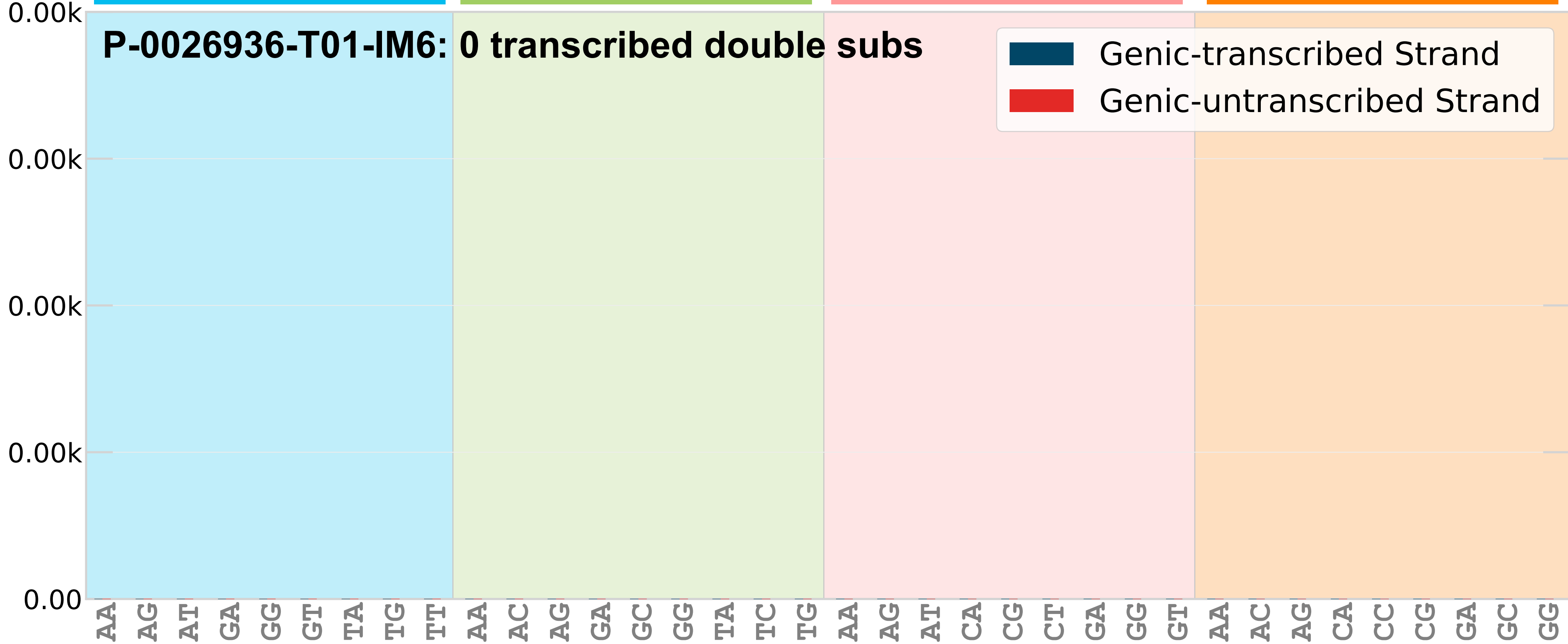


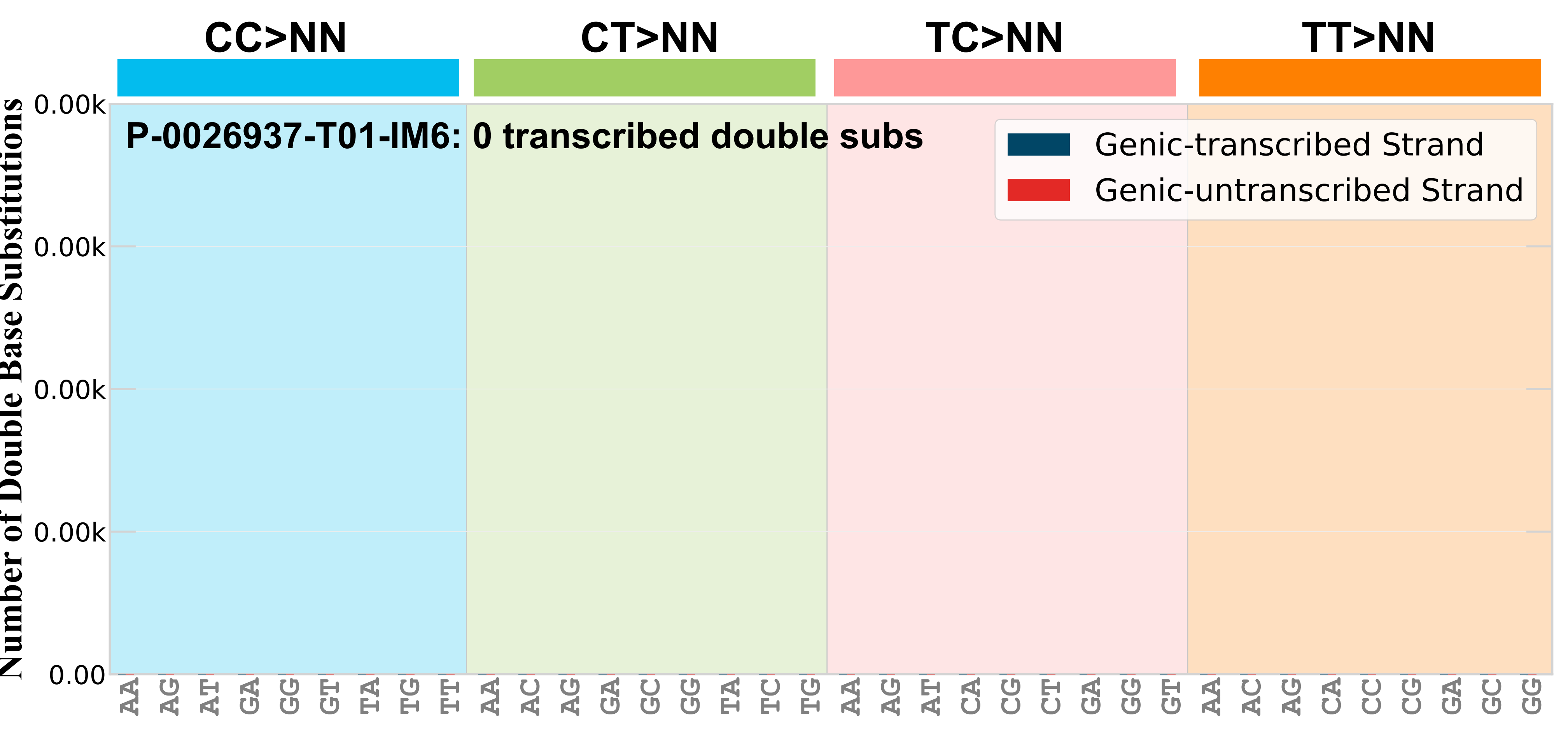


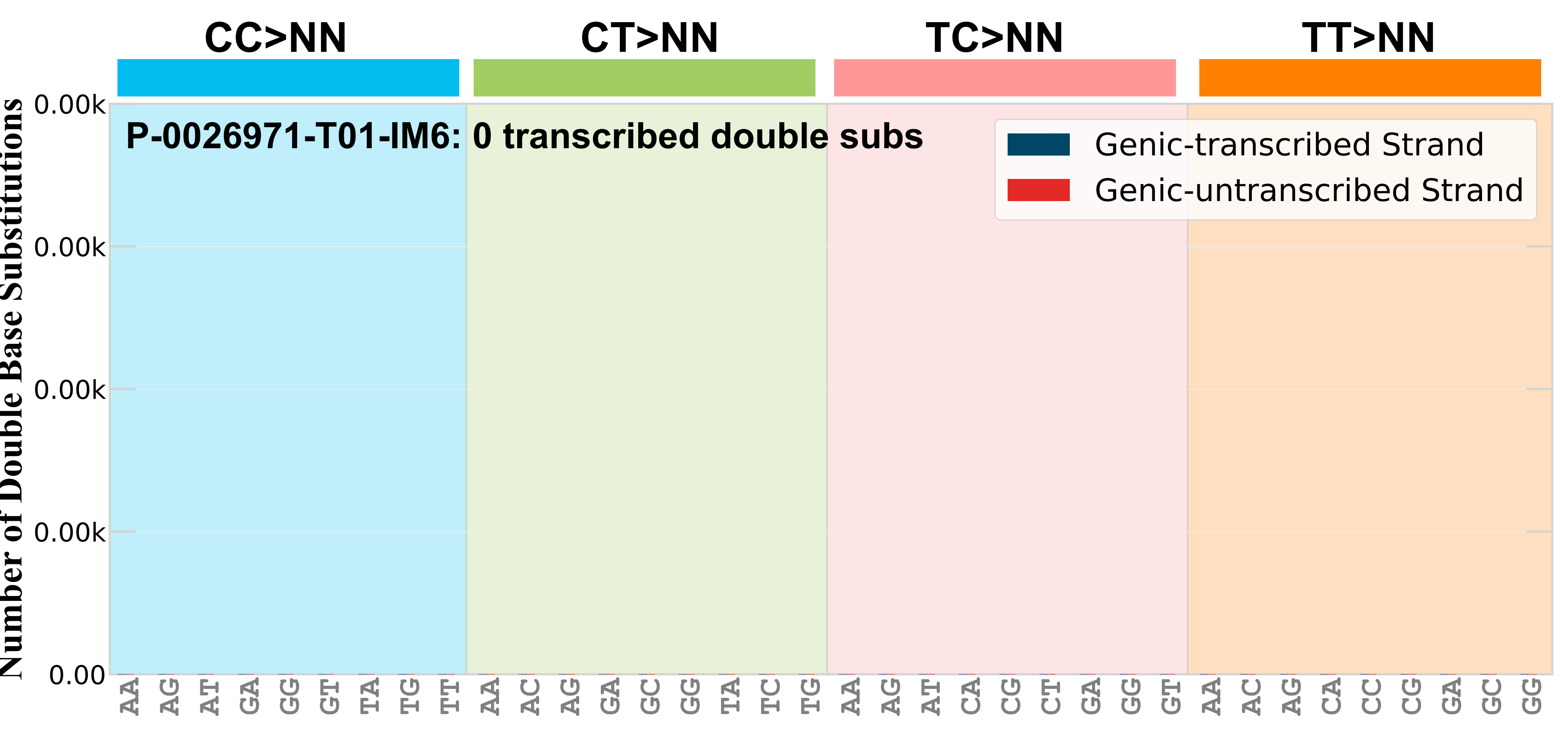
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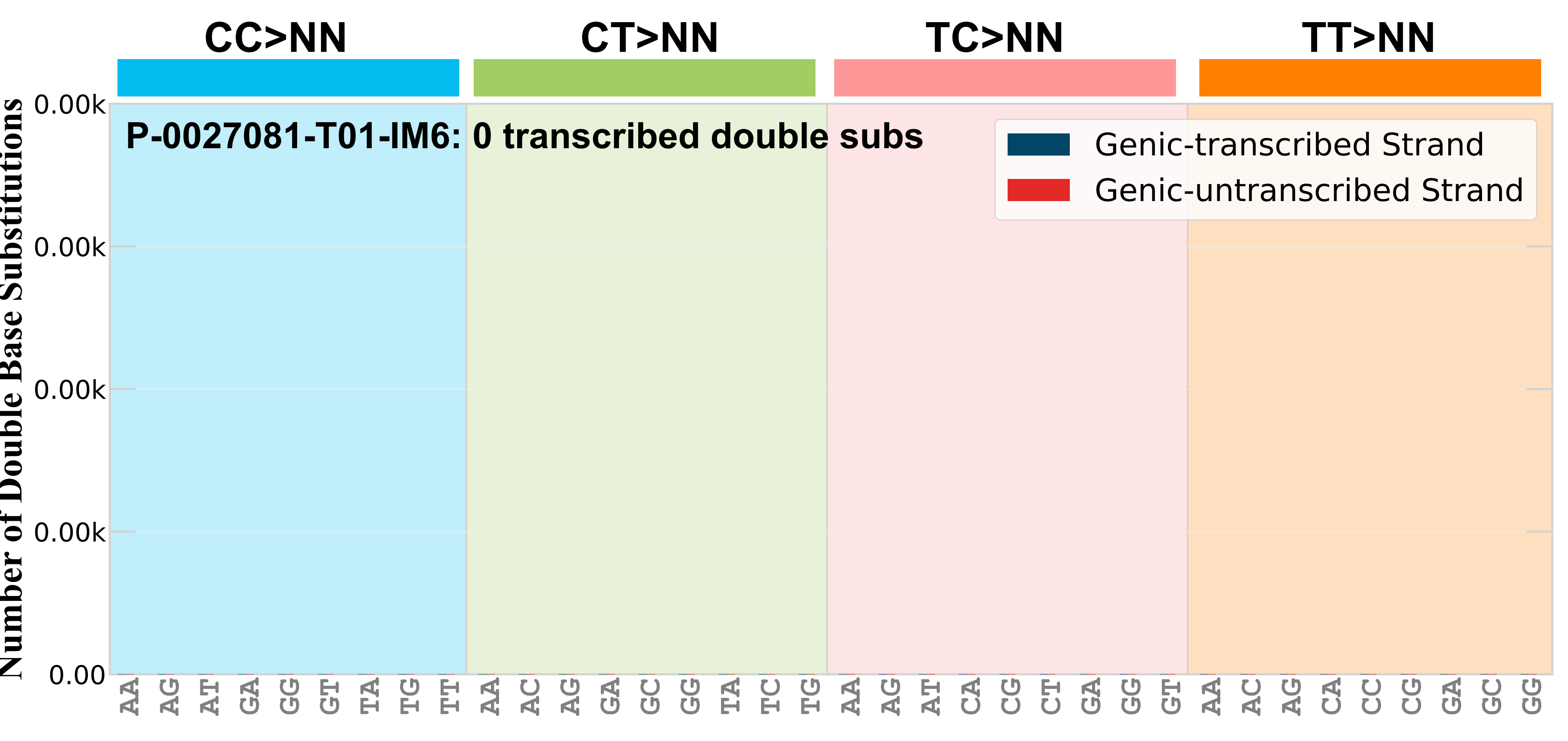


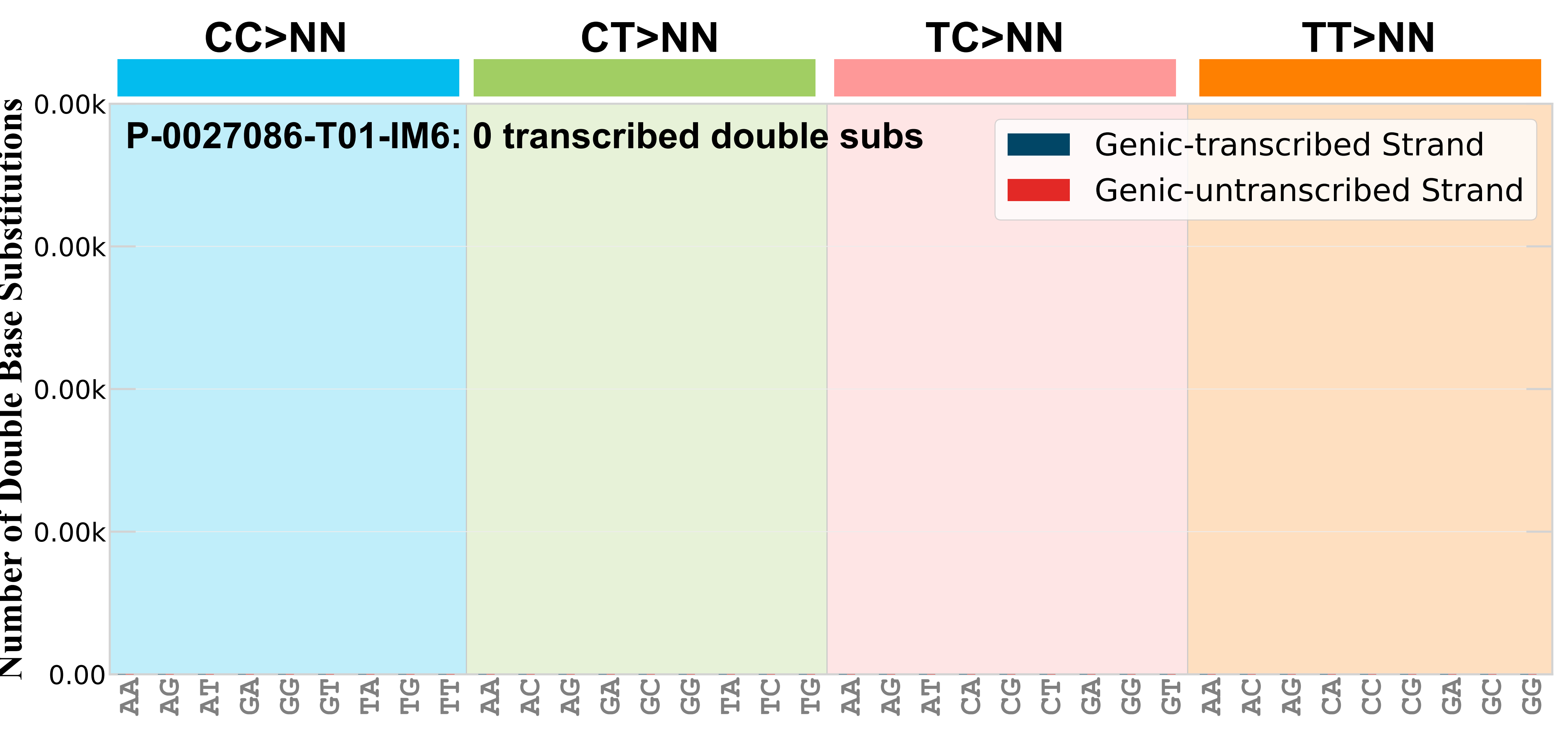
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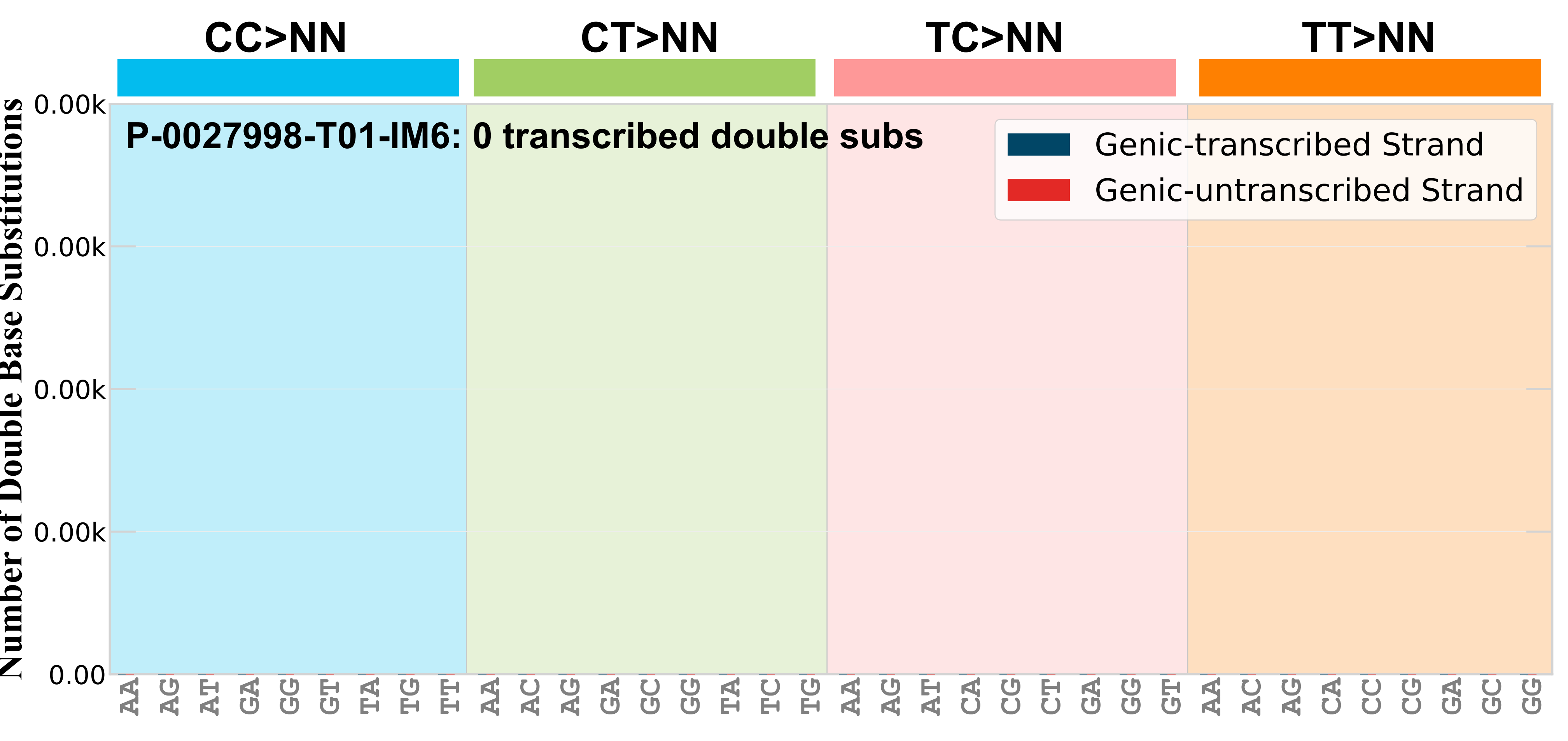


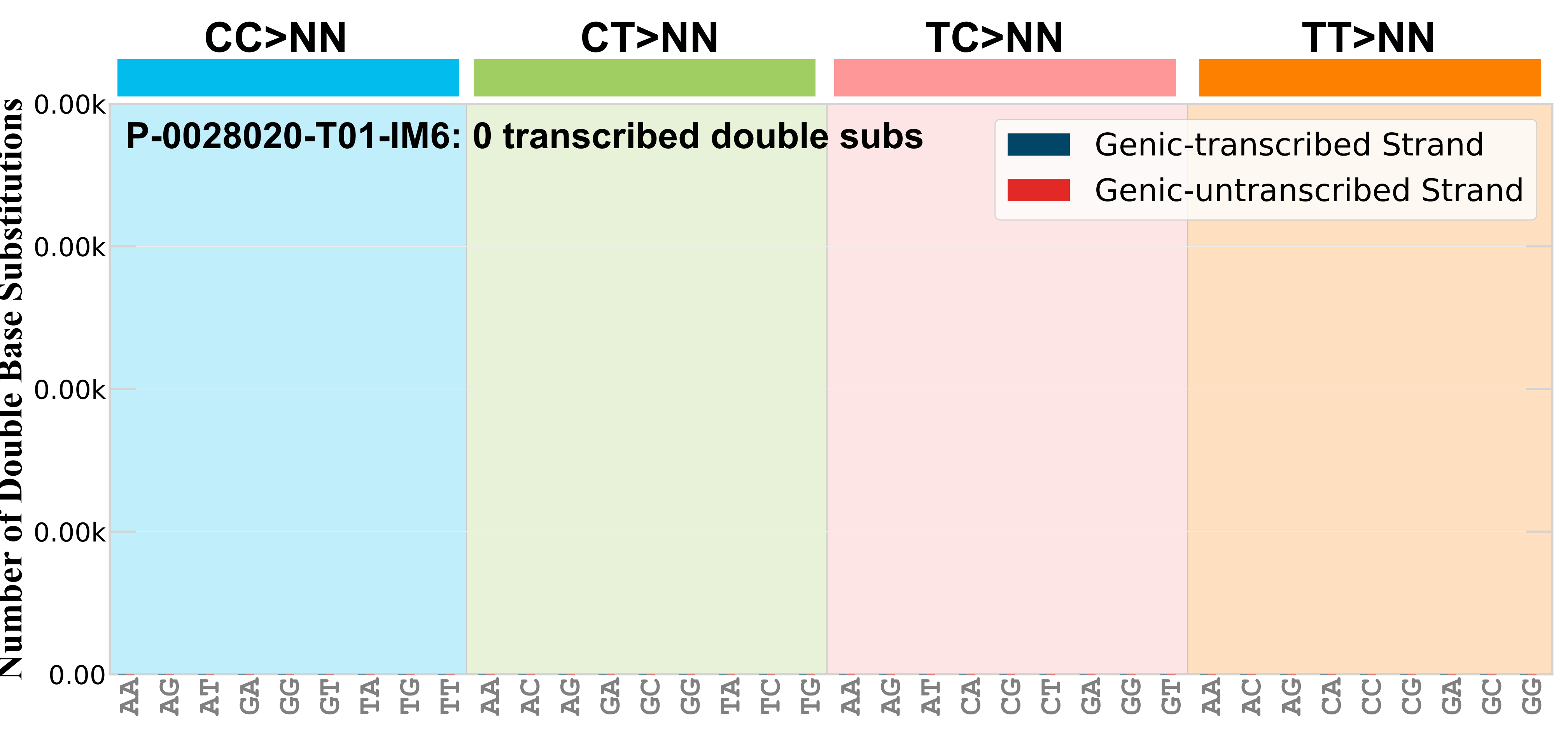




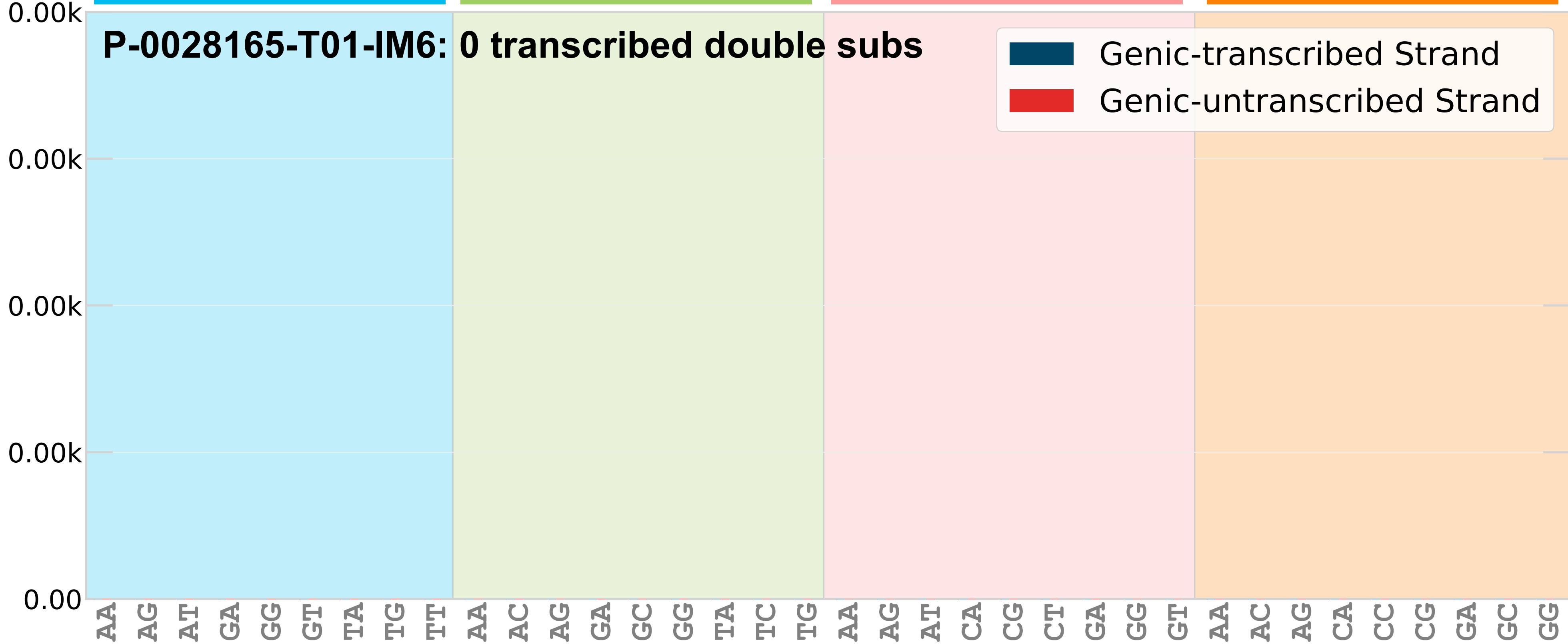


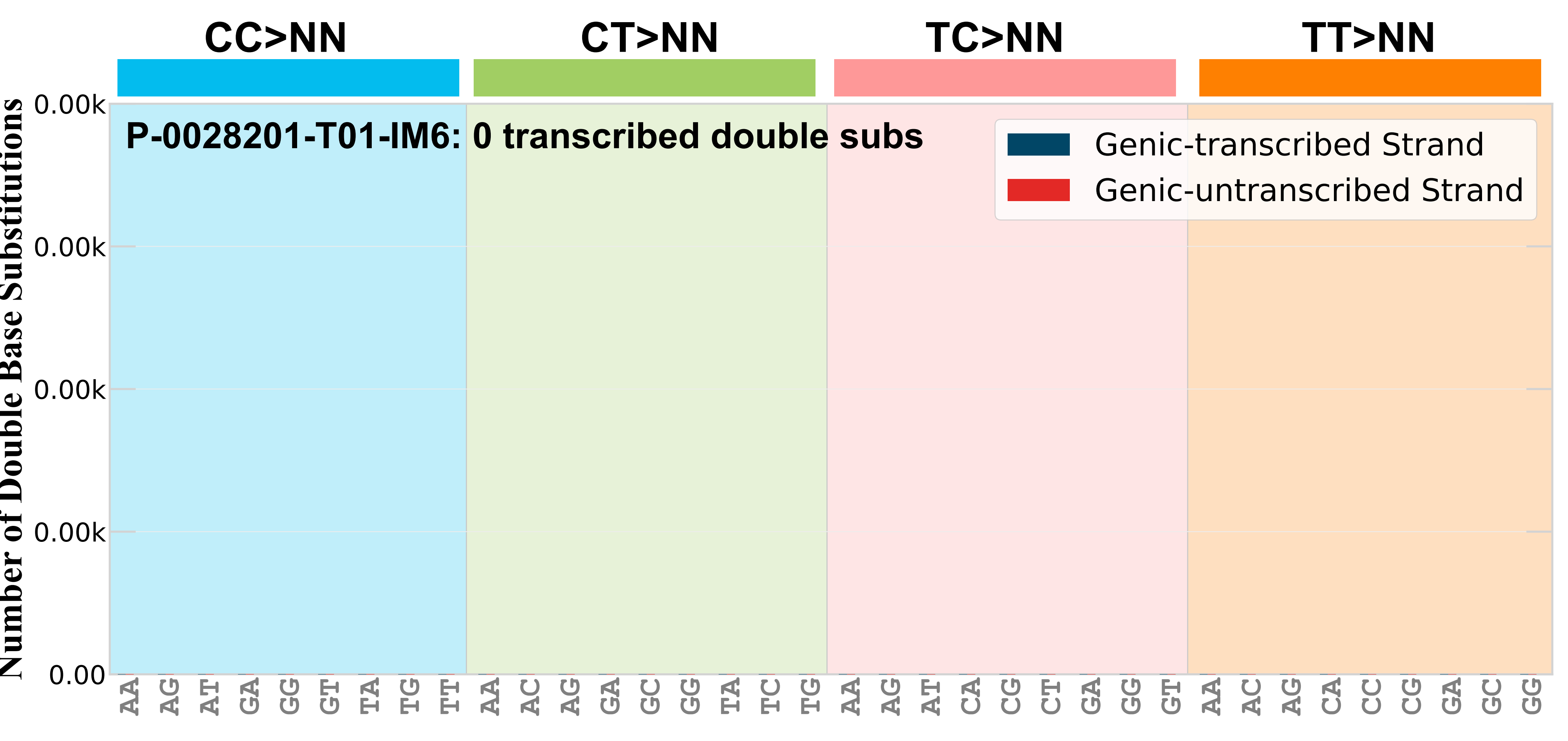




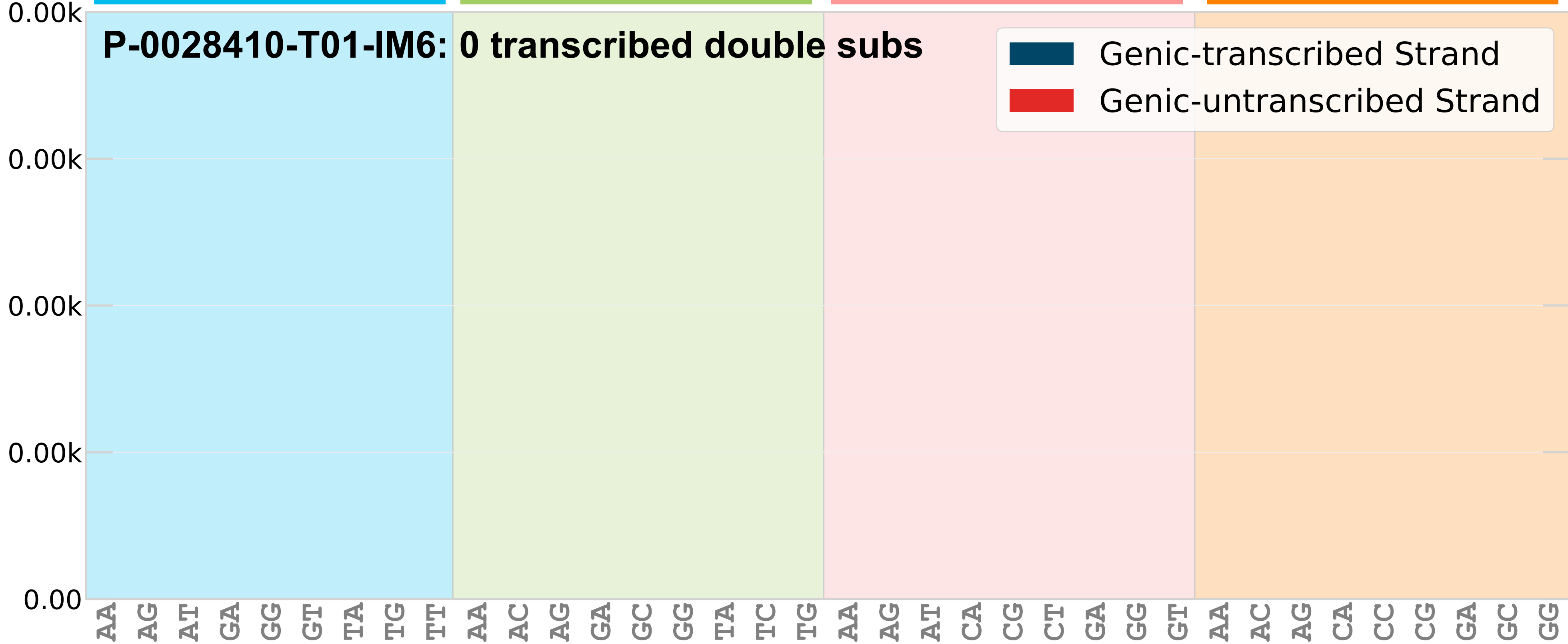


TT>NN





TT>NN



TT>NN

