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5'

3'

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85

CLN5 >

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170

CLN5 >

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255

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340

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425

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510

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1190

CLN5

Sanger Sequencing

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PCR Forward

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CLN5

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1445

CLN5

CLN5-201

1
M A
ENSE0...
CLN5-201

gRNA Protospacer

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Donor Template WT -> SNV

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1530

CLN5

CLN5-201

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ENSE0003712901

CLN5-201

Donor Template WT -> SNV

Protospacer Sequence

PAM

SNV

Donor Template WT -> SNV

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1615

CLN5

CLN5-201

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ENSE0003712901

CLN5-201

Donor Template WT -> SNV

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1700

CLN5

CLN5-201

CLN5-201

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1785

CLN5

CLN5-201

CLN5-201

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1870

CLN5

CLN5-201

CLN5-201

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1955

FBXL3

CLN5

CLN5-201

CLN5-201

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2040

FBXL3

CLN5

CLN5-201

CLN5-201

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FBXL3

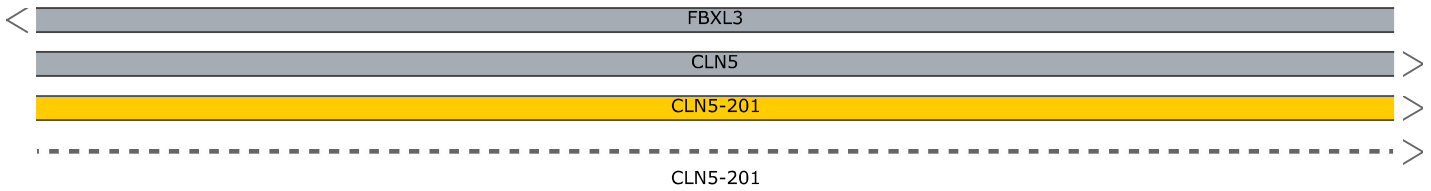
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CLN5-201

CLN5-201

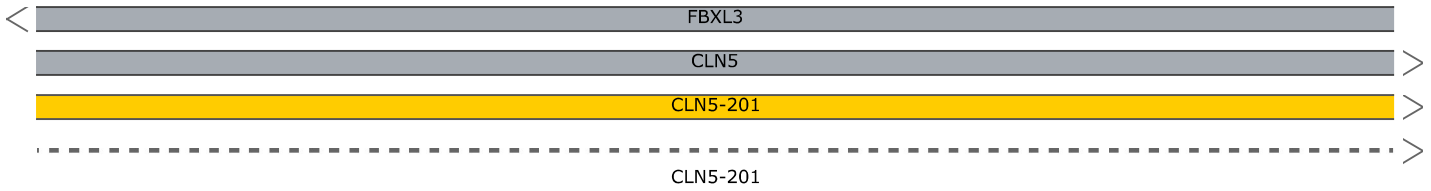
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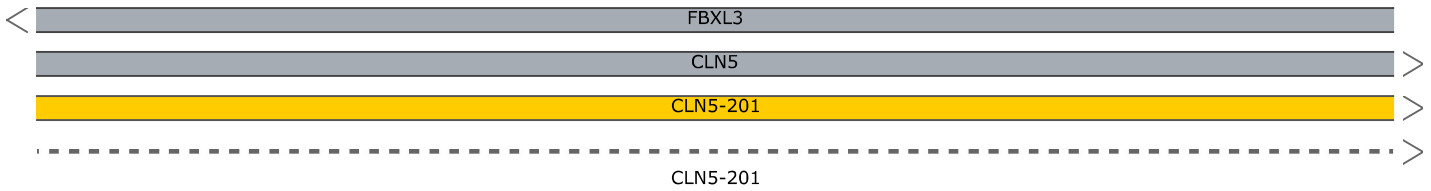
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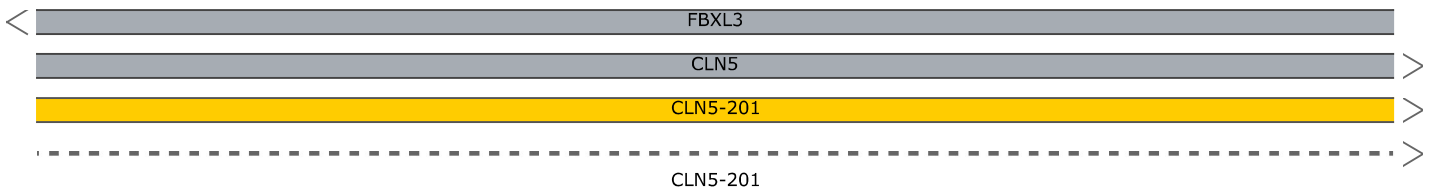
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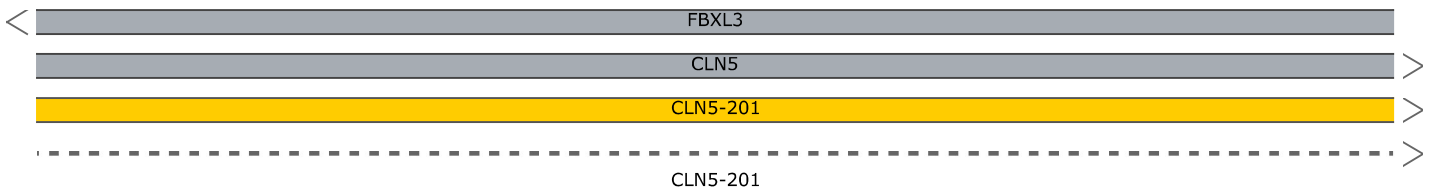
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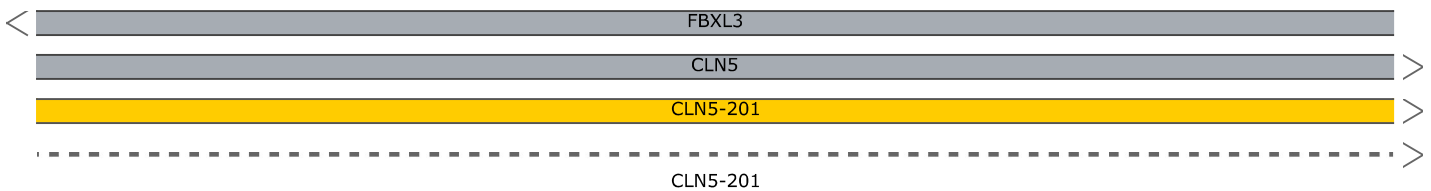
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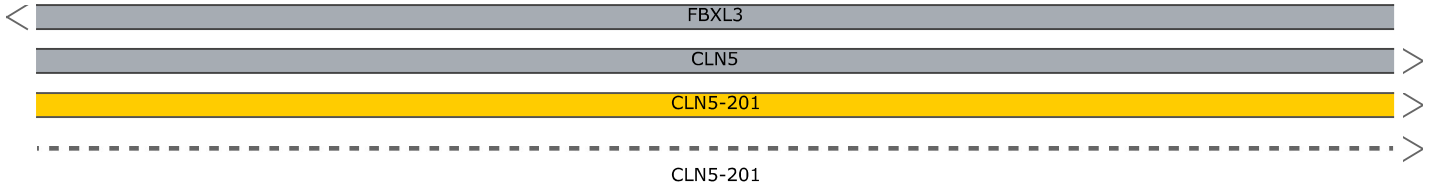
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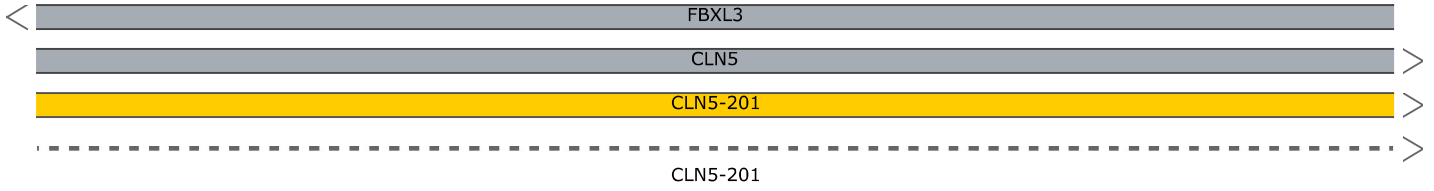
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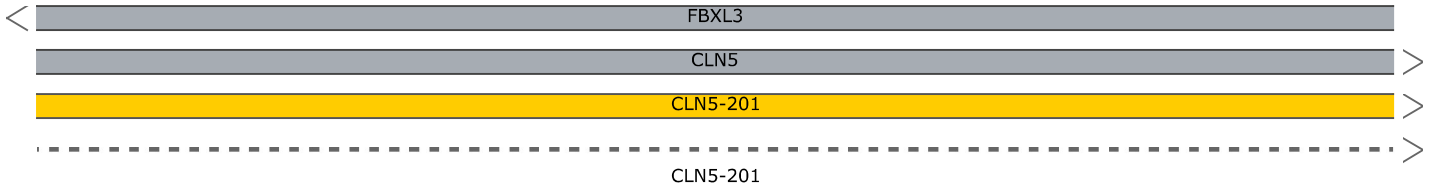
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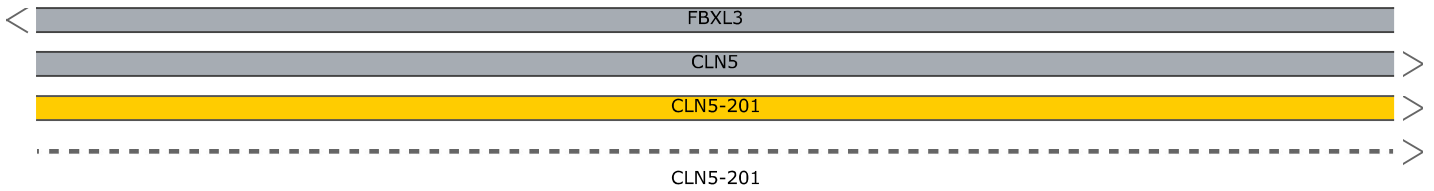
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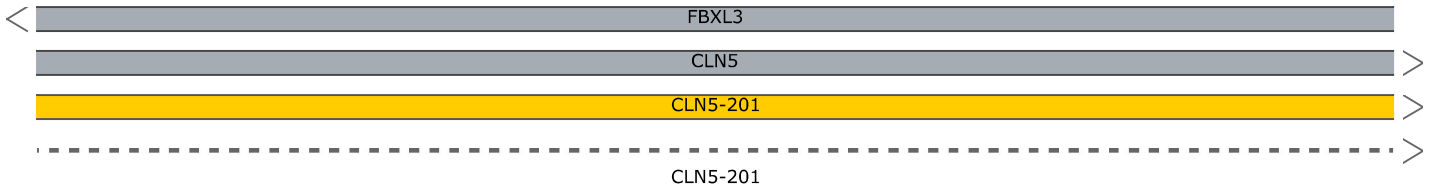
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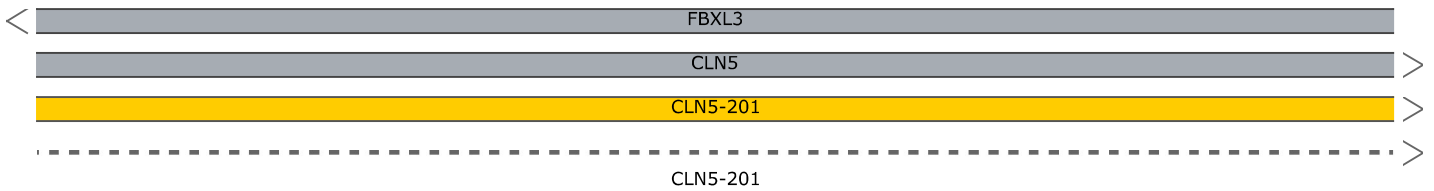
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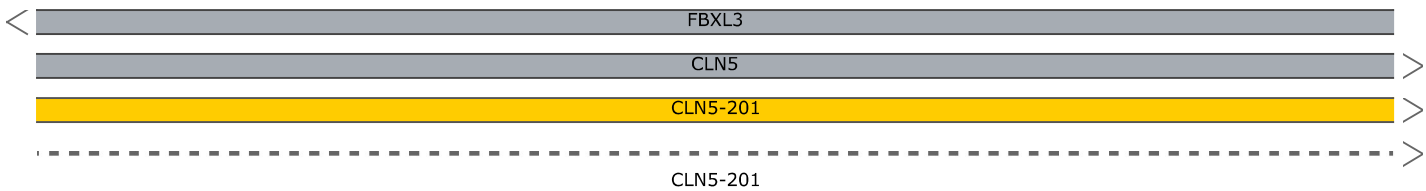
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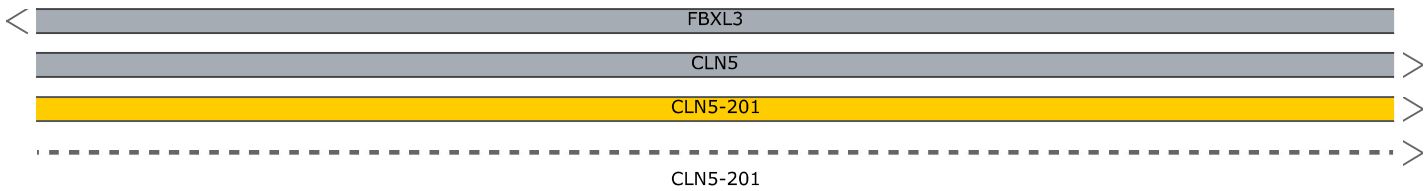
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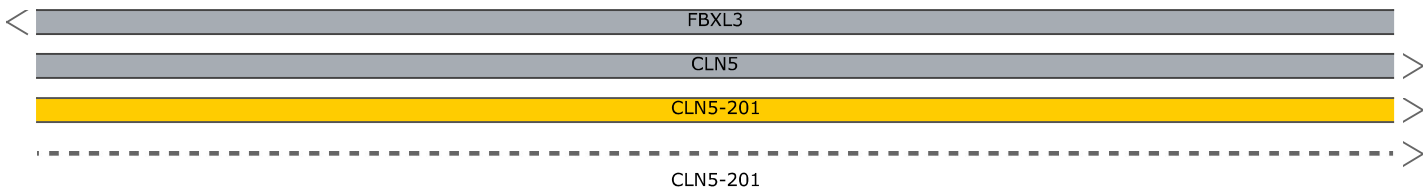
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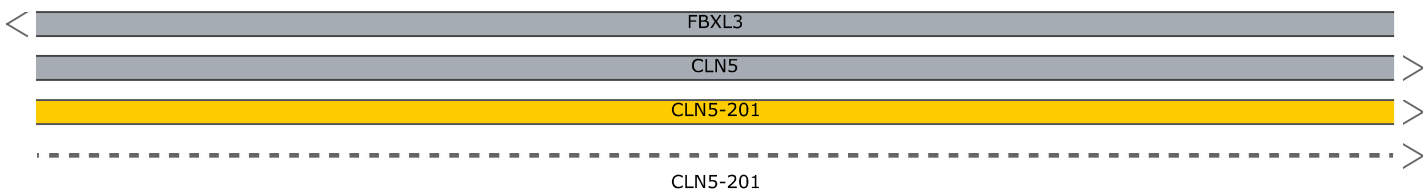
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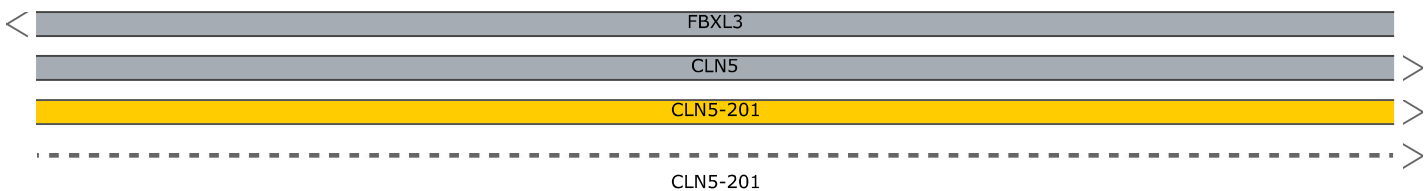
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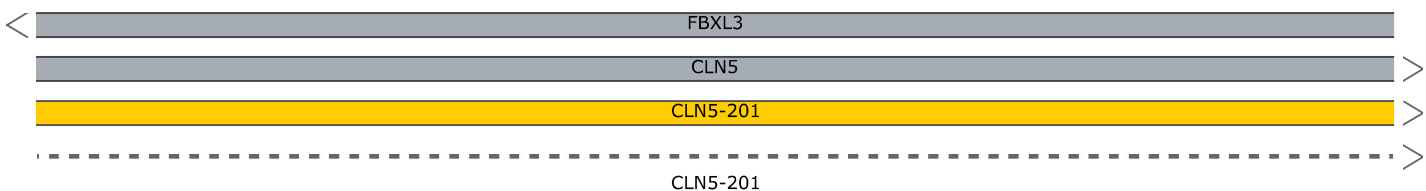
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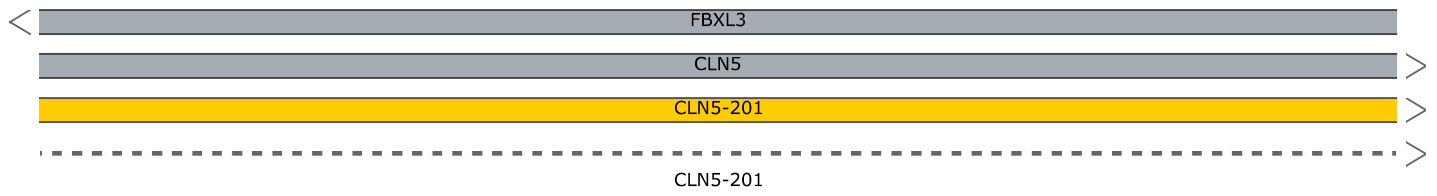
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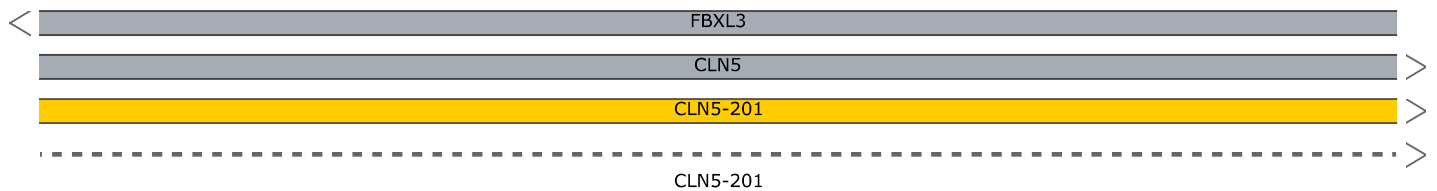
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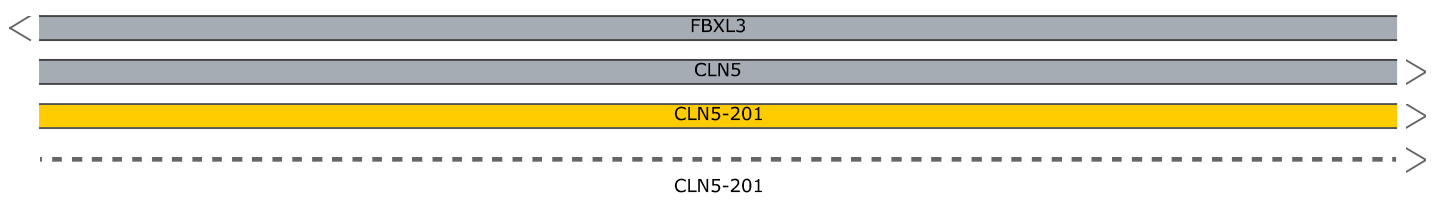
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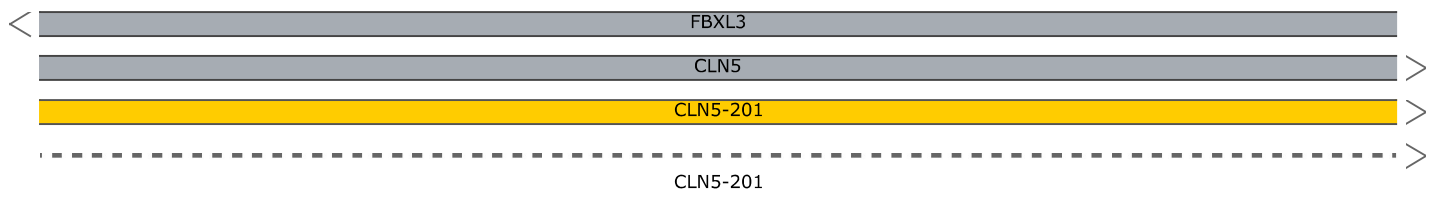
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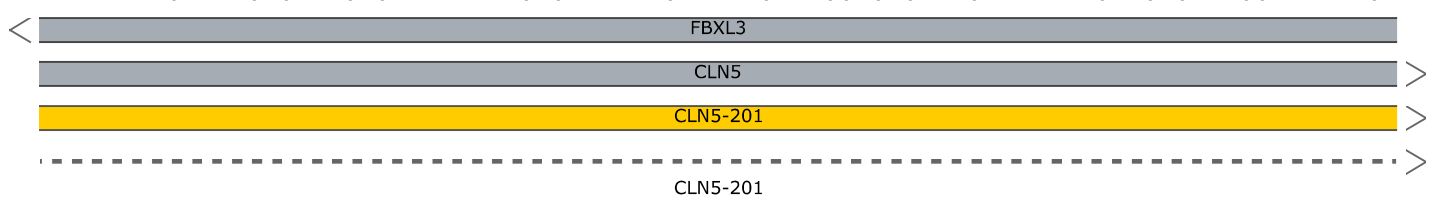
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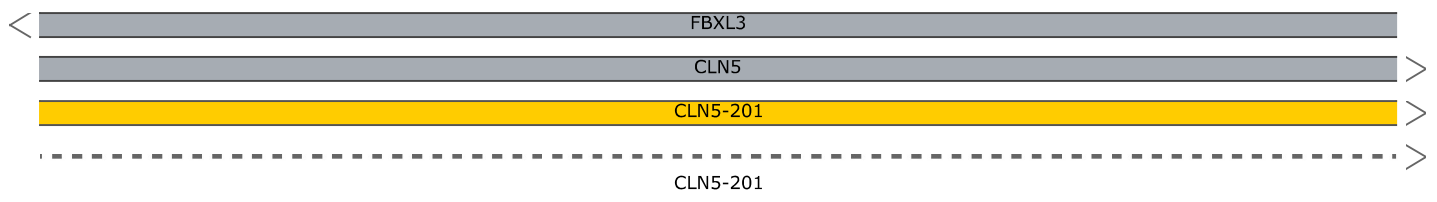
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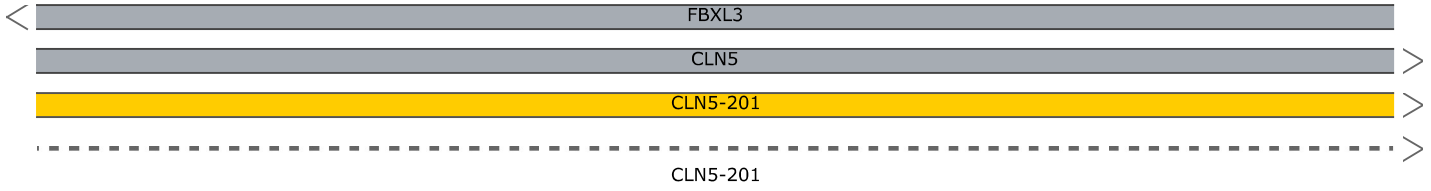
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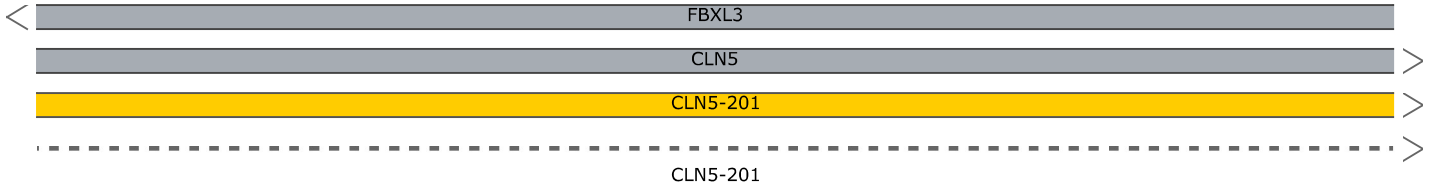
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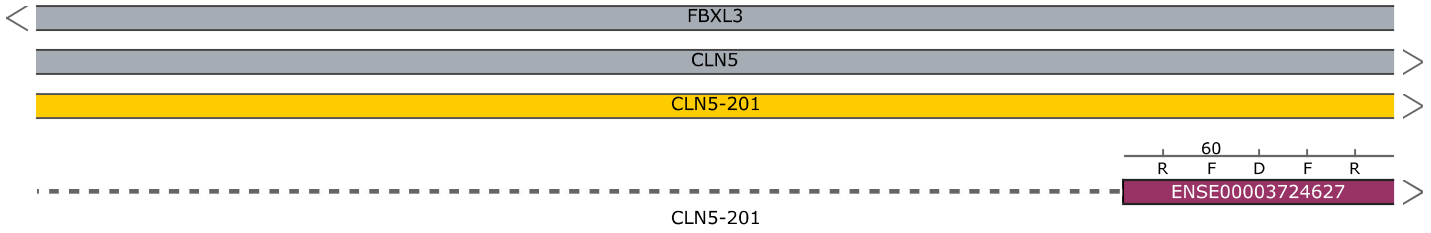
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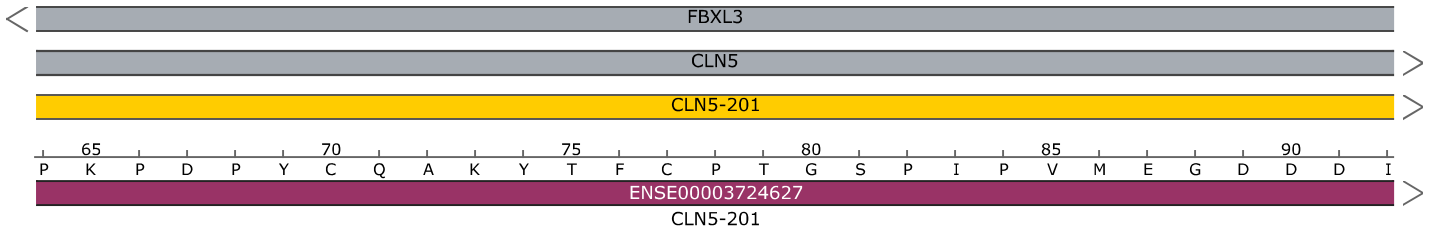
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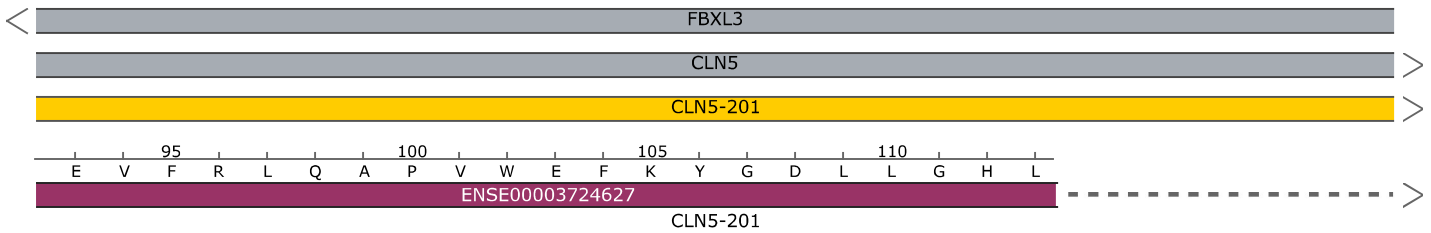
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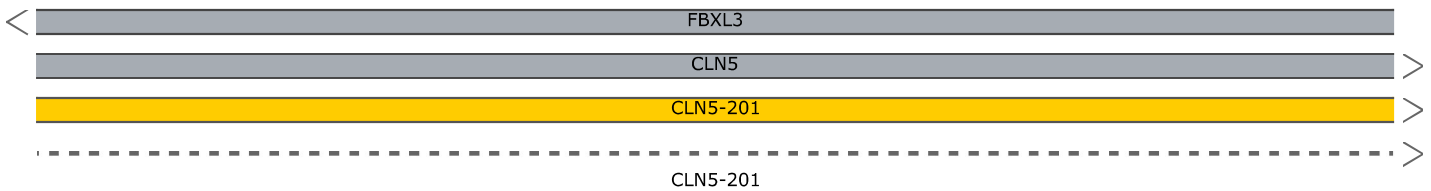
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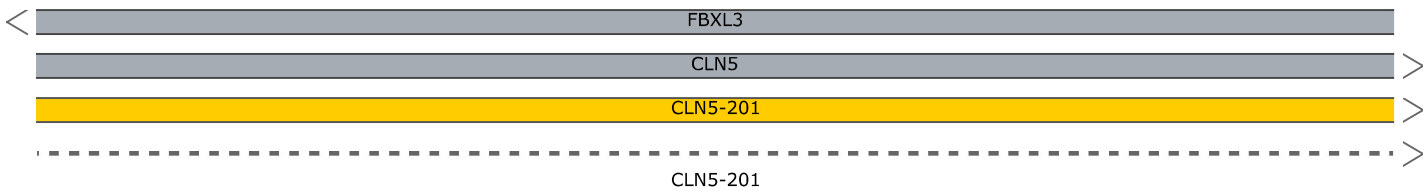
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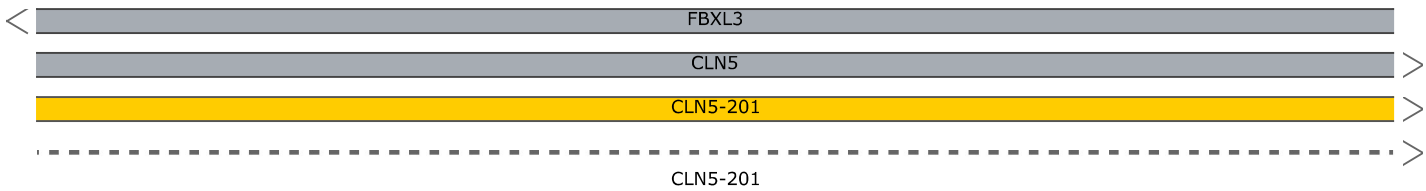
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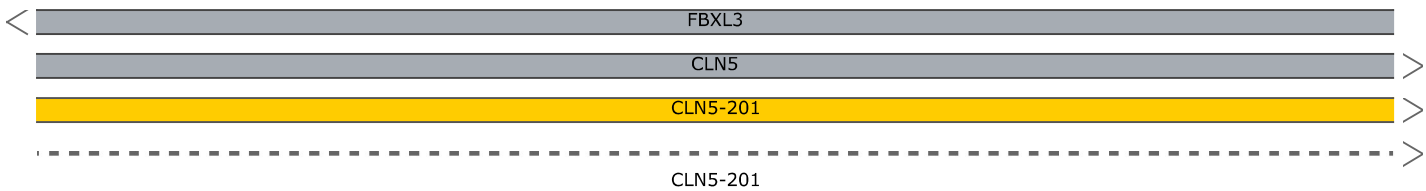
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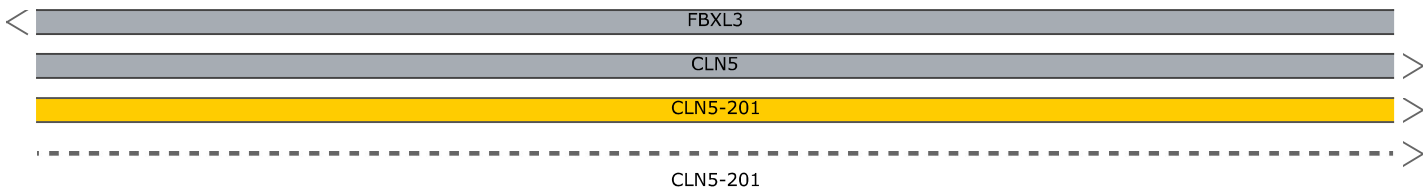
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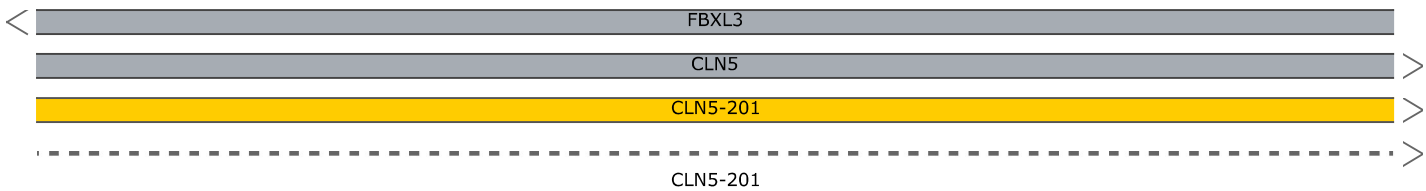
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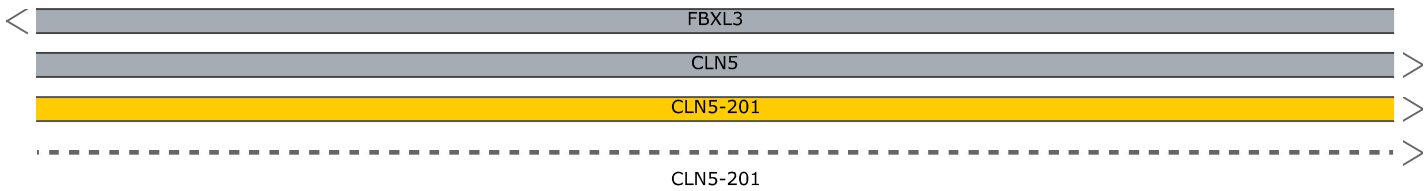
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5185



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FBXL3

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CLN5-201

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FBXL3

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CLN5-201

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FBXL3

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CLN5-201

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CLN5-201

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CLN5-201

CLN5-201

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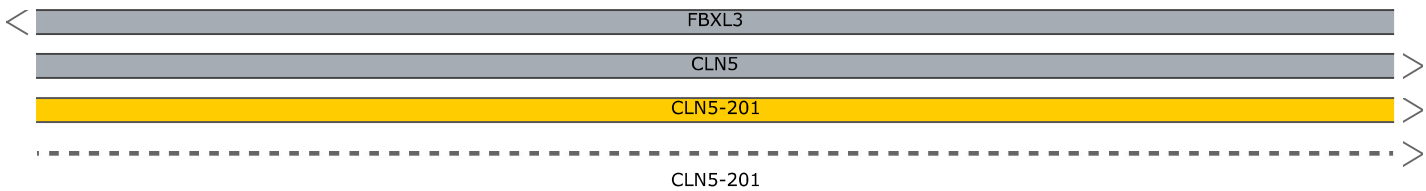
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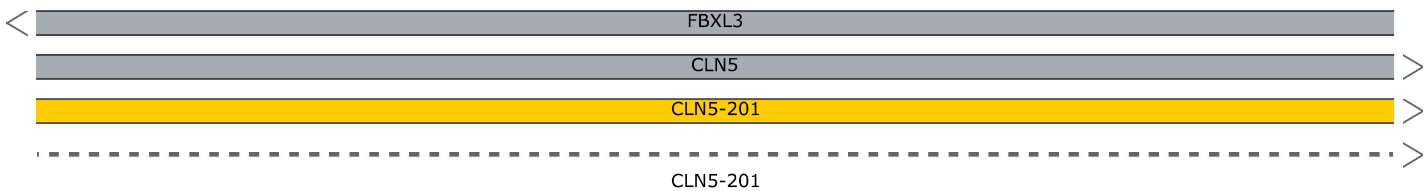
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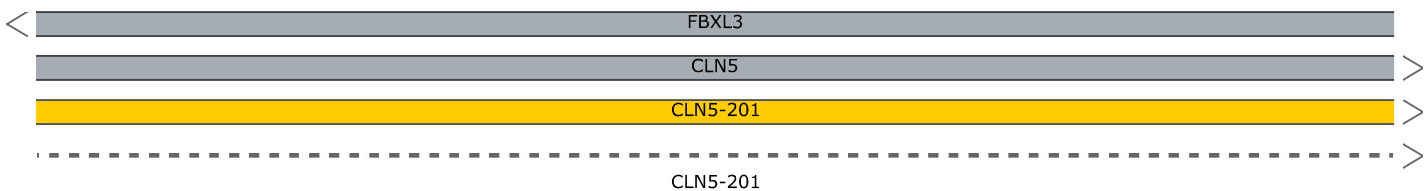
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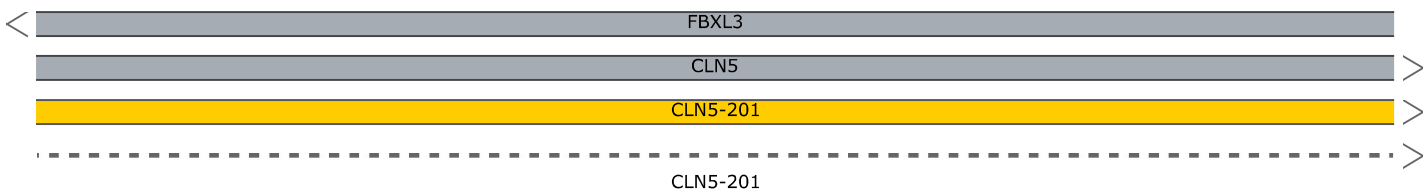
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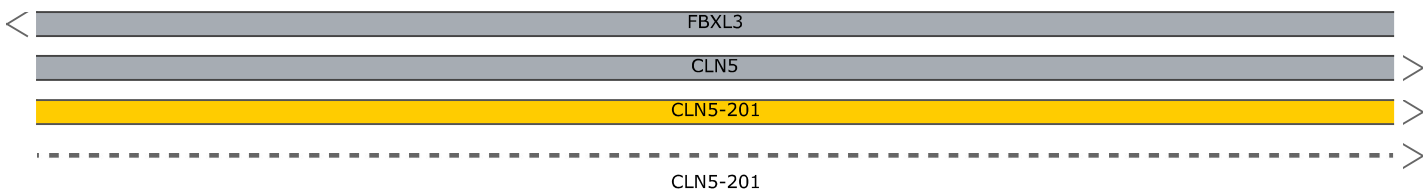
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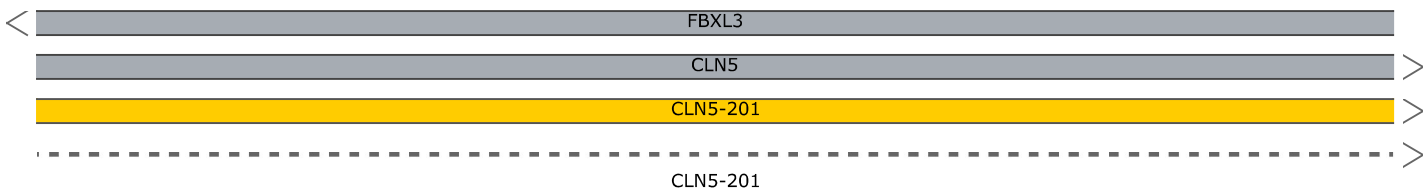
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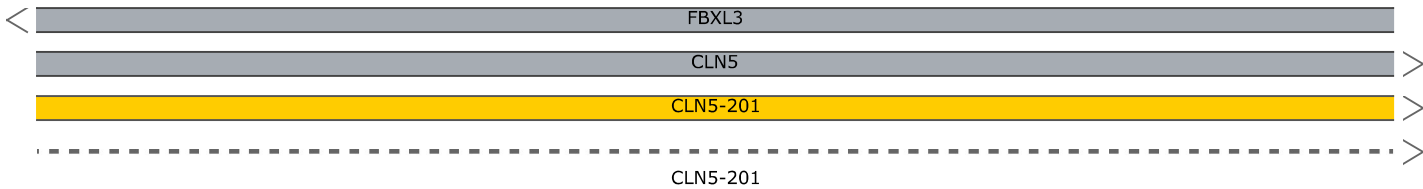
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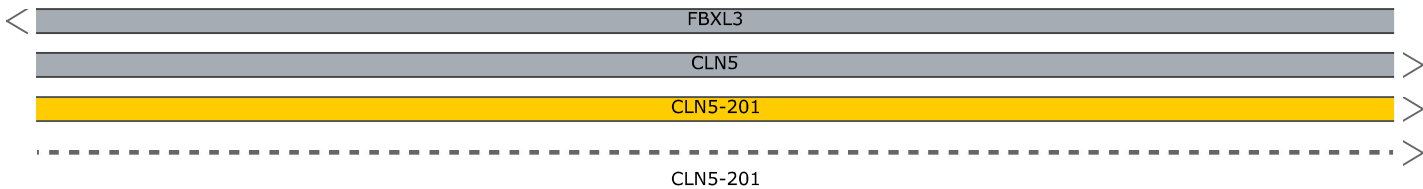
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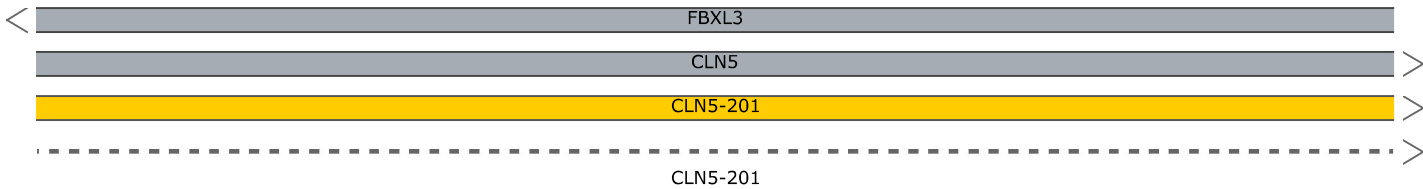
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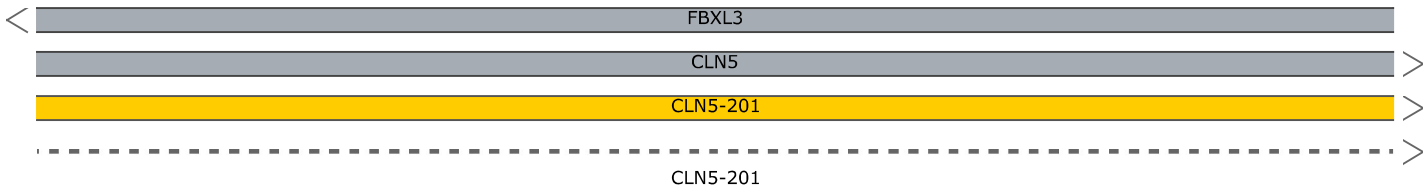
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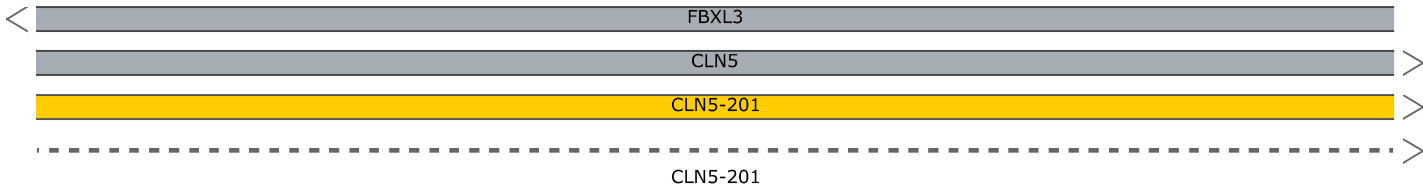
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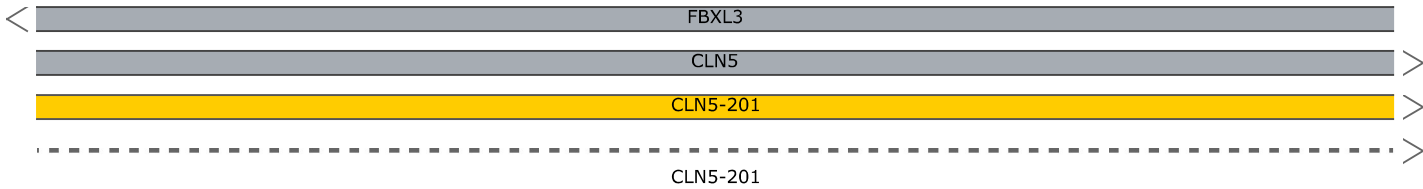
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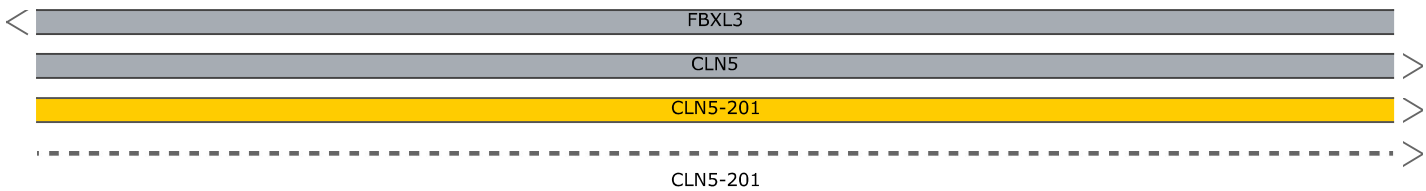
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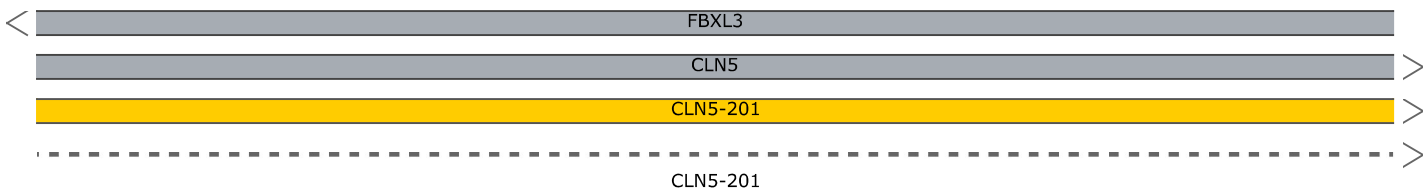
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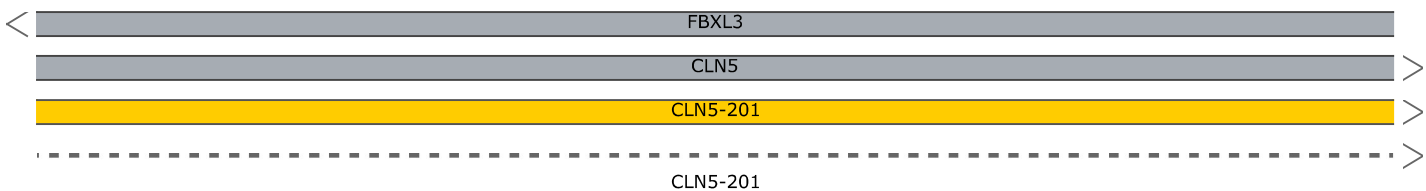
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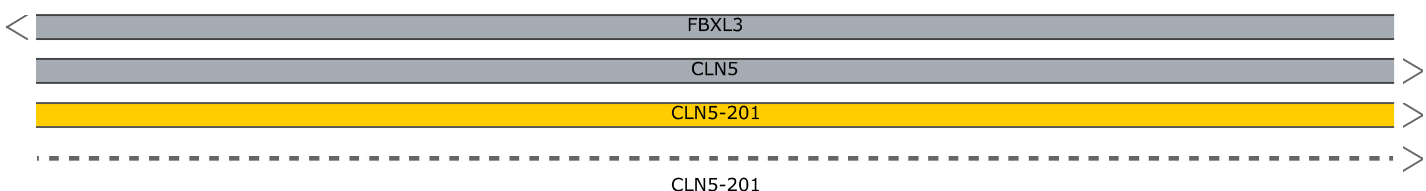
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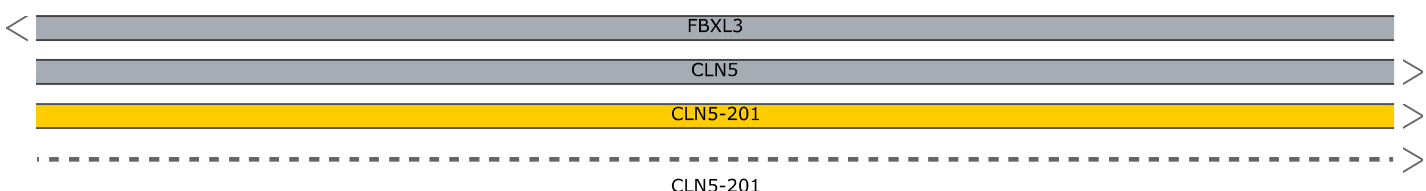
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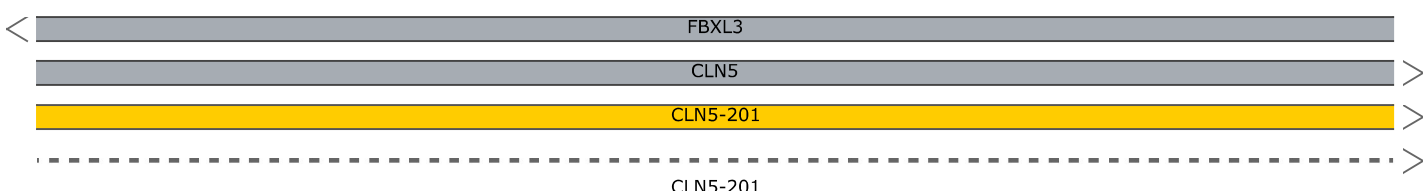
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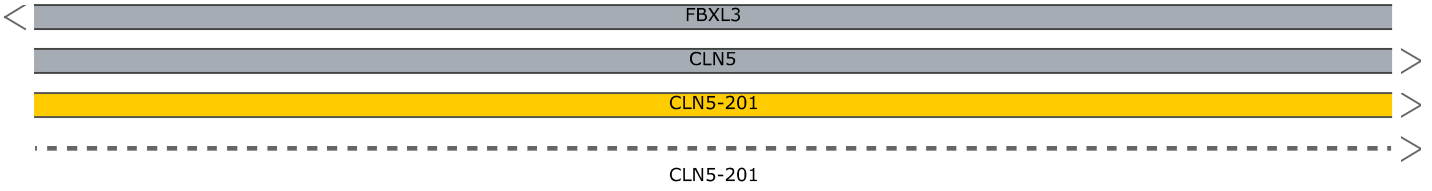
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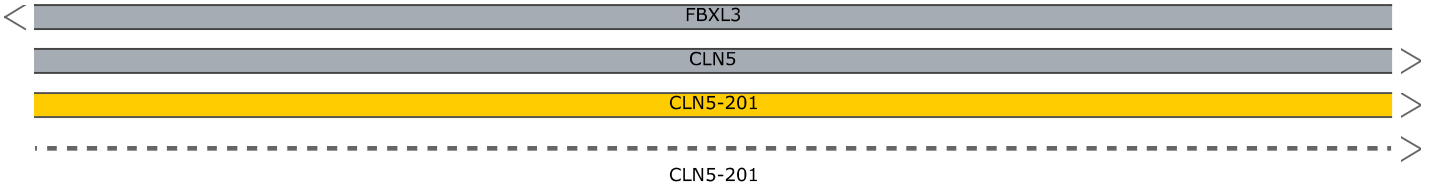
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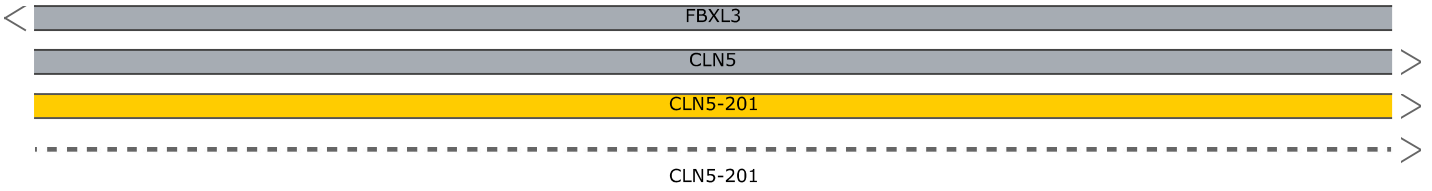
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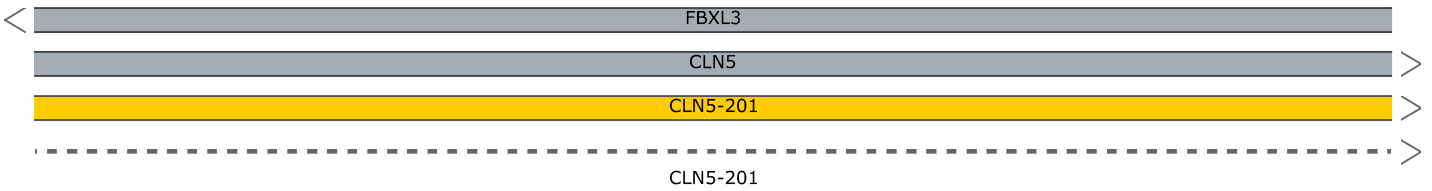
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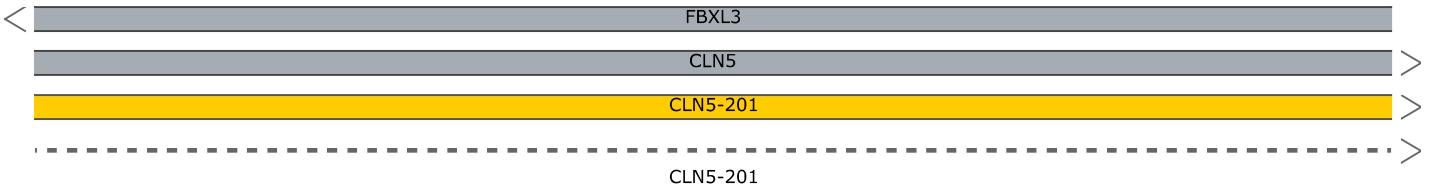
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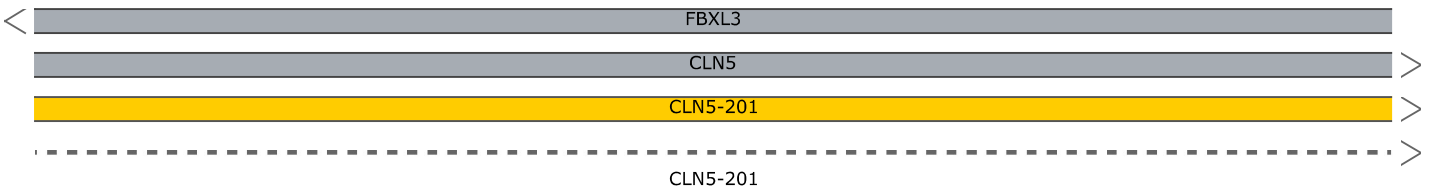
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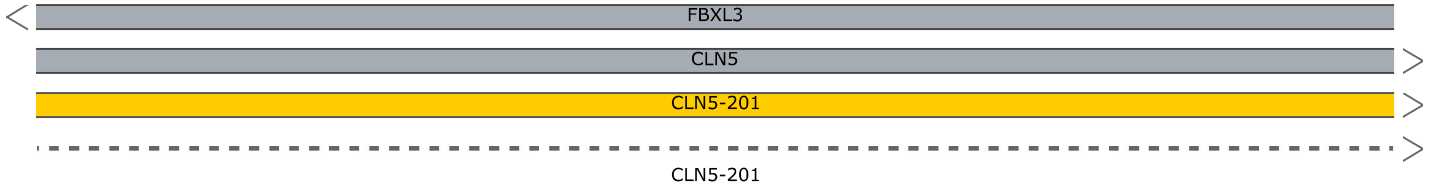
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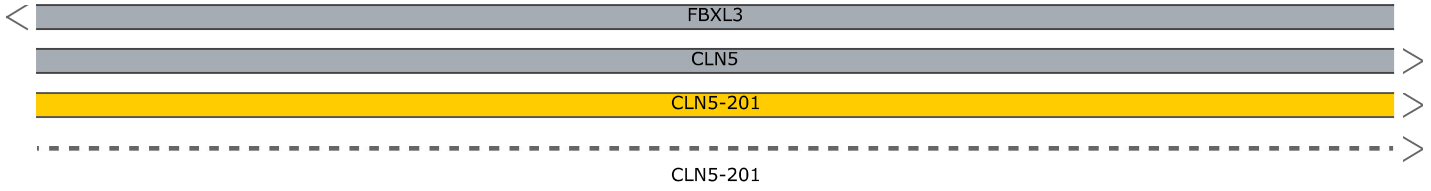
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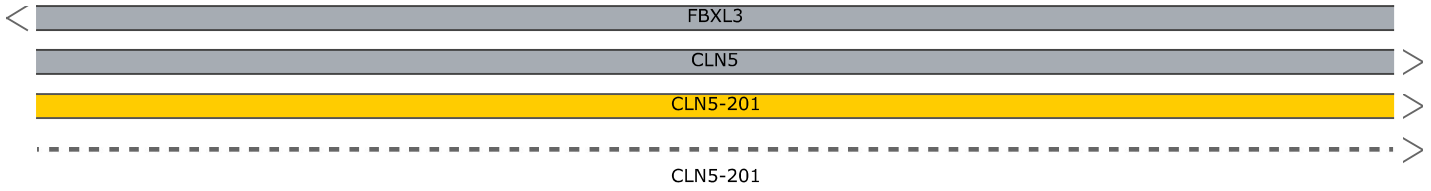
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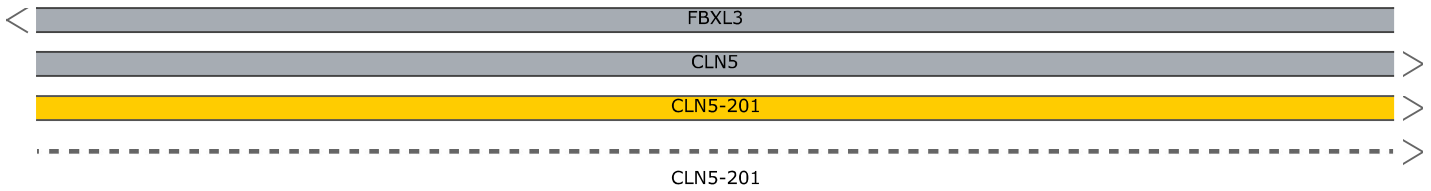
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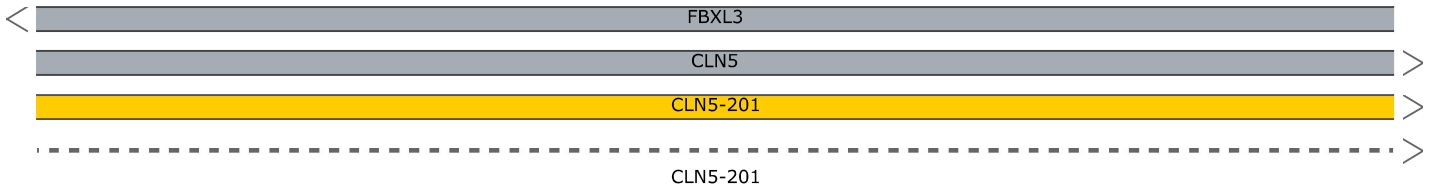
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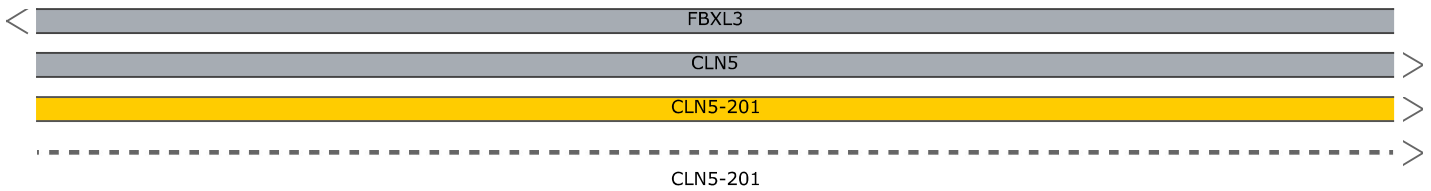
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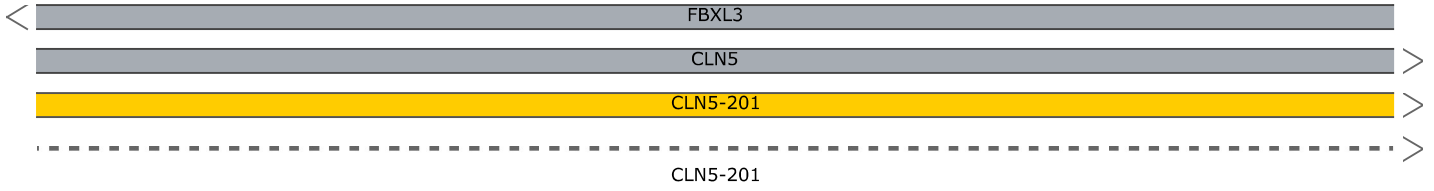
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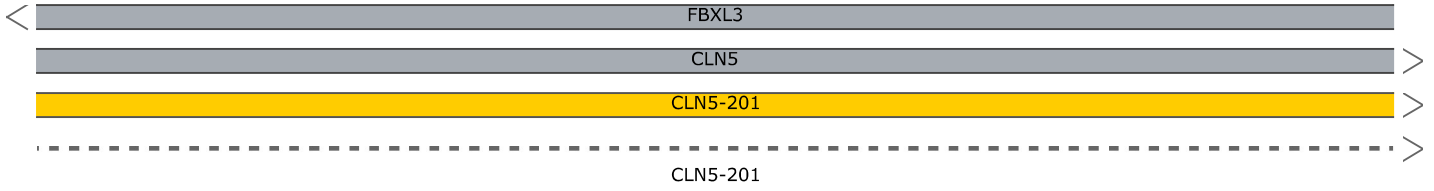
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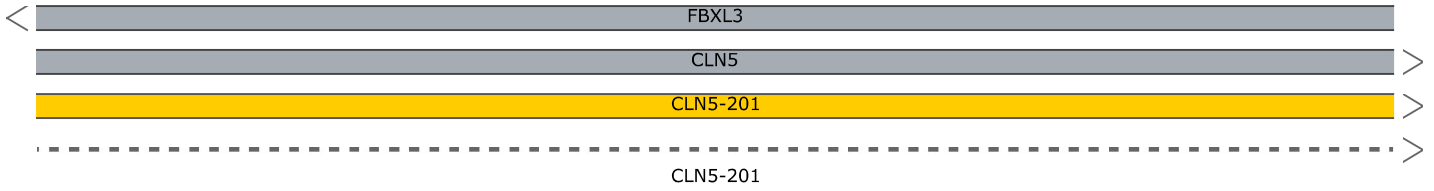
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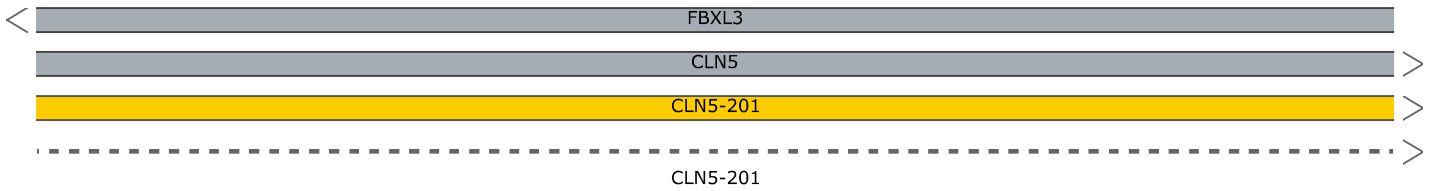
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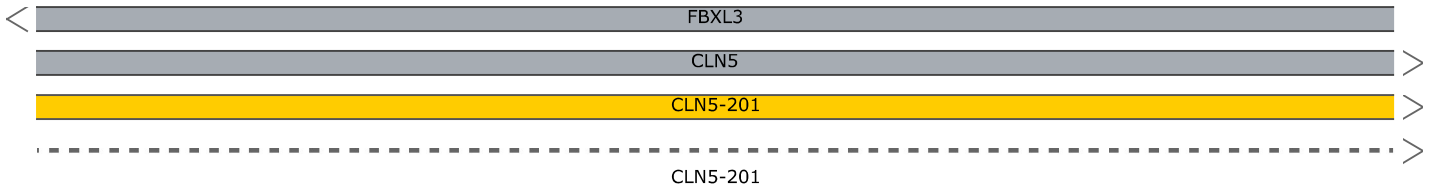
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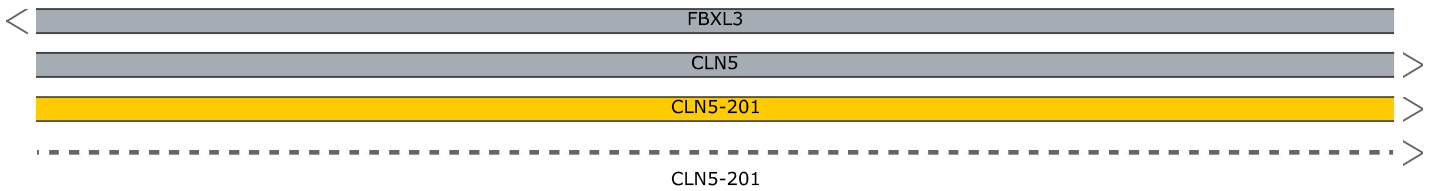
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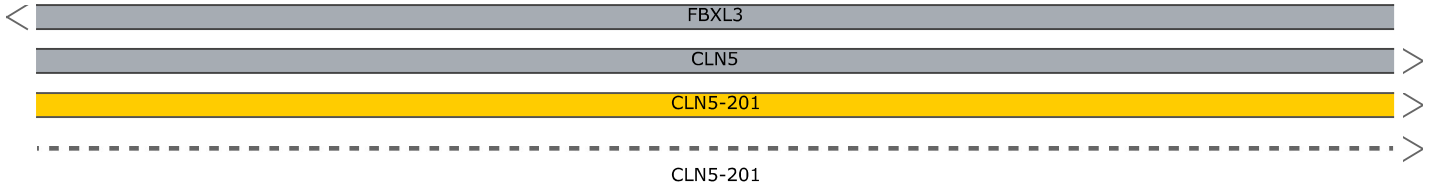
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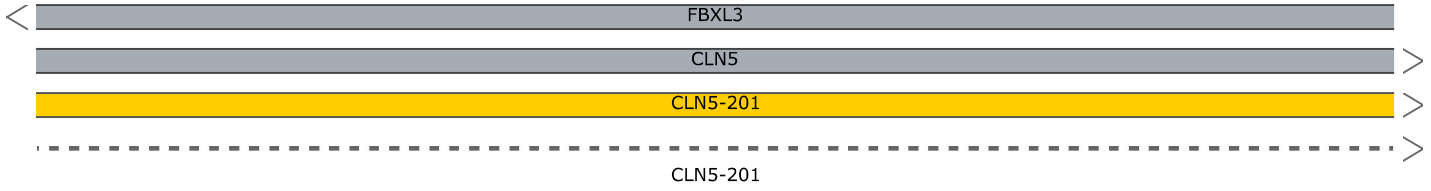
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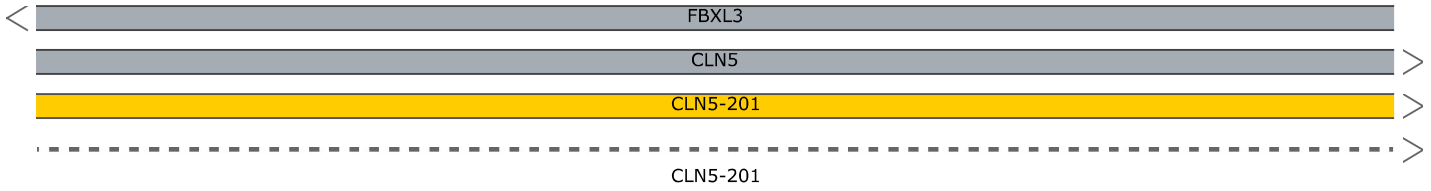
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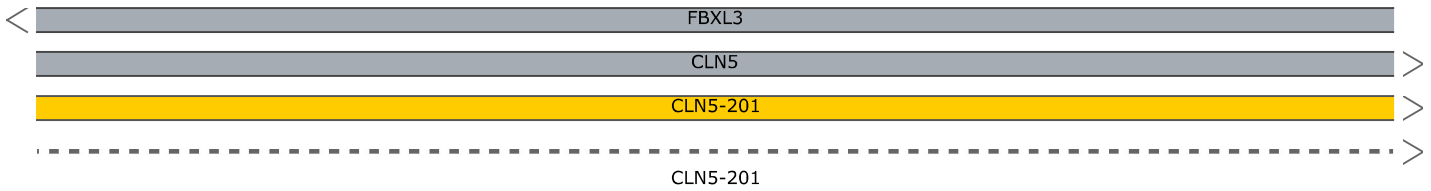
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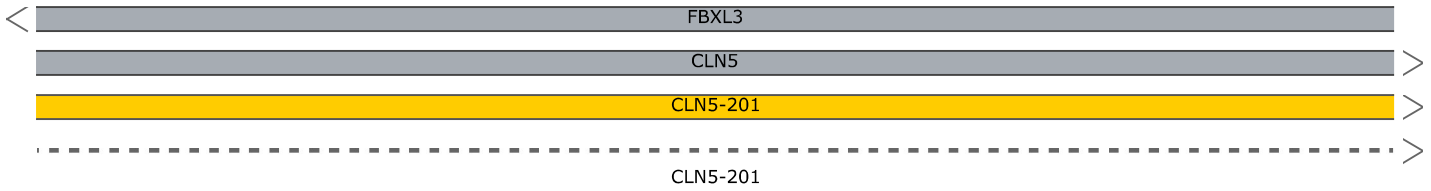
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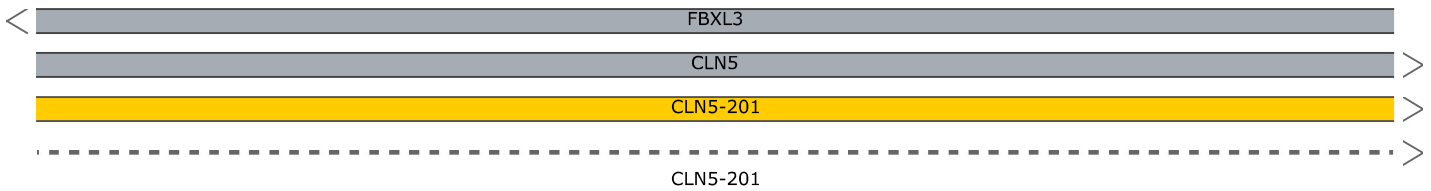
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9180



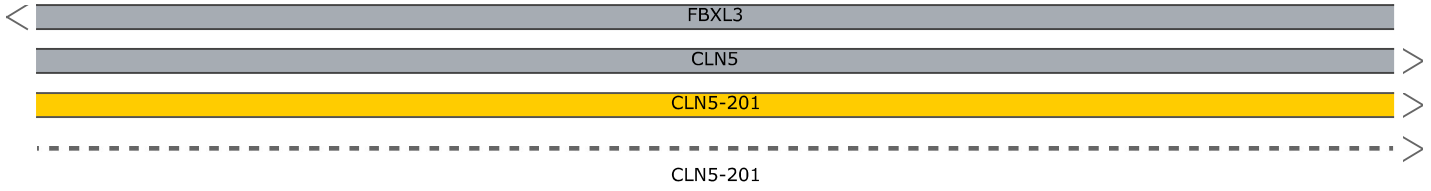
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9265



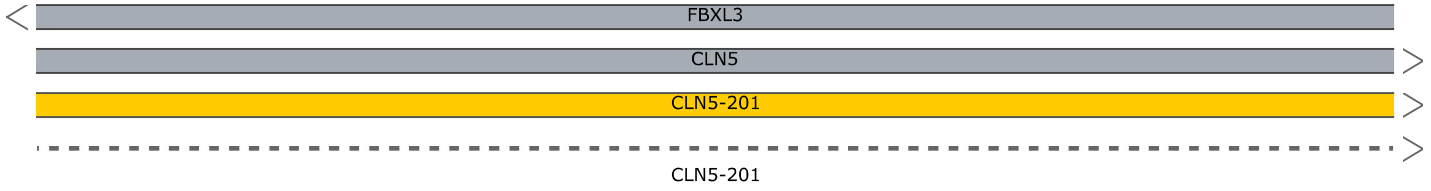
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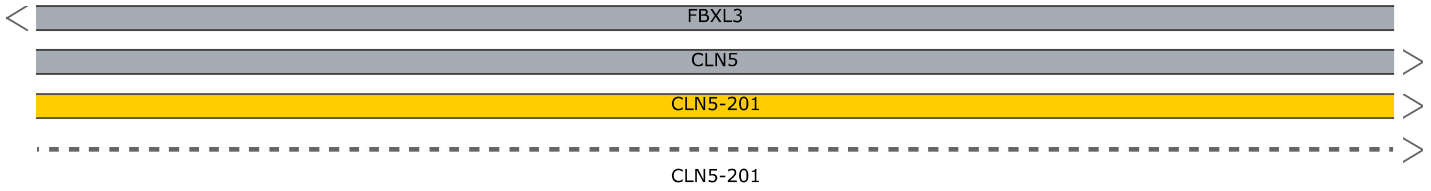
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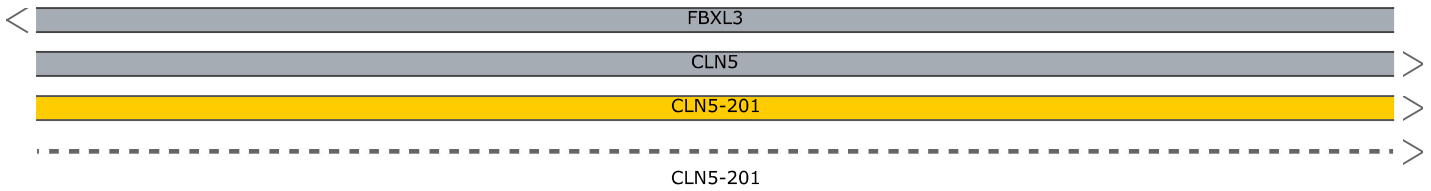
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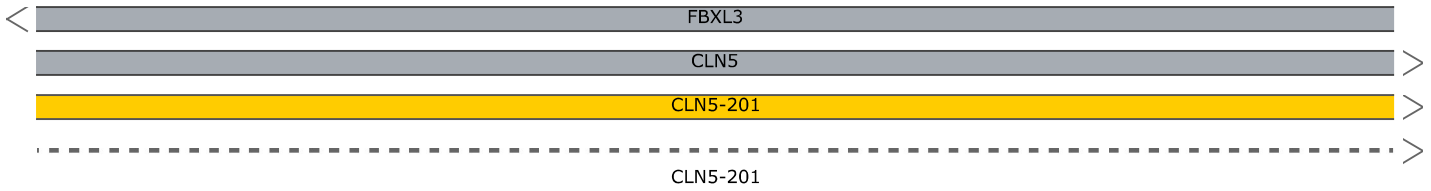
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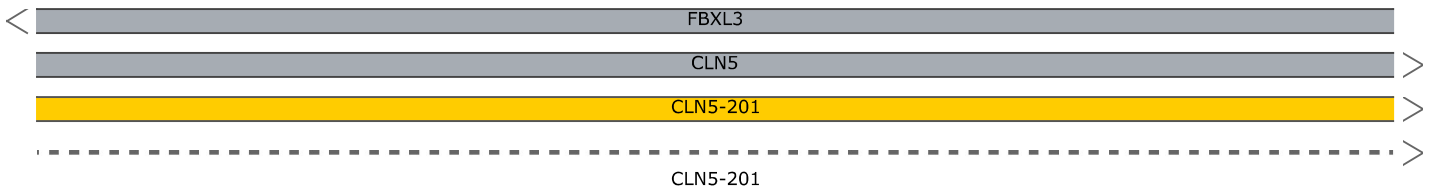
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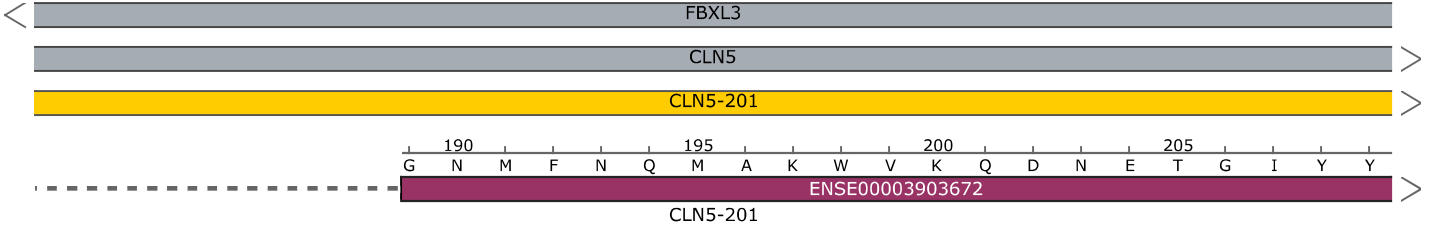


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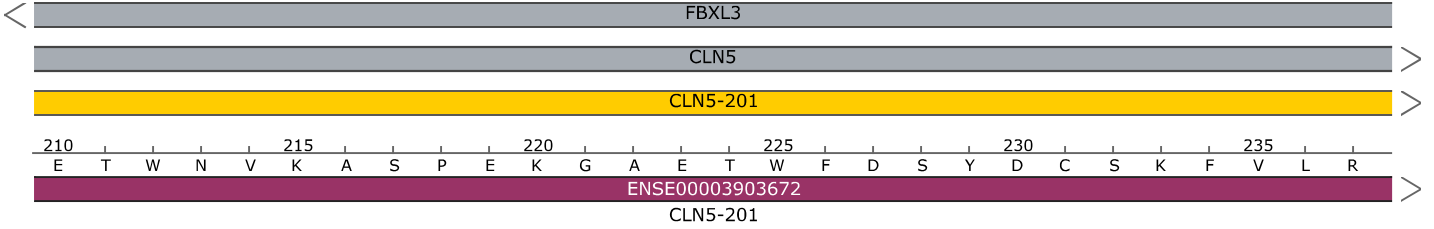
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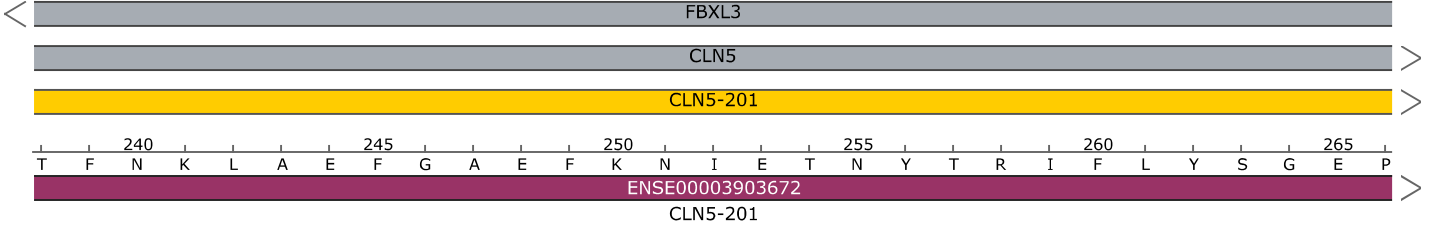
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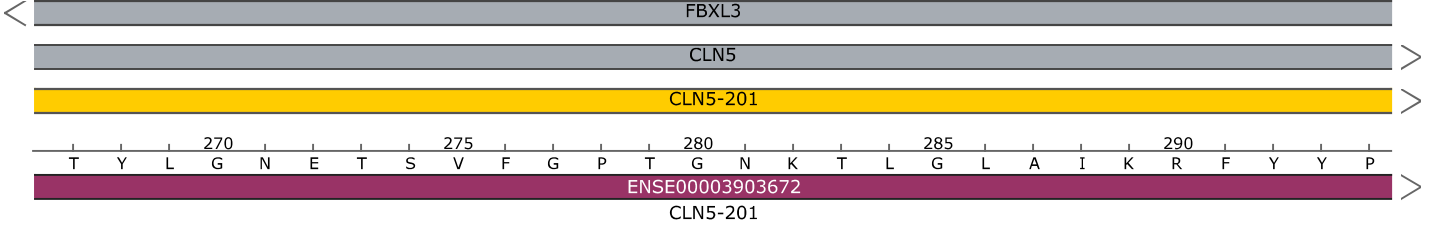
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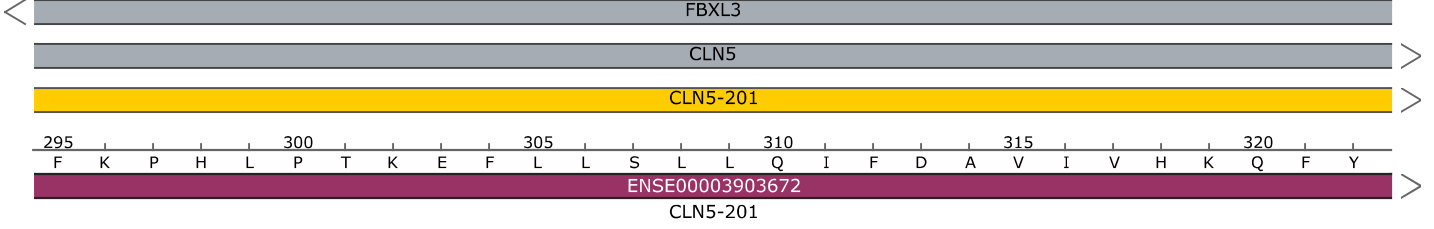
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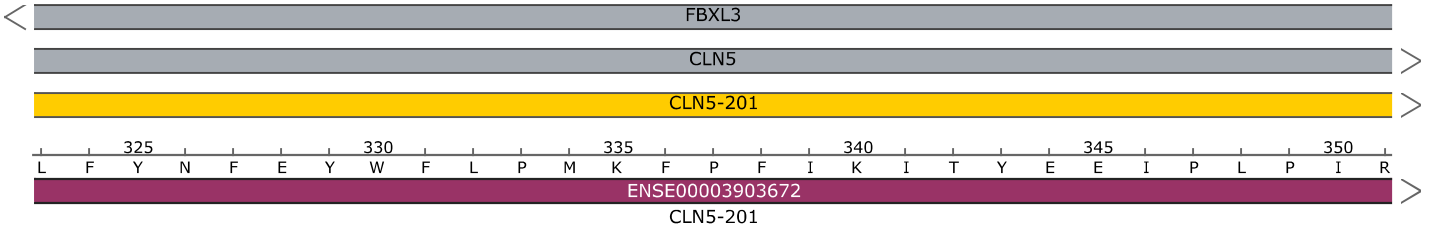


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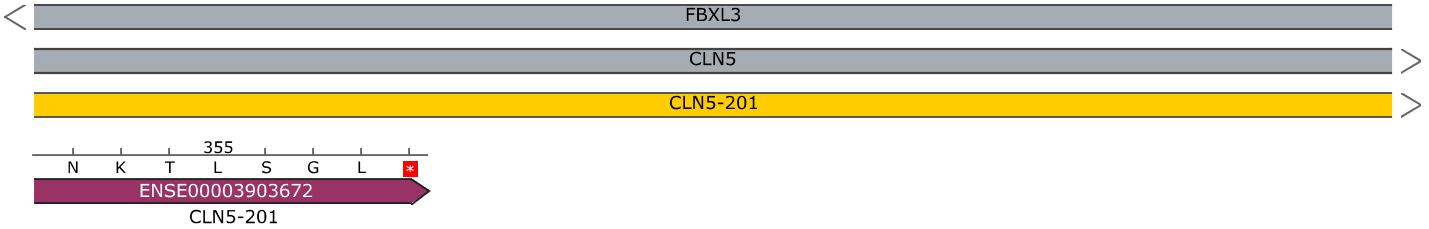
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10,285



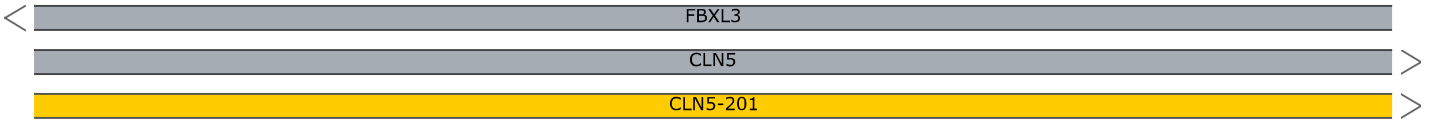
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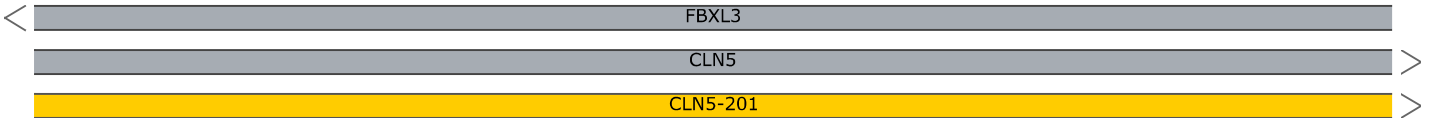
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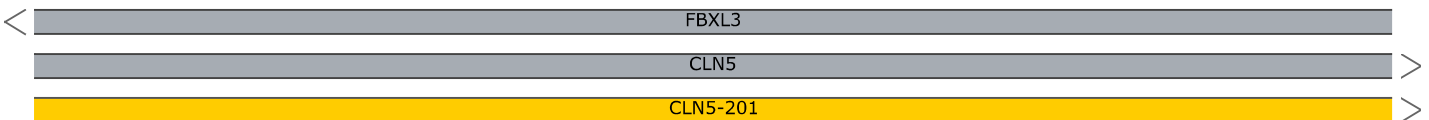
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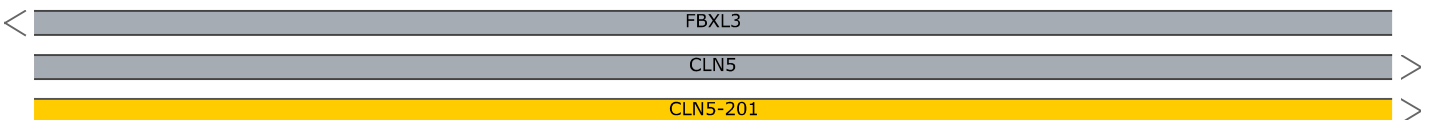
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10,625



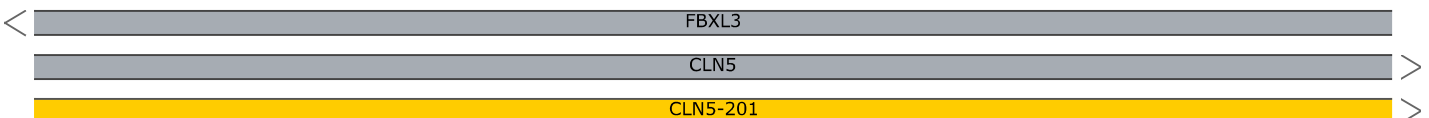
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10,710



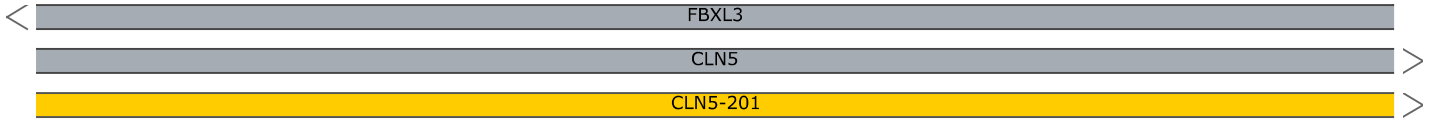
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10,795



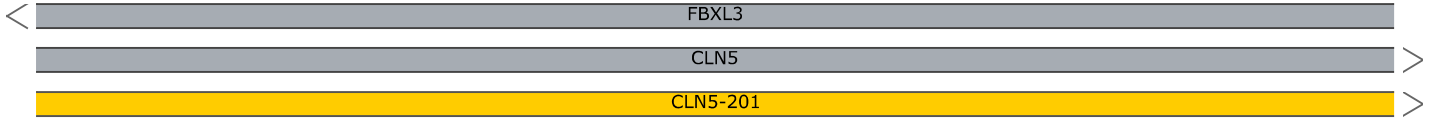
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10,880



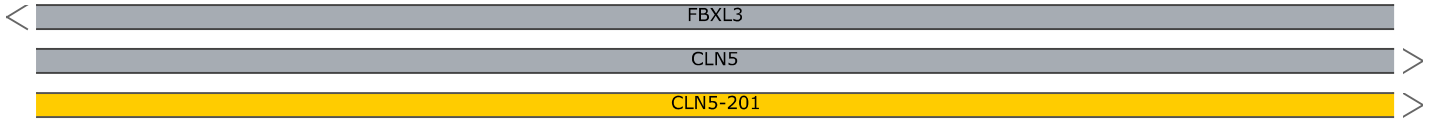
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10,965



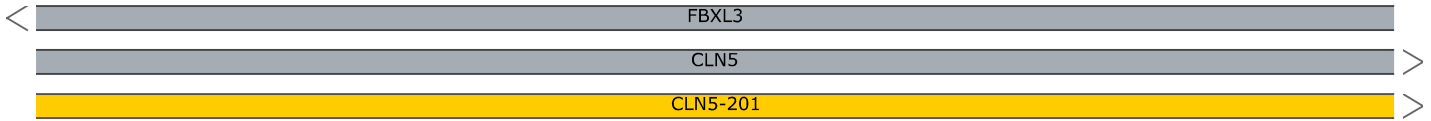
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11,050



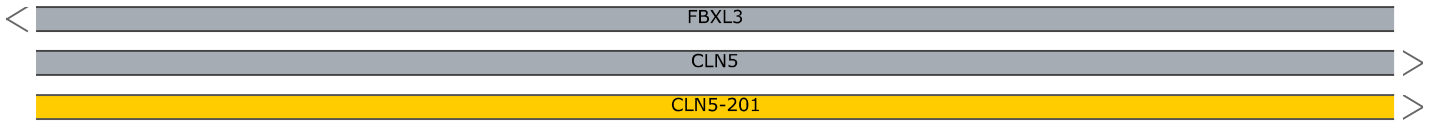
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11,135



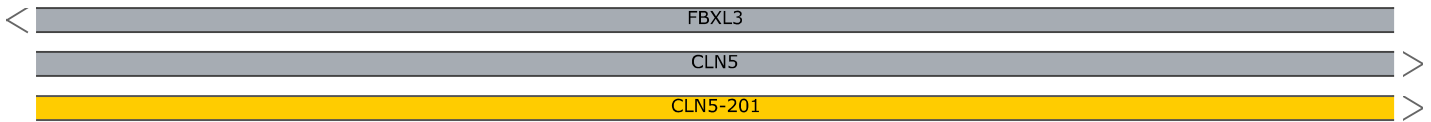
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11,220



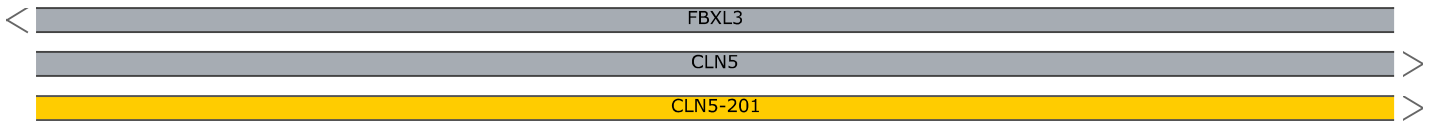
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11,305



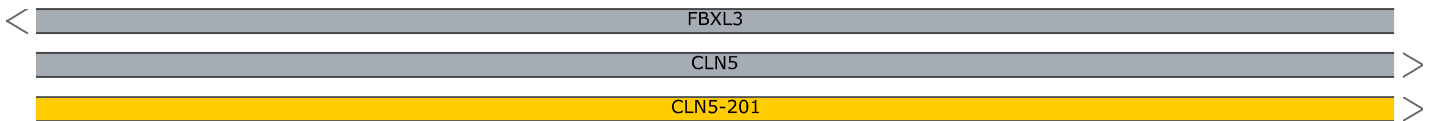
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11,390



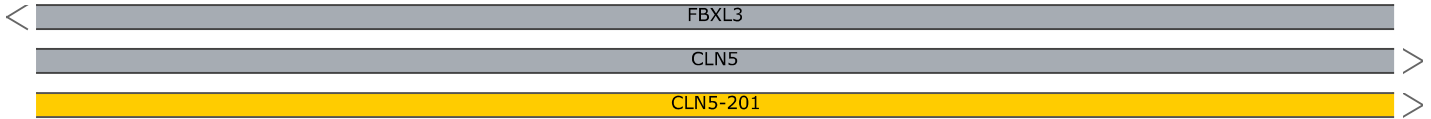
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11,475



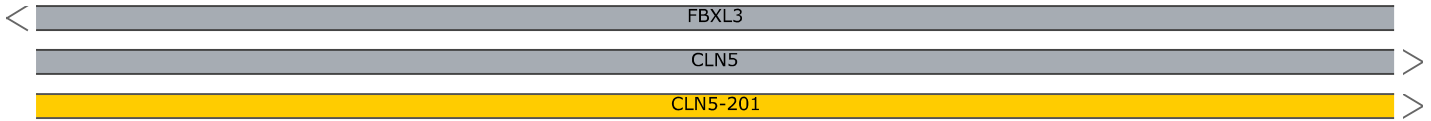
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11,560



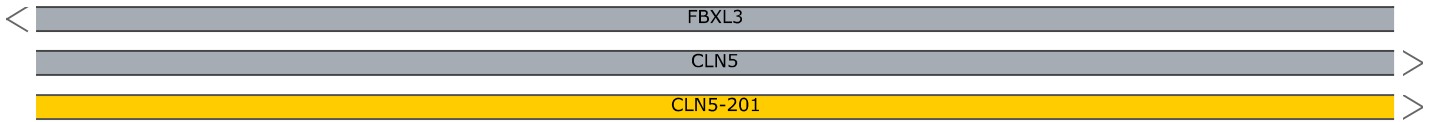
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11,645



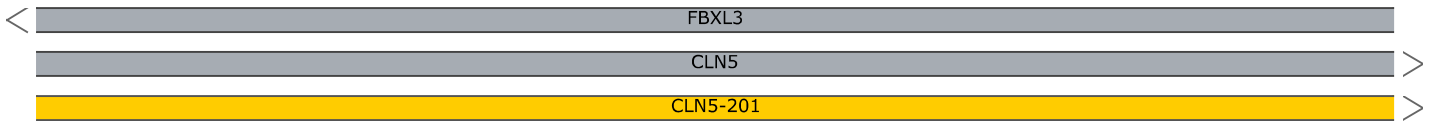
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11,730



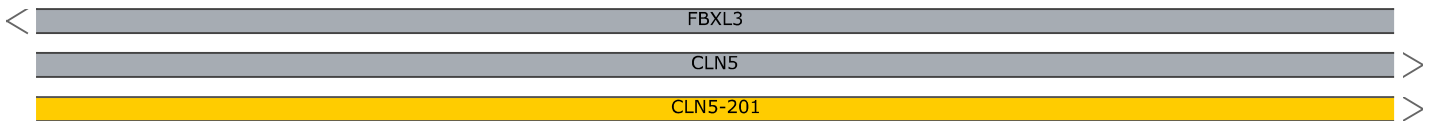
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11,815



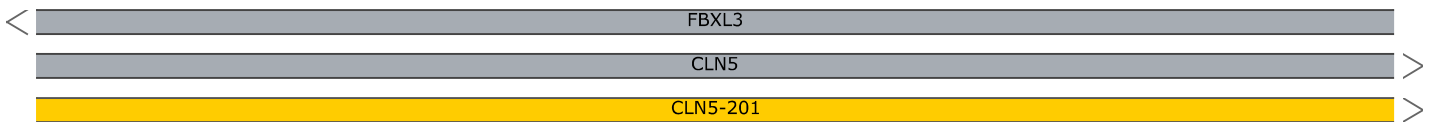
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11,900



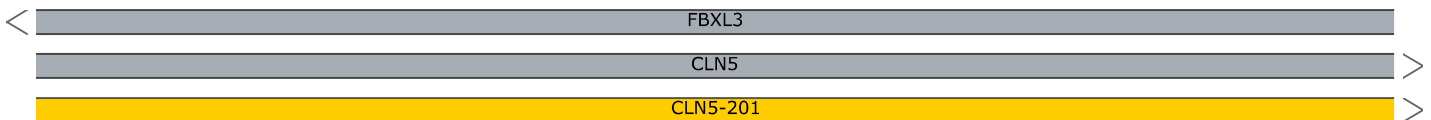
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11,985



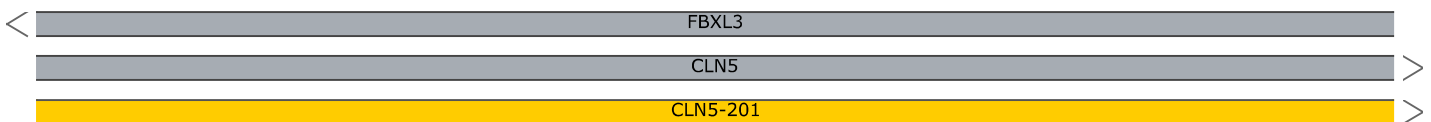
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12,070



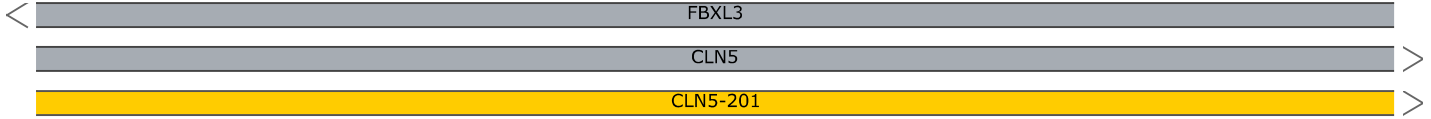
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12,155



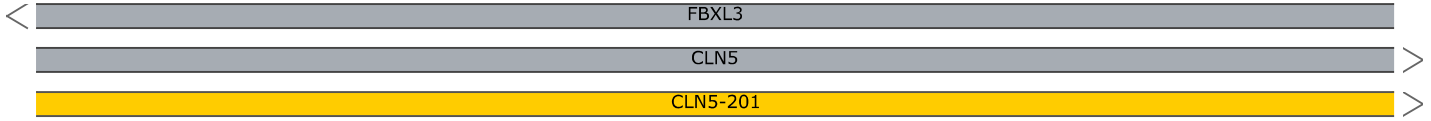
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12,240



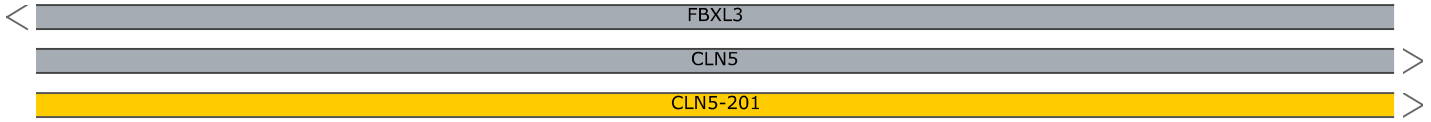
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12,325



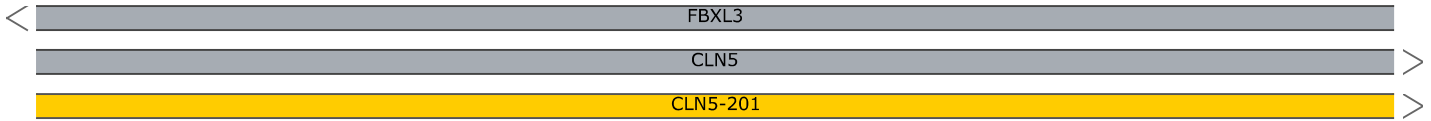
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12,410



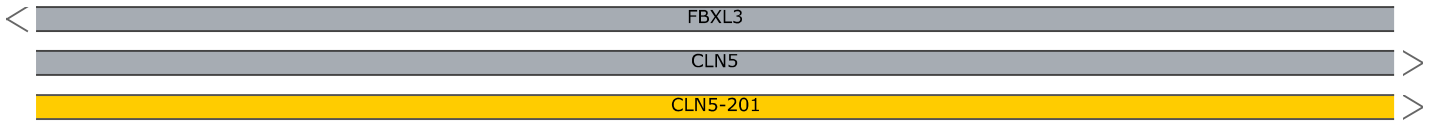
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12,495



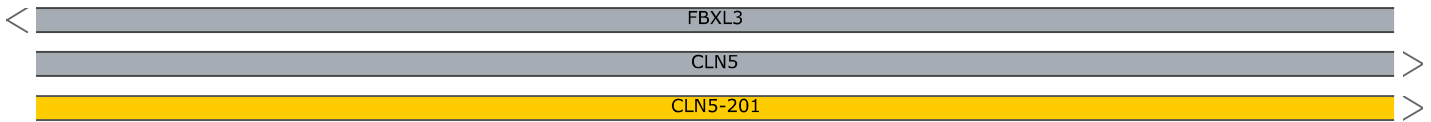
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12,580



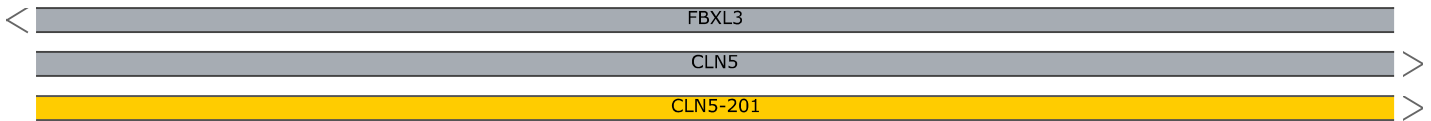
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12,665



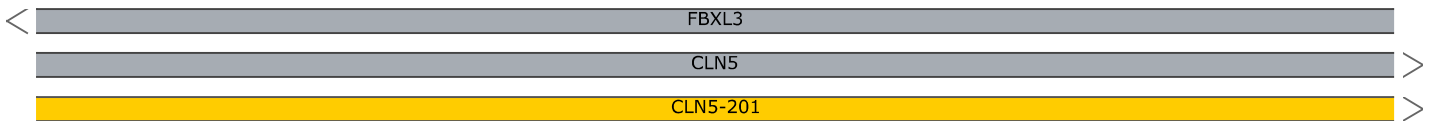
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12,750



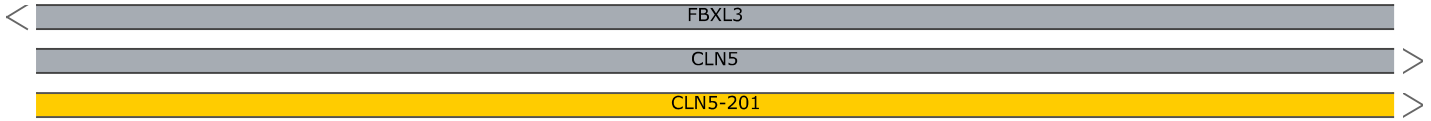
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12,835



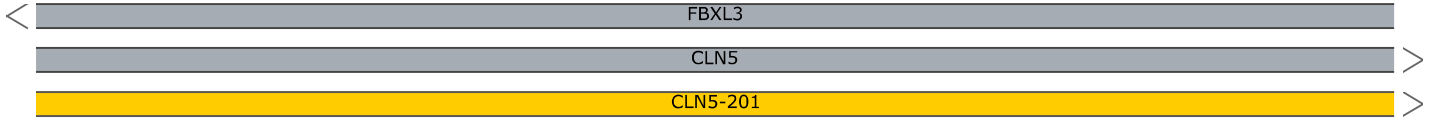
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12,920



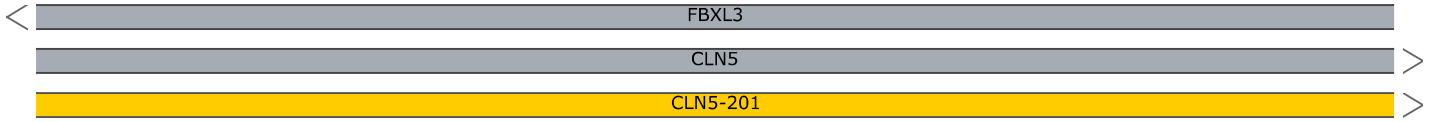
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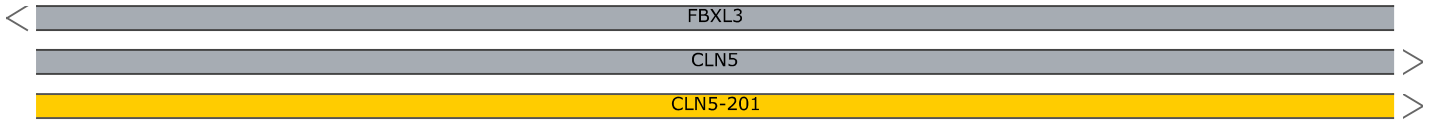
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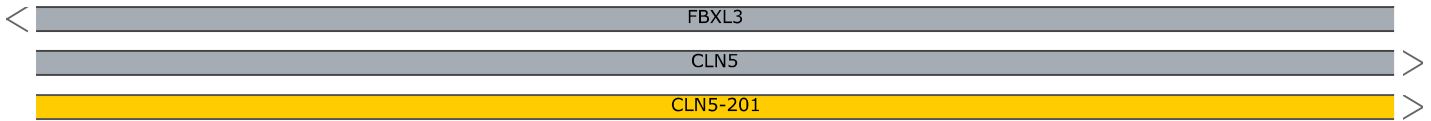
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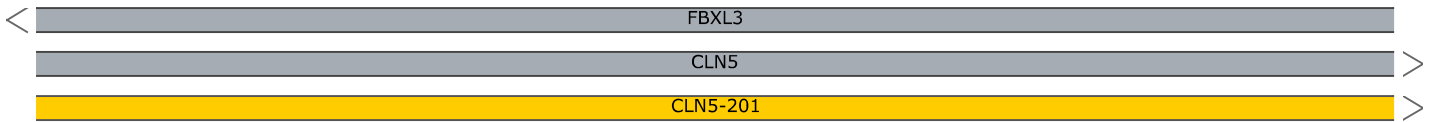
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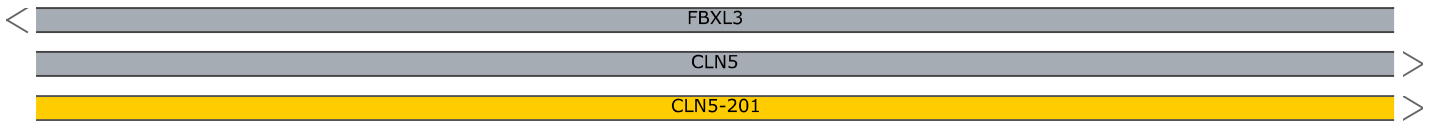
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13,345



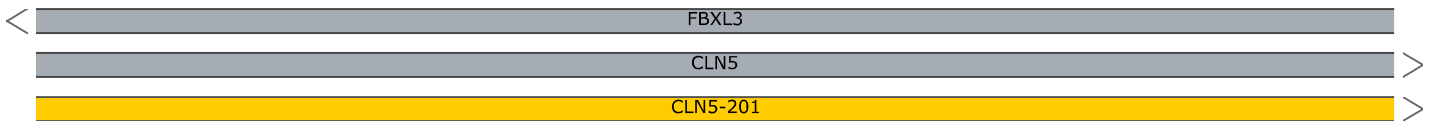
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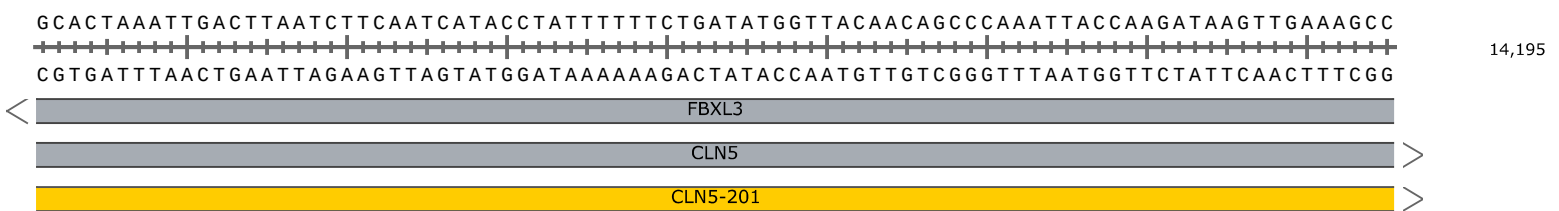
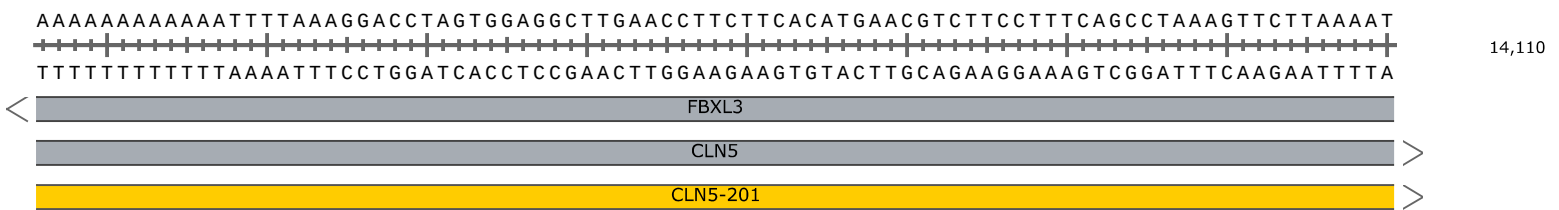
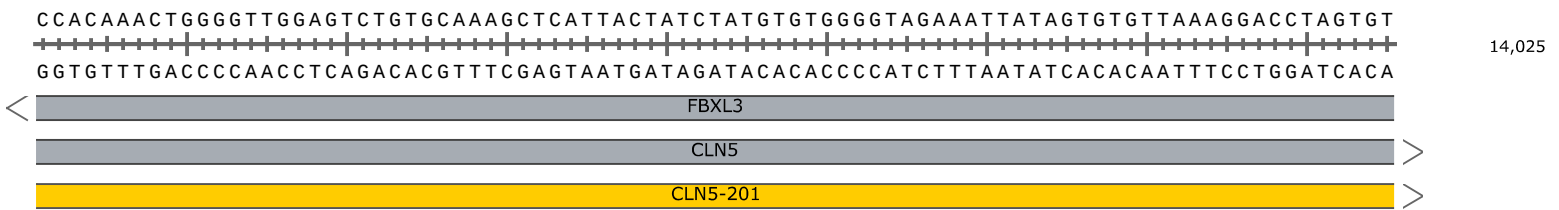
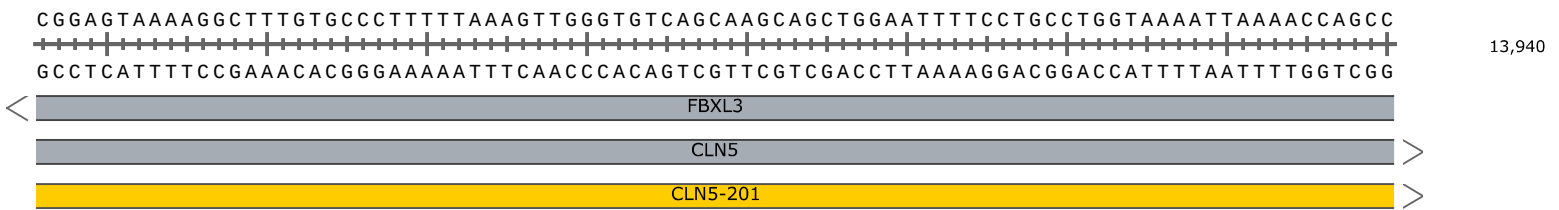
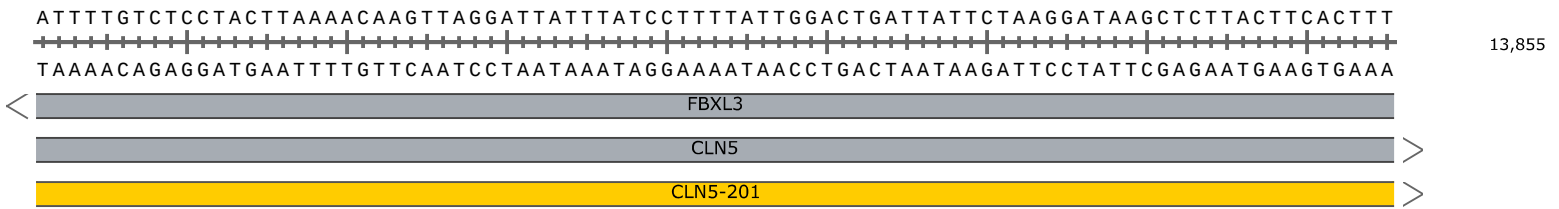
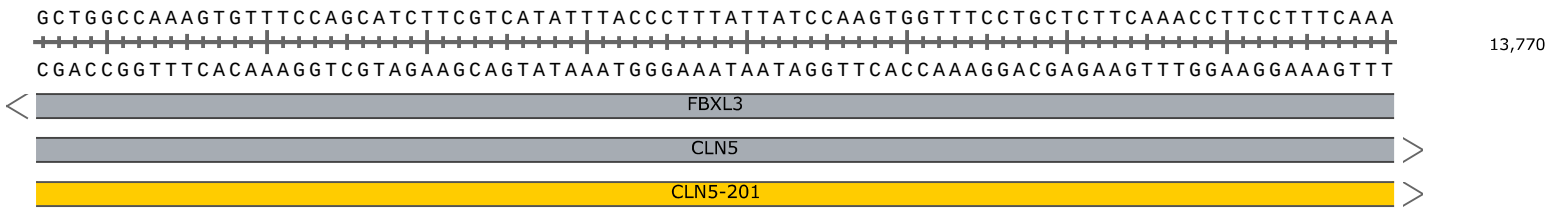
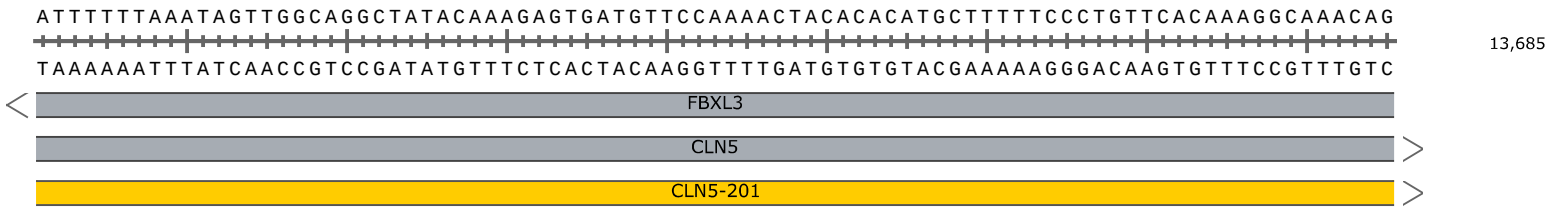
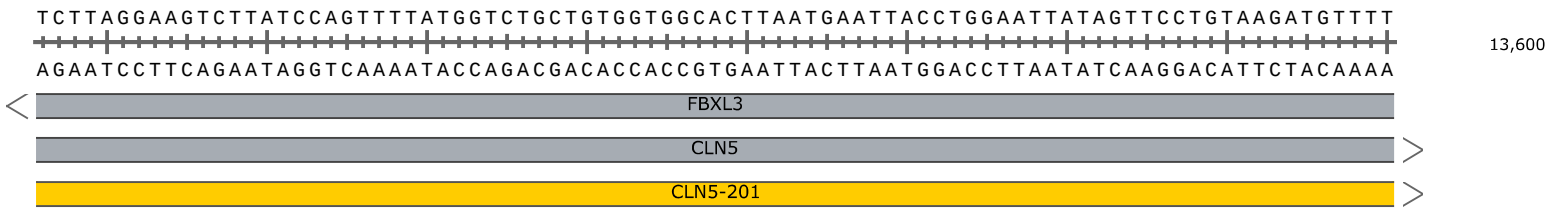
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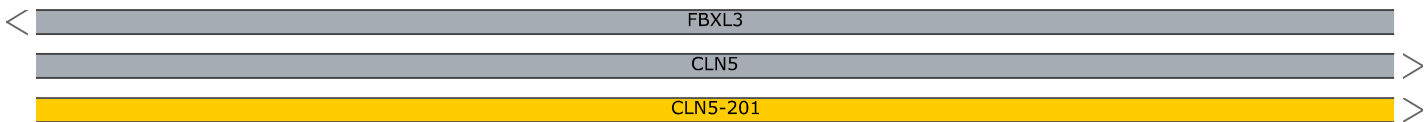
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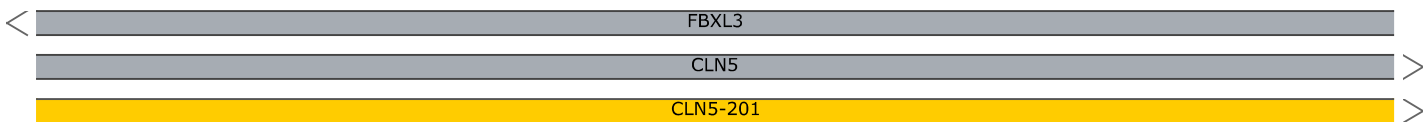
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14,280



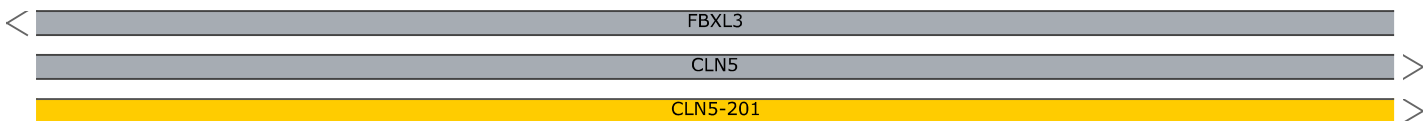
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14,365



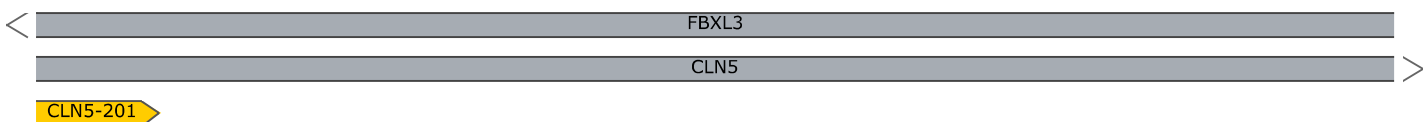
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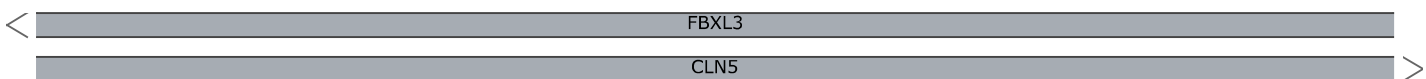
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14,535



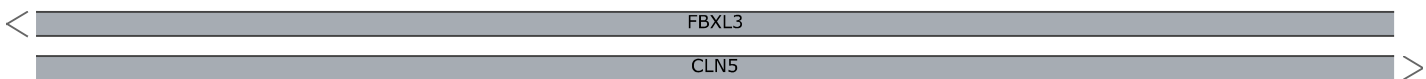
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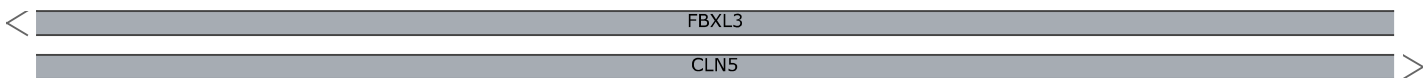
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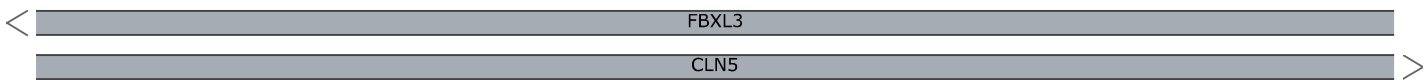
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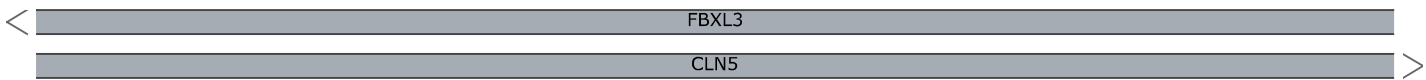
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14,875



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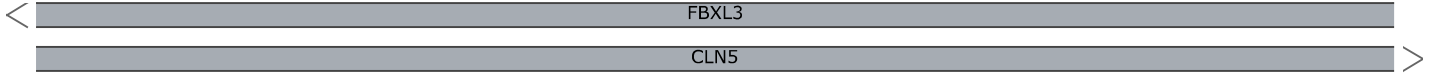
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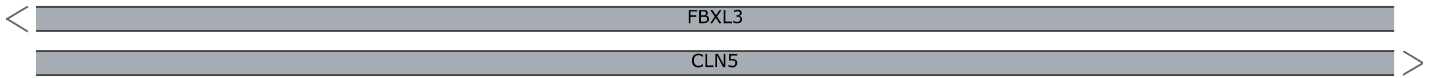
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15,895



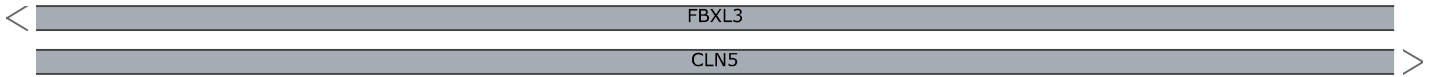
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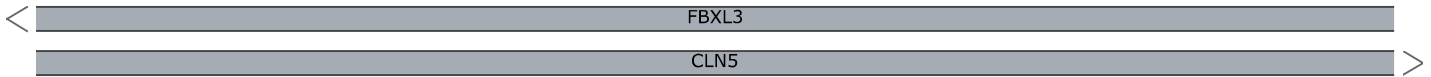
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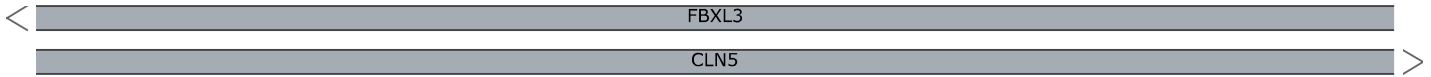
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16,150



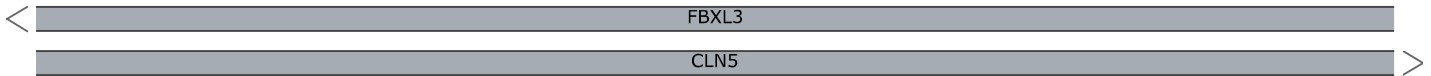
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16,235



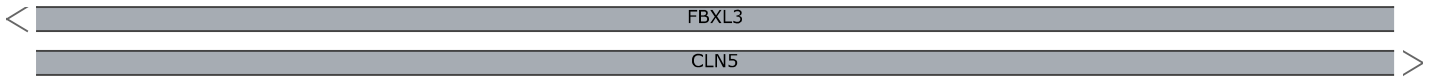
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16,320



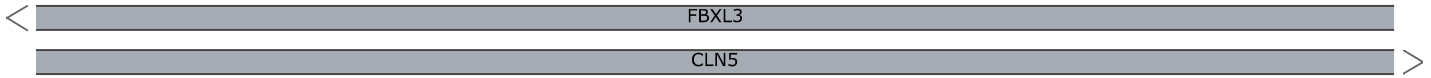
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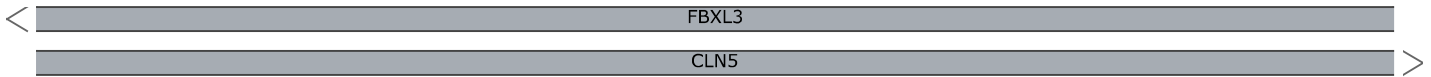
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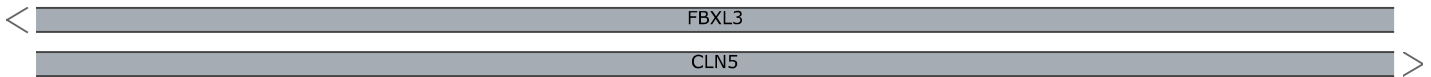
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16,575



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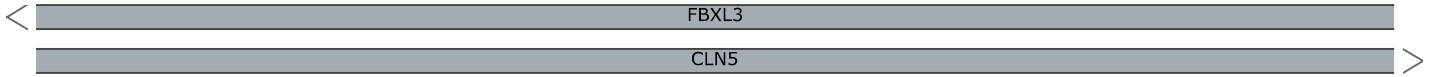






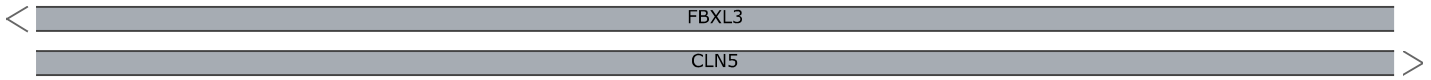
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20,145



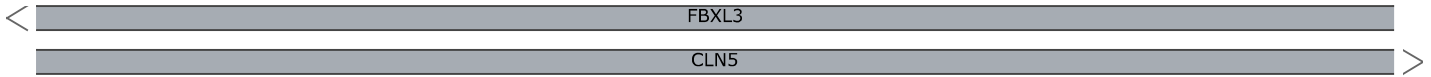
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20,230



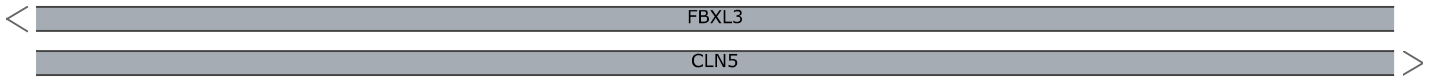
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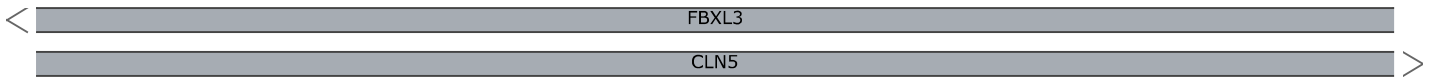
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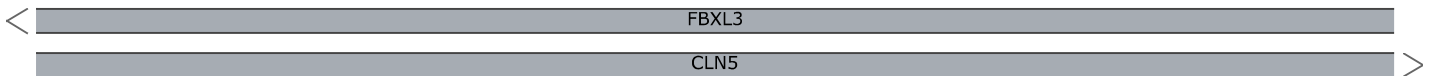
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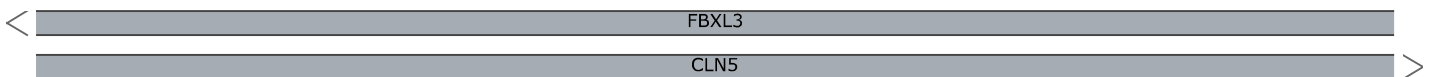
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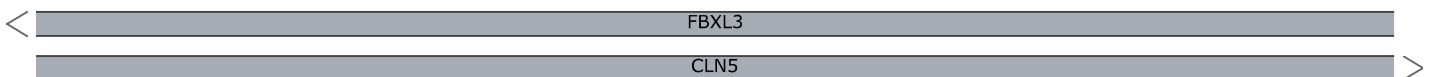
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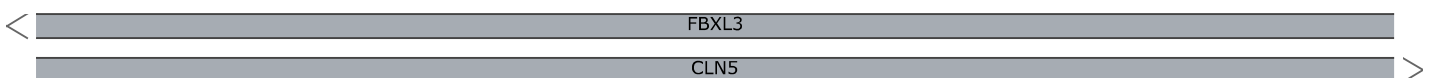
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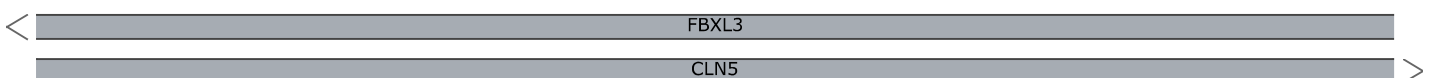
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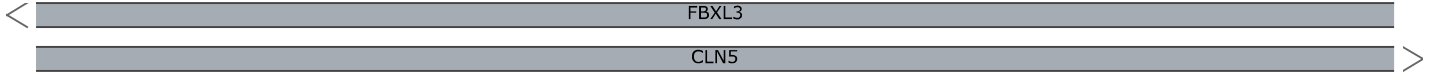
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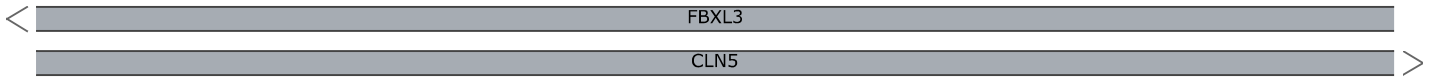
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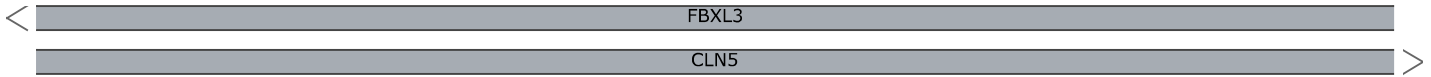
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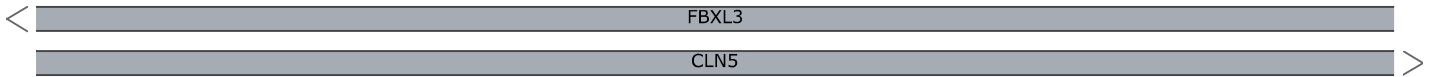
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21,165



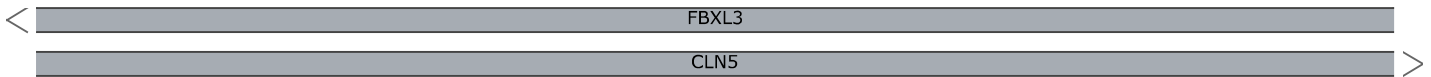
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21,250



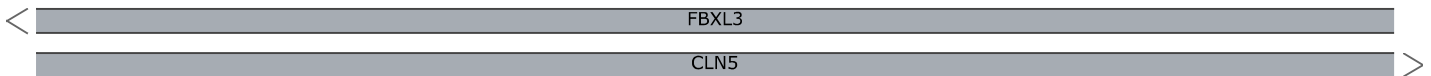
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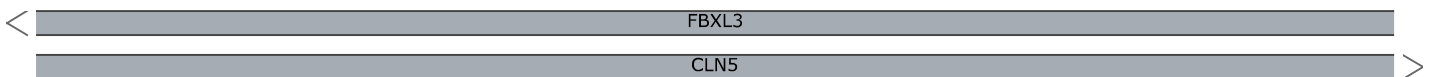
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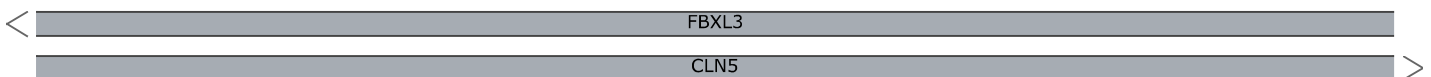
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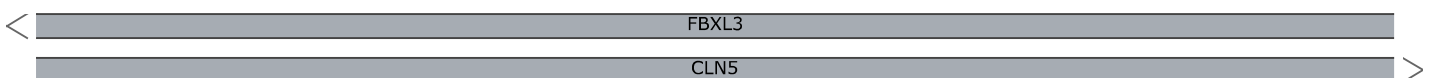
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21,590



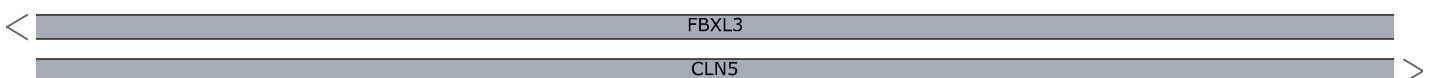
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21,675



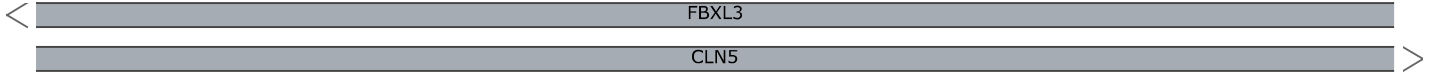
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21,760



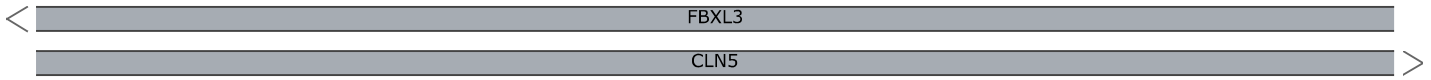
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21,845



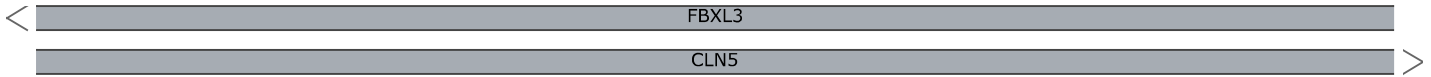
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21,930



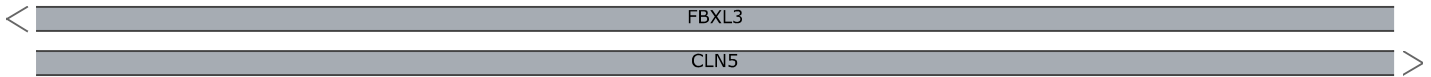
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22,015



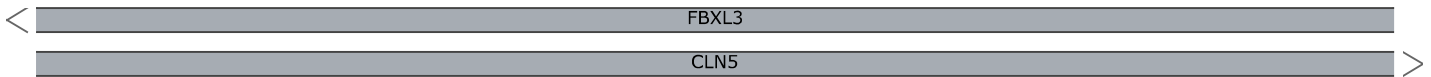
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22,100



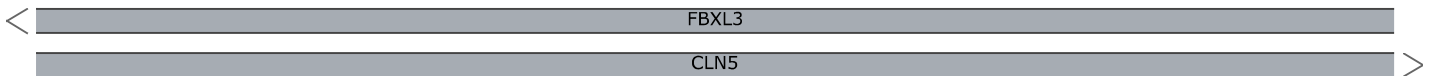
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22,185



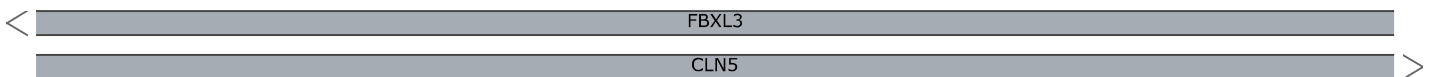
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22,270



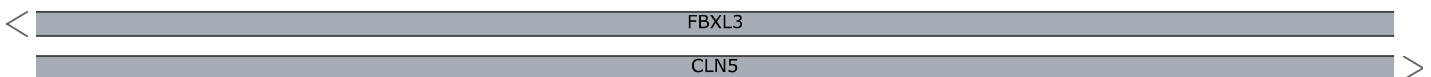
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22,355



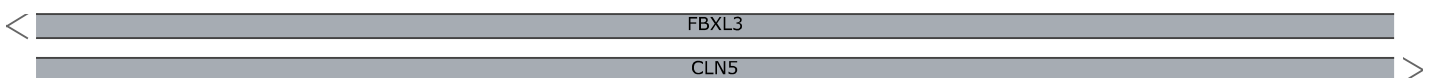
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22,440



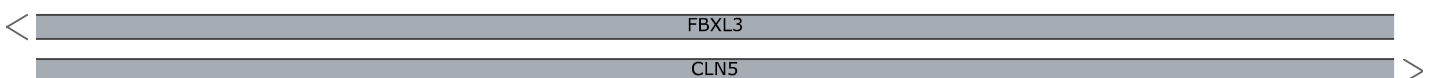
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22,525



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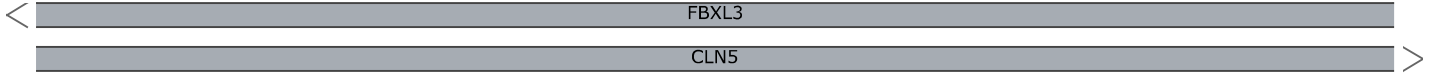
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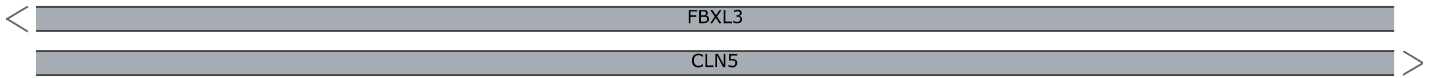
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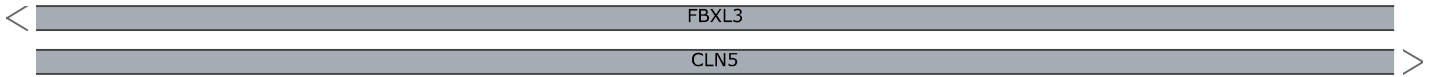
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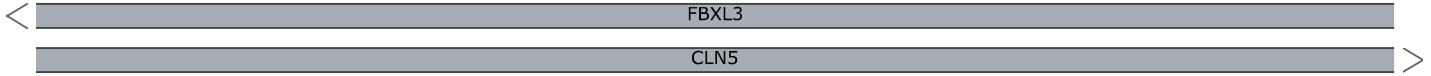
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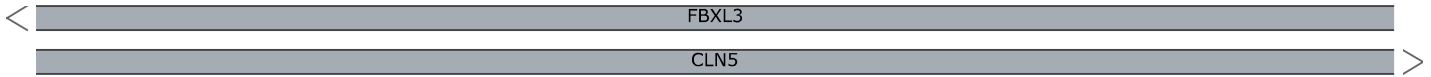
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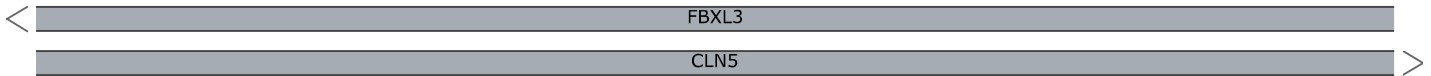
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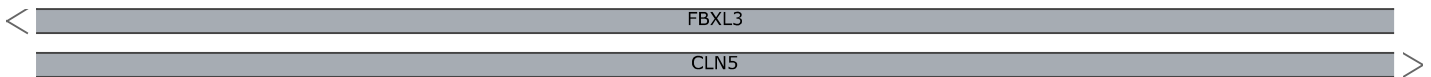
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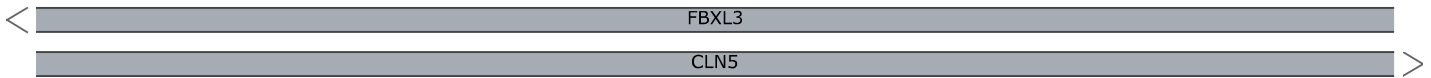
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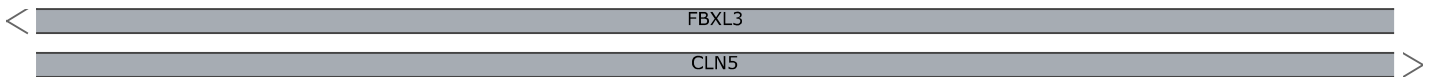
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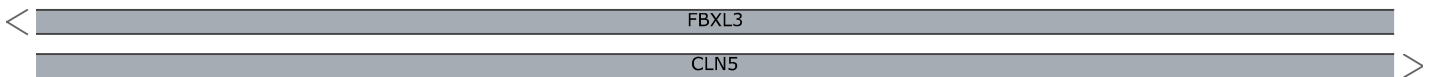
23,375

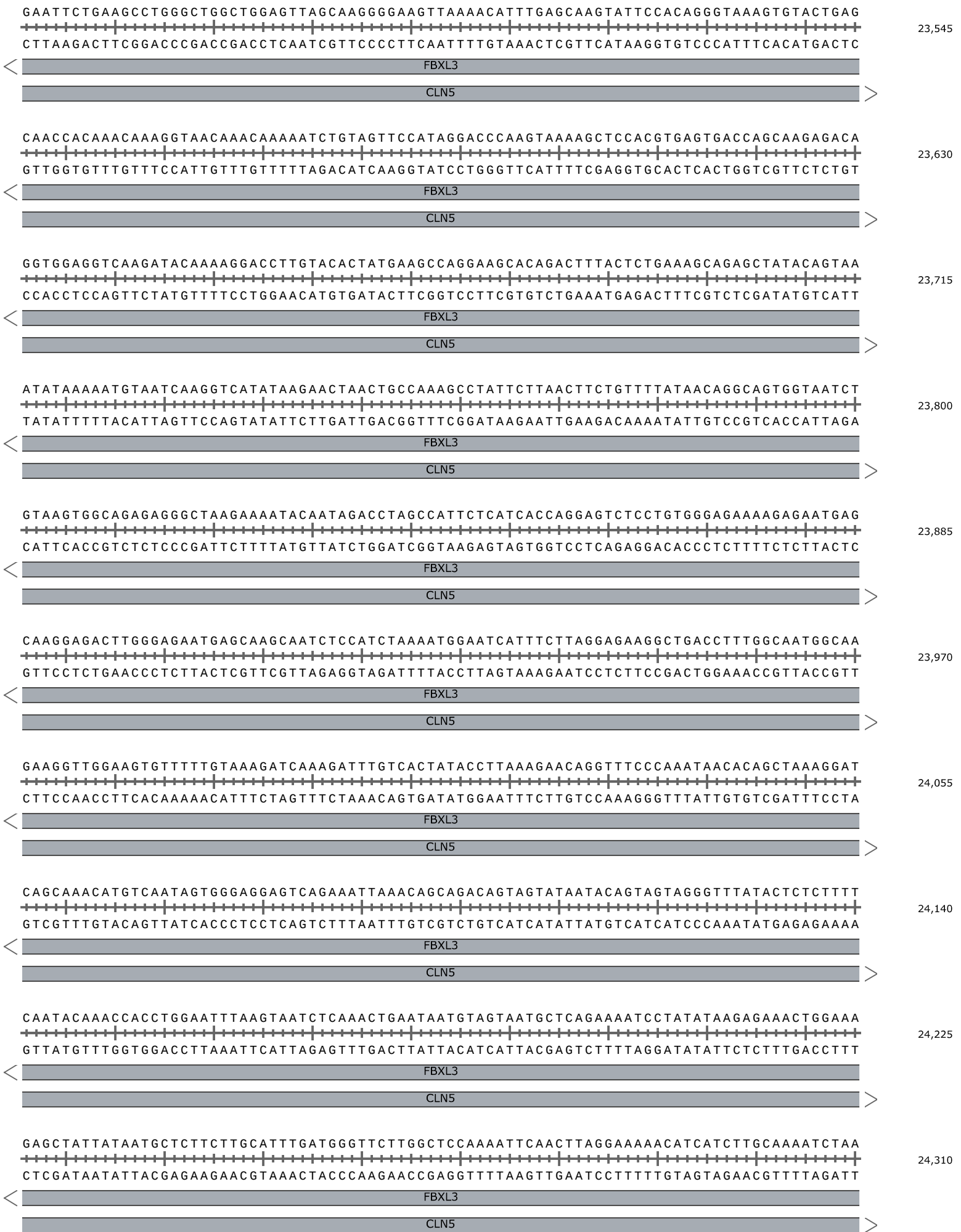


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23,460

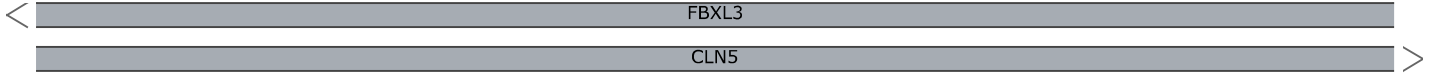






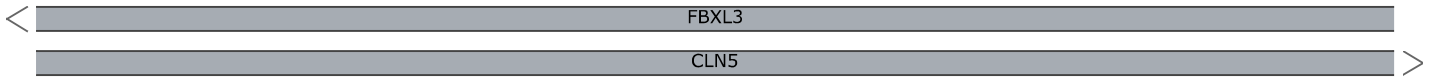
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25,245



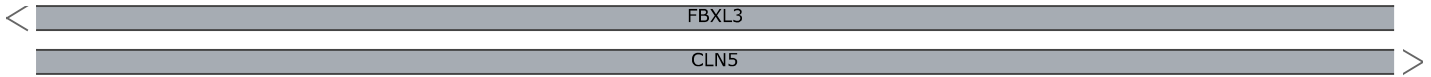
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25,330



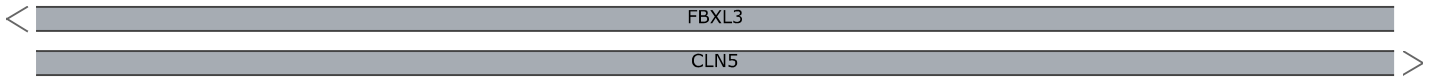
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25,415



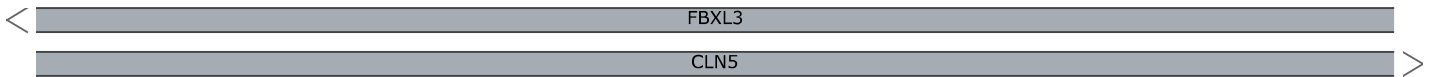
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25,500



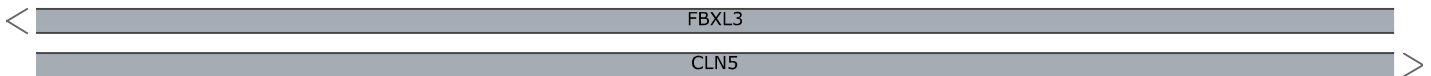
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25,585



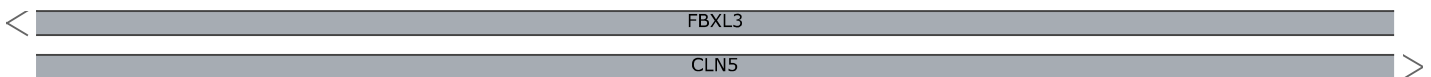
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25,670



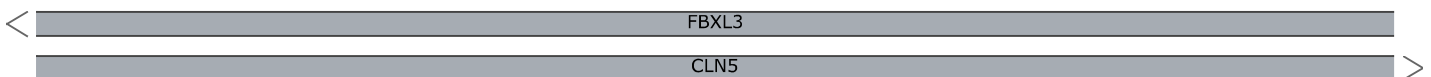
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25,755



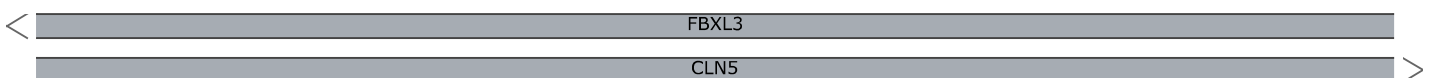
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25,840



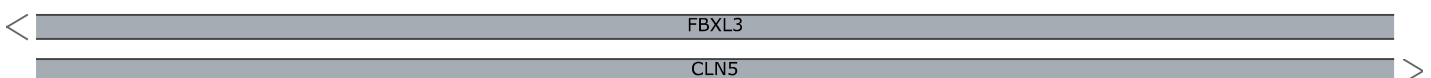
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25,925



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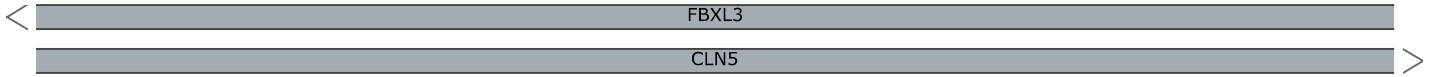
26,010





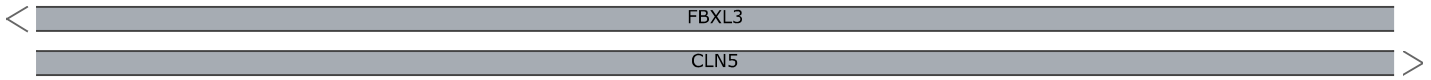
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26,945



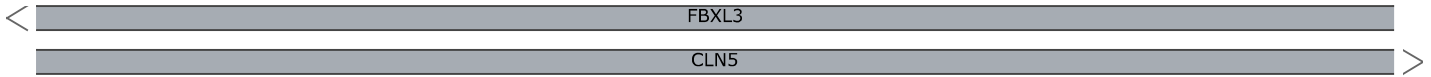
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27,030



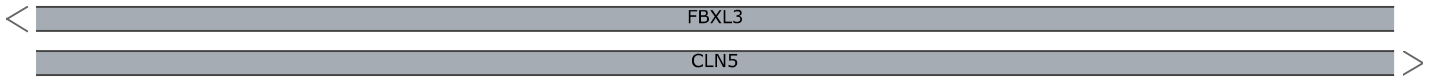
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27,115



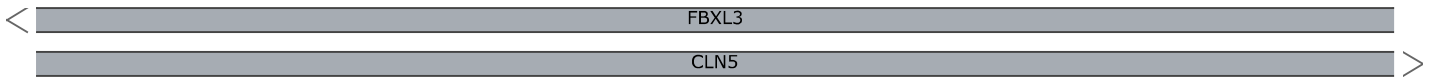
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27,200



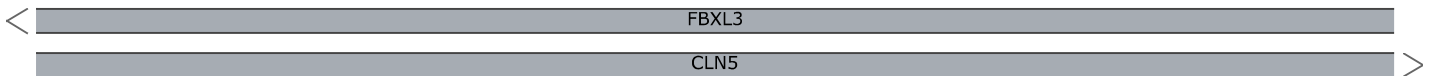
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27,285



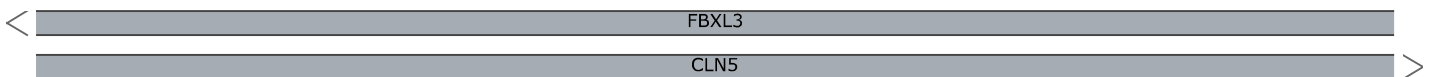
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27,370



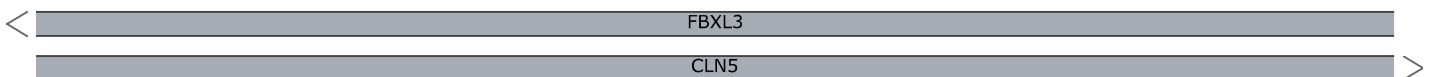
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27,455



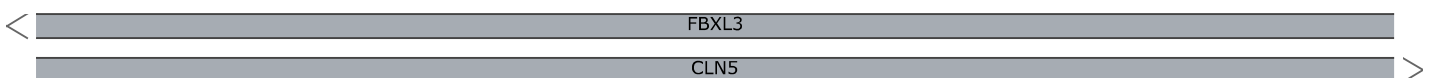
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27,540



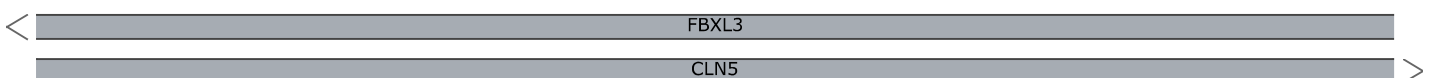
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27,625



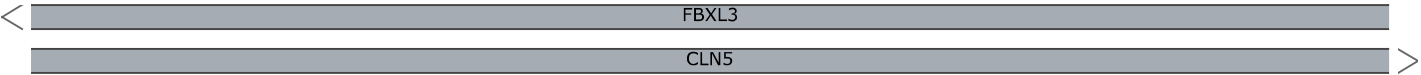
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27,710



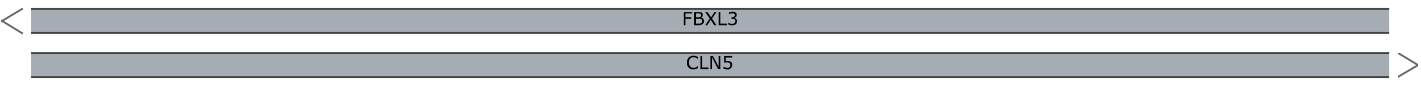
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27,795



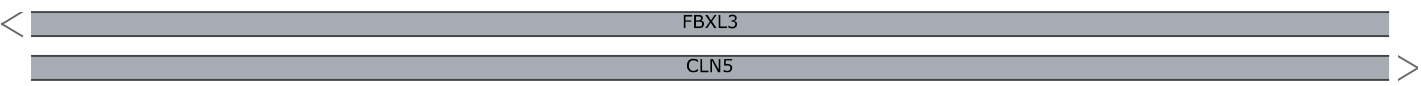
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27,880



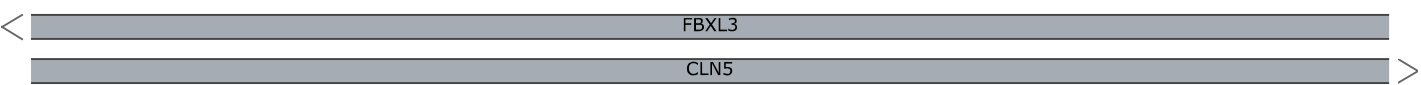
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27,965



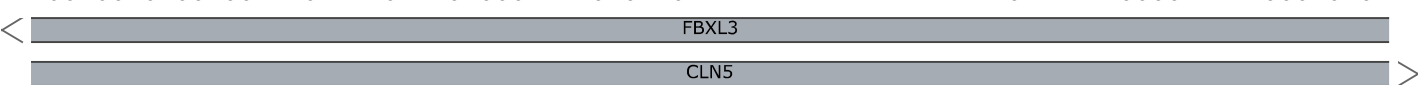
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28,050



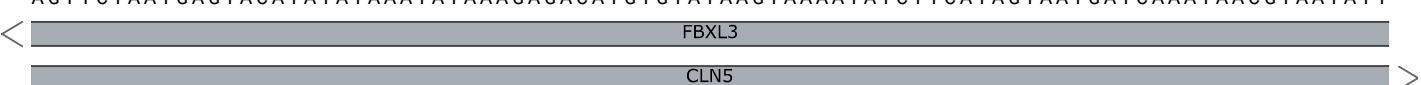
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28,135



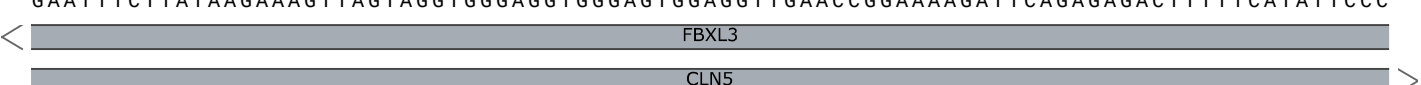
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28,220



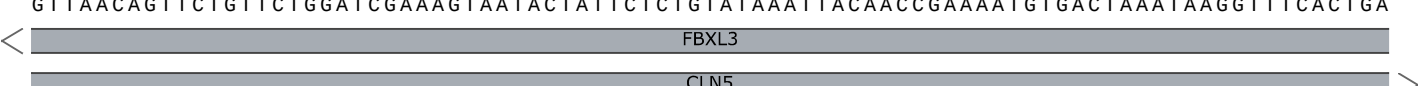
CTTAAAGAATATTCTTTCAATCATCCACCCTCCACCCTCACCTCCAACCTTGGCCTTTTCTAAGTCTCTCTGAAAAAGTATAAGGG
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28,305



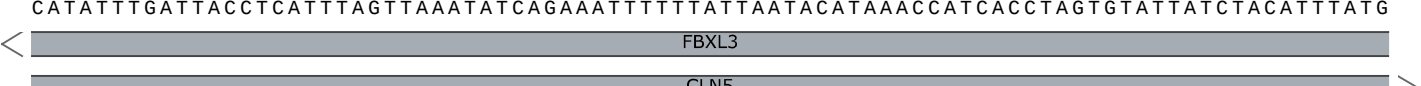
CAATTGTCAAGACAAGACCTAGCTTTTCATTATGATAAGAGACATATTTAATGTTGGCTTTTACACTGATTTATTCCAAAAGTGACT
GTTAACAGTTCTGTTCTGGATCGAAAGTAATACTATTCTCTGTATAAATTACAACCGAAAATGTGACTAAATAAGGTTTCACTGA

28,390



GTATAAACTAATGGAGTAAATCAATTTATAGTCTTTAAAAAATAATTATGTATTTGGTAGTGGATCACATAATAGATGTAAATAC
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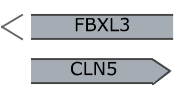
28,475



AGTGTCTAT 3'

TCACAGATA 5'

28,484



| Feature | Location | Size | Type |
|-----------------------|---|------------|-----------------|
| ✓ CLN5 | 1 .. 28,484 | 28,484 bp | gene |
| /note | = gene ENSG00000102805 Protein coding | | |
| CLN5-208 | 1 .. 14,458 | 14,458 bp | prim_transcript |
| /note | = primary transcript ENST00000636183 | | |
| CLN5-216 | 1385 .. 11,818 | 10,434 bp | prim_transcript |
| /note | = primary transcript ENST00000636780 | | |
| CLN5-202 | 1400 .. 7204 | 5805 bp | prim_transcript |
| /note | = primary transcript ENST00000485938 | | |
| | 1419 .. 138,930 | 137,512 bp | gene |
| /note | = gene ENSG00000283208 Protein coding | | |
| | 1419 .. 87,366 | 85,948 bp | prim_transcript |
| /note | = primary transcript ENST00000638147 Protein coding | | |
| CLN5-219 | 1419 .. 9317 | 7899 bp | prim_transcript |
| /note | = primary transcript ENST00000637537 | | |
| ✓ CLN5-201 | 1422 .. 14,458 | 13,037 bp | prim_transcript |
| /note | = primary transcript ENST00000377453 | | |
| CLN5-218 | 1428 .. 26,472 | 25,045 bp | prim_transcript |
| /note | = primary transcript ENST00000637397 | | |
| CLN5-207 | 1430 .. 5440 | 4011 bp | prim_transcript |
| /note | = primary transcript ENST00000635989 | | |
| CLN5-203 | 1432 .. 11,686 | 10,255 bp | prim_transcript |
| /note | = primary transcript ENST00000616833 | | |
| CLN5-211 | 1437 .. 28,484 | 27,048 bp | prim_transcript |
| /note | = primary transcript ENST00000636525 | | |
| CLN5-215 | 1439 .. 27,707 | 26,269 bp | prim_transcript |
| /note | = primary transcript ENST00000636767 | | |
| CLN5-205 | 1439 .. 20,309 | 18,871 bp | prim_transcript |
| /note | = primary transcript ENST00000635905 Retained intron | | |
| CLN5-211 | 1440 .. 26,486 | 25,047 bp | CDS |
| ▶ 5 segments = 813 bp | | | |
| /note | = coding sequence ENSP00000490078 | | |
| /translation | = MAQEVDTAQQGAEMRRGAGAARGRASWCWALALLWLAVVPGWSRVSGIPSRRHWPVPHYK,,RFDFRPKDPYQCQAKYTFCTGSPIPVME GDDDIIEVFRLQAPVWEFKYGDLLGHL,,KIMHDAIGFRSTLTGKNYTMWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWK ENGLTVQVATIS,,GFHHVGGQDSIELRTSSDPPILASQSAGITDVSHCTRPTIRILPQRGTYLYL,,LWTKTFLCLSLQFSWDFQNIATPYFNLL 248 amino acids = 30.7 kDa | | |
| CLN5-215 | 1440 .. 26,087 | 24,648 bp | CDS |
| ▶ 5 segments = 747 bp | | | |
| /note | = coding sequence ENSP00000489855 | | |
| /translation | = MAQEVDTAQQGAEMRRGAGAARGRASWCWALALLWLAVVPGWSRVSGIPSRRHWPVPHYK,,RFDFRPKDPYQCQAKYTFCTGSPIPVME GDDDIIEVFRLQAPVWEFKYGDLLGHL,,KIMHDAIGFRSTLTGKNYTMWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWK ENGLTVQVATIS,,GFHHVGGQDSIELRTSSDPPILASQSAGITDVSHCTRPTIRILPQRGTYLYL,,RWVLLCCPG* 248 amino acids = 28.0 kDa | | |
| CLN5-218 | 1440 .. 22,246 | 20,807 bp | CDS |
| ▶ 5 segments = 822 bp | | | |
| /note | = coding sequence ENSP00000490422 | | |
| /translation | = MAQEVDTAQQGAEMRRGAGAARGRASWCWALALLWLAVVPGWSRVSGIPSRRHWPVPHYK,,RFDFRPKDPYQCQAKYTFCTGSPIPVME GDDDIIEVFRLQAPVWEFKYGDLLGHL,,KIMHDAIGFRSTLTGKNYTMWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWK ENGLTVQVATIS,,GFHHVGGQDSIELRTSSDPPILASQSAGITDVSHCTRPTIRILPQRGTYLYL,,SLALLPGWSTVVRRLTATSA SRIQTIF 270 amino acids = 30.7 kDa | | |

| Feature | Location | Size | Type |
|--------------------------------------|--|-----------|-----------------|
| ✓ CLN5-201 | 1440 .. 10,310 | 8871 bp | CDS |
| ▶ 4 segments = 1077 bp | | | |
| /note | = coding sequence ENSP00000366673 | | |
| /translation | = MAQEVDTAQGAEMRRGAGAARGRASWCWALALLWLAVVPGWSRVSGIPSRRHWPVPYK,,RFDFRPKDPYCYQAKYTFCTGSPIPVME GDDDIIEVFRLQAPVWEFKYGDLLGHL,,KIMHDAIGFRSTLTGKNYTMWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWK ENGLTVQVATIS,,GNMFNQMAKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETNYTRIFLYSGE PTYLGNETSVMFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLQIFDAVIVHKQFYLFYNFEYWFLPMKFPFIKITYEEIPLIRNKTLISGL* 358 amino acids = 41.5 kDa | | |
| CLN5-208 | 1440 .. 10,310 | 8871 bp | CDS |
| ▶ 4 segments = 1077 bp | | | |
| /note | = coding sequence ENSP00000490181 | | |
| /translation | = MAQEVDTAQGAEMRRGAGAARGRASWCWALALLWLAVVPGWSRVSGIPSRRHWPVPYK,,RFDFRPKDPYCYQAKYTFCTGSPIPVME GDDDIIEVFRLQAPVWEFKYGDLLGHL,,KIMHDAIGFRSTLTGKNYTMWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWK ENGLTVQVATIS,,GNMFNQMAKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETNYTRIFLYSGE PTYLGNETSVMFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLQIFDAVIVHKQFYLFYNFEYWFLPMKFPFIKITYEEIPLIRNKTLISGL* 358 amino acids = 41.5 kDa | | |
| CLN5-203 | 1440 .. 9329 | 7890 bp | CDS |
| ▶ 4 segments = 624 bp | | | |
| /note | = coding sequence ENSP00000479547 | | |
| /translation | = MAQEVDTAQGAEMRRGAGAARGRASWCWALALLWLAVVPGWSRVSGIPSRRHWPVPYK,,RFDFRPKDPYCYQAKYTFCTGSPIPVME GDDDIIEVFRLQAPVWEFKYGDLLGHL,,KIMHDAIGFRSTLTGKNYTMWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWK ENGLTVQVATIS,,GNMFNQMAKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETNYTRIFLYSGE PTYLGNETSVMFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLQIFDAVIVHKQFYLFYNFEYWFLPMKFPFIKITYEEIPLIRNKTLISGL* 358 amino acids = 41.5 kDa | | |
| CLN5-216 | 1440 .. 7412 | 5973 bp | CDS |
| ▶ 4 segments = 594 bp | | | |
| /note | = coding sequence ENSP00000489809 | | |
| /translation | = MAQEVDTAQGAEMRRGAGAARGRASWCWALALLWLAVVPGWSRVSGIPSRRHWPVPYK,,RFDFRPKDPYCYQAKYTFCTGSPIPVME GDDDIIEVFRLQAPVWEFKYGDLLGHL,,KIMHDAIGFRSTLTGKNYTMWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWK ENGLTVQVATIS,,GNMFNQMAKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETNYTRIFLYSGE PTYLGNETSVMFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLQIFDAVIVHKQFYLFYNFEYWFLPMKFPFIKITYEEIPLIRNKTLISGL* 358 amino acids = 41.5 kDa | | |
| CLN5-219 | 1440 .. 7412 | 5973 bp | CDS |
| ▶ 4 segments = 594 bp | | | |
| /note | = coding sequence ENSP00000489711 | | |
| /translation | = MAQEVDTAQGAEMRRGAGAARGRASWCWALALLWLAVVPGWSRVSGIPSRRHWPVPYK,,RFDFRPKDPYCYQAKYTFCTGSPIPVME GDDDIIEVFRLQAPVWEFKYGDLLGHL,,KIMHDAIGFRSTLTGKNYTMWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWK ENGLTVQVATIS,,GNMFNQMAKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETNYTRIFLYSGE PTYLGNETSVMFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLQIFDAVIVHKQFYLFYNFEYWFLPMKFPFIKITYEEIPLIRNKTLISGL* 358 amino acids = 41.5 kDa | | |
| CLN5-202 | 1440 .. 5479 | 4040 bp | CDS |
| ▶ 3 segments = 576 bp | | | |
| /note | = coding sequence ENSP00000482959 | | |
| /translation | = MAQEVDTAQGAEMRRGAGAARGRASWCWALALLWLAVVPGWSRVSGIPSRRHWPVPYK,,RFDFRPKDPYCYQAKYTFCTGSPIPVME GDDDIIEVFRLQAPVWEFKYGDLLGHL,,KIMHDAIGFRSTLTGKNYTMWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWK ENGLTVQVATIS,,GNMFNQMAKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETNYTRIFLYSGE PTYLGNETSVMFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLQIFDAVIVHKQFYLFYNFEYWFLPMKFPFIKITYEEIPLIRNKTLISGL* 358 amino acids = 41.5 kDa | | |
| ✓ Donor Template WT -> SNV | 1485 .. 1549 | 65 bp | misc_feature |
| CLN5-206 | 1501 .. 11,752 | 10,252 bp | prim_transcript |
| /note | = primary transcript ENST00000635915 Nonsense mediated decay | | |
| ✓ Protospacer Sequence | 1502 .. 1521 | 20 bp | misc_feature |
| ✓ SNV | 1517 .. 1517 | 1 bp | misc_feature |
| /note | = WT = G SNV = A | | |
| ✓ PAM | 1522 .. 1524 | 3 bp | misc_feature |
| CLN5-209 | 1698 .. 4208 | 2511 bp | prim_transcript |
| /note | = primary transcript ENST00000636405 | | |
| CLN5-213 | 1726 .. 10,672 | 8947 bp | prim_transcript |
| /note | = primary transcript ENST00000636681 Nonsense mediated decay | | |
| CLN5-214 | 1914 .. 11,805 | 9892 bp | prim_transcript |
| /note | = primary transcript ENST00000636705 | | |

| Feature | Location | Size | Start | End | Type |
|-----------------------|--|------------|-------|-----|-----------------|
| CLN5-214 | 1914 .. 10,310 | 8397 bp | ■ | → | CDS |
| ▶ 4 segments = 913 bp | | | | | |
| /note | = coding sequence ENSP00000490937 | | | | |
| /translation | = WVQ,,AL*LPSKT*SLLSS*VYFLSNWLTPSYGG***H*SFSITSPSMGI*IWRPPGTL,,ENYA*CHWIQKYINWQELHNGMV*TFPTWQL YISPST*NGCPFLV*SRRCLLF*GN**CSLEGKWDISSSNYIR,,KHVQPNGKVGETGQ*NRNLL*DMECKSQPRKGGDMV*FLRLFQI CVKDL*QVG*IWSRVQEHRNQLYKNISLQWRTYLSGK*NICFWANRQKDSWFSHKILLPLQTTFAN*RISVESLANF*CSDCAQTVLFV 504 codons (27 internal stop codons) | | | | |
| FBXL3 | 1939 .. 36,536 | 34,598 bp | ■ | ← | gene |
| /note | = gene ENSG00000005812 Protein coding | | | | |
| FBXL3-206 | 1939 .. 24,922 | 22,984 bp | ■ | ← | prim_transcript |
| /note | = primary transcript ENST00000485797 | | | | |
| CLN5-210 | 3392 .. 9280 | 5889 bp | ■ | → | prim_transcript |
| /note | = primary transcript ENST00000636520 Retained intron | | | | |
| CLN5-212 | 4570 .. 5618 | 1049 bp | ■ | → | prim_transcript |
| /note | = primary transcript ENST00000636602 Retained intron | | | | |
| CLN5-217 | 4578 .. 11,770 | 7193 bp | ■ | → | prim_transcript |
| /note | = primary transcript ENST00000637278 Retained intron | | | | |
| | 5256 ..138,930 | 133,675 bp | ■ | → | prim_transcript |
| /note | = primary transcript ENST00000637192 Nonsense mediated decay | | | | |
| | 5295 .. 85,539 | 80,245 bp | ■ | → | prim_transcript |
| /note | = primary transcript ENST00000635838 Protein coding | | | | |
| | 5300 ..109,741 | 104,442 bp | ■ | → | prim_transcript |
| /note | = primary transcript ENST00000638101 Protein coding | | | | |
| FBXL3-205 | 8478 .. 28,027 | 19,550 bp | ■ | ← | prim_transcript |
| /note | = primary transcript ENST00000477982 | | | | |
| CLN5-204 | 9123 .. 9724 | 602 bp | ■ | → | prim_transcript |
| /note | = primary transcript ENST00000635761 | | | | |
| FBXL3-201 | 14,601 .. 36,500 | 21,900 bp | ■ | ← | prim_transcript |
| /note | = primary transcript ENST00000355619 Protein coding | | | | |
| FBXL3-202 | 16,906 .. 36,536 | 19,631 bp | ■ | ← | prim_transcript |
| /note | = primary transcript ENST00000417323 Protein coding | | | | |
| | 17,943 .. 86,519 | 68,577 bp | ■ | → | prim_transcript |
| /note | = primary transcript ENST00000461131 Retained intron | | | | |
| FBXL3-203 | 24,506 .. 28,085 | 3580 bp | ■ | ← | prim_transcript |
| /note | = primary transcript ENST00000470210 | | | | |
| FBXL3-204 | 24,852 .. 36,426 | 11,575 bp | ■ | ← | prim_transcript |
| /note | = primary transcript ENST00000472949 | | | | |

| Primer | Length |  | Binding Sites |  | Tm | Date Added |
|--------------------------------------|--------|---|---------------|---|------|--------------|
| ✓ PCR Forward | 20-mer | | 1228 .. 1247 |  | 56°C | Oct 16, 2022 |
| /sequence | = | GACCAAAGCACCTTCCTGGA 55% GC / 6071.0 Da | | | | |
| ✓ Sanger Sequencing | 20-mer | | 1228 .. 1247 |  | 56°C | Oct 16, 2022 |
| /sequence | = | GACCAAAGCACCTTCCTGGA 55% GC / 6071.0 Da | | | | |
| ✓ Donor Template WT -> SNV | 65-mer | | 1485 .. 1549 |  | 88°C | Oct 13, 2022 |
| /sequence | = | GGCGCGGGCGCGGCTCGGGGACGCGCTTCCTGATGCTGGGCCCTGGCGCTGCTTTGGCTCGCGGT 77% GC / 20,138.9 Da | | | | |
| ✓ gRNA Protospacer | 20-mer | | 1502 .. 1521 |  | 67°C | Oct 16, 2022 |
| /sequence | = | GGGACGCGCTTCCTGGTGCT 70% GC / 6141.0 Da | | | | |
| ✓ PCR Reverse | 19-mer | | 1654 .. 1672 |  | 58°C | Oct 16, 2022 |
| /sequence | = | CCCATCCCCCATCGTCAAC 63% GC / 5613.7 Da | | | | |