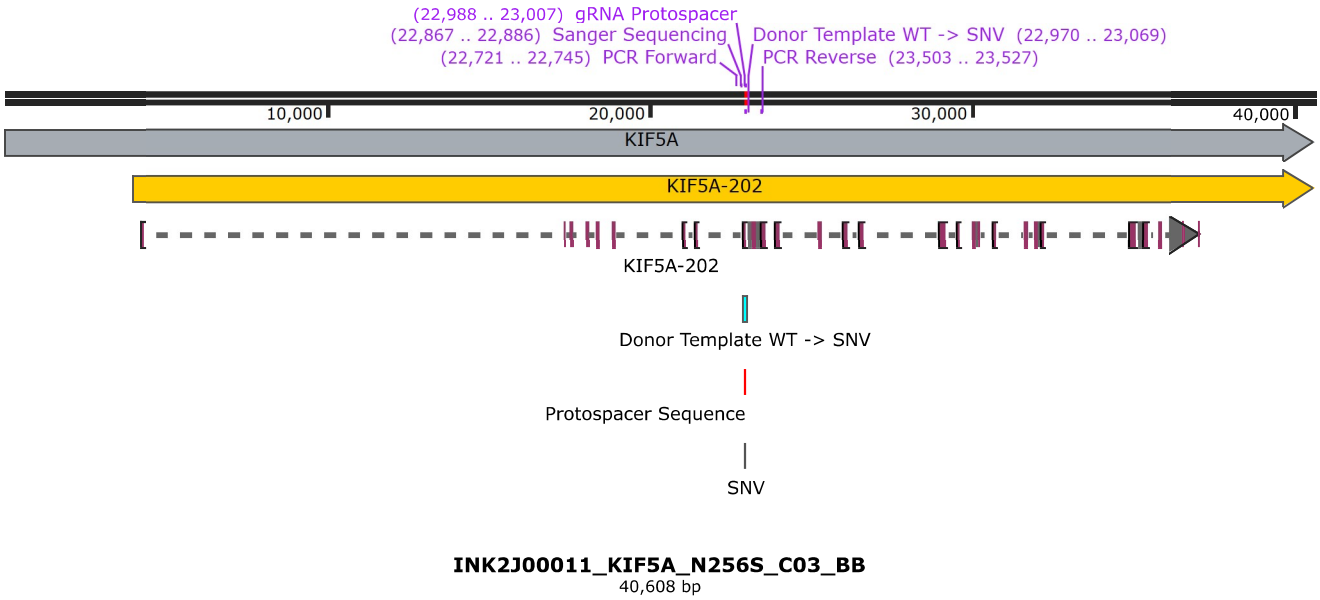

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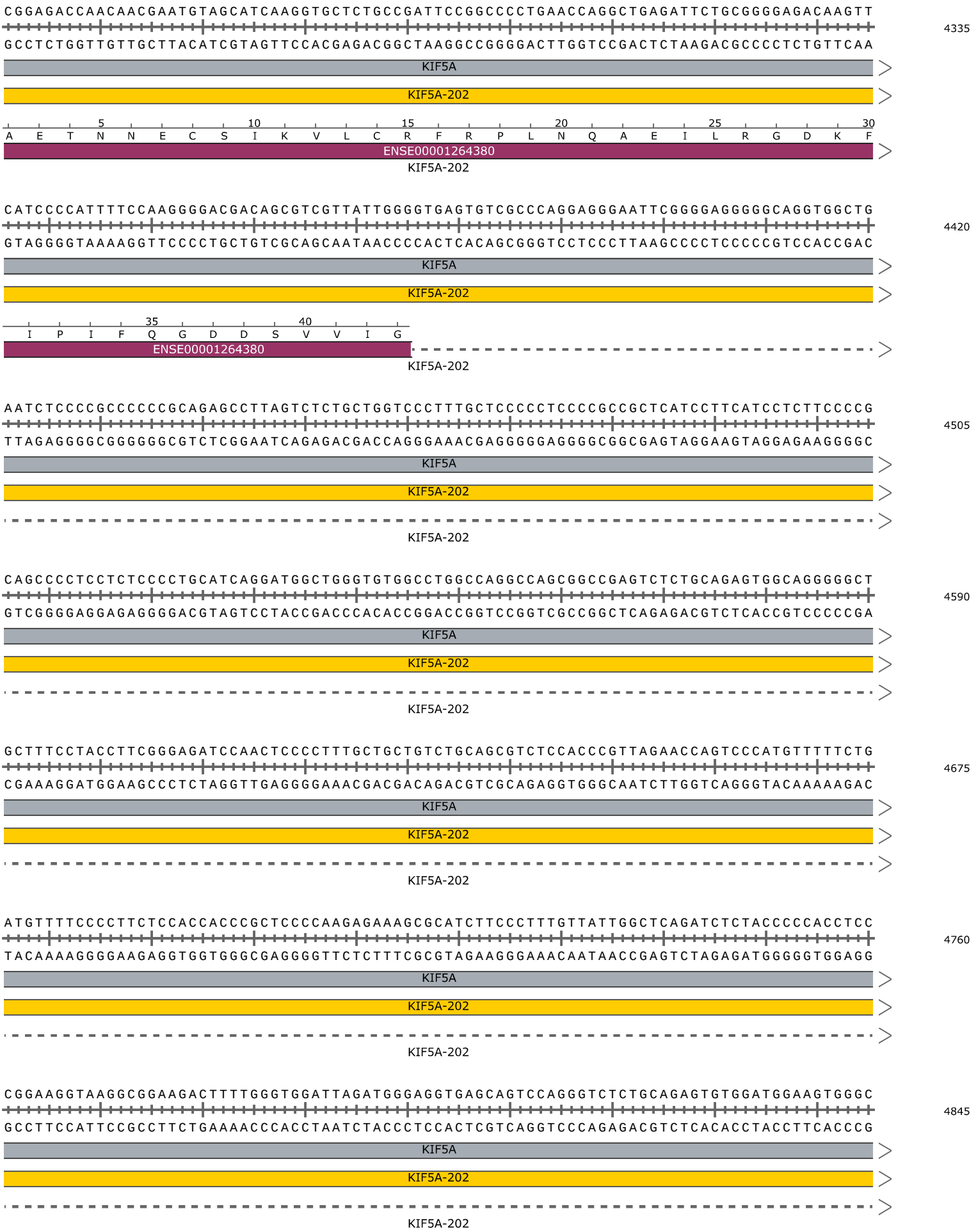
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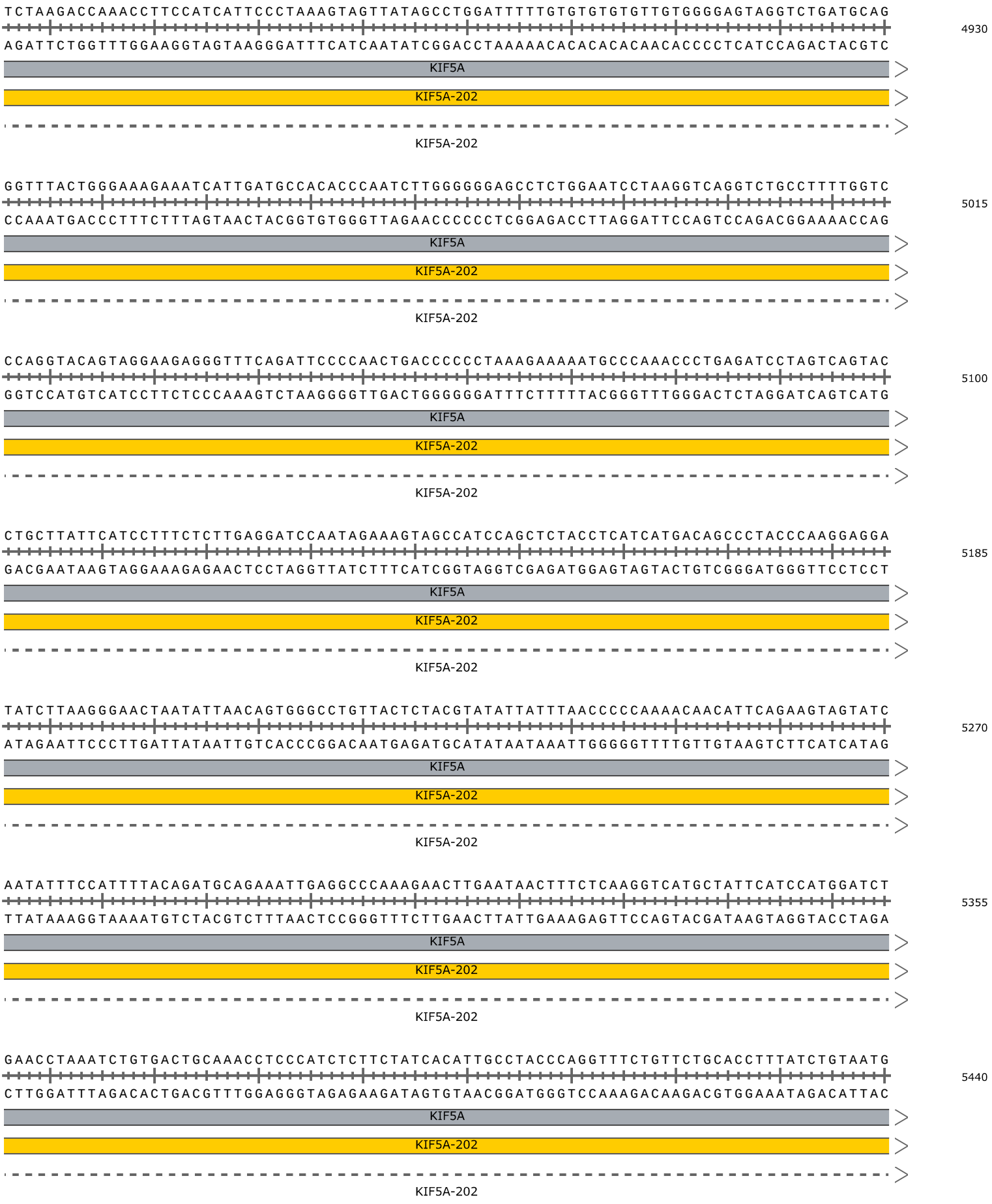
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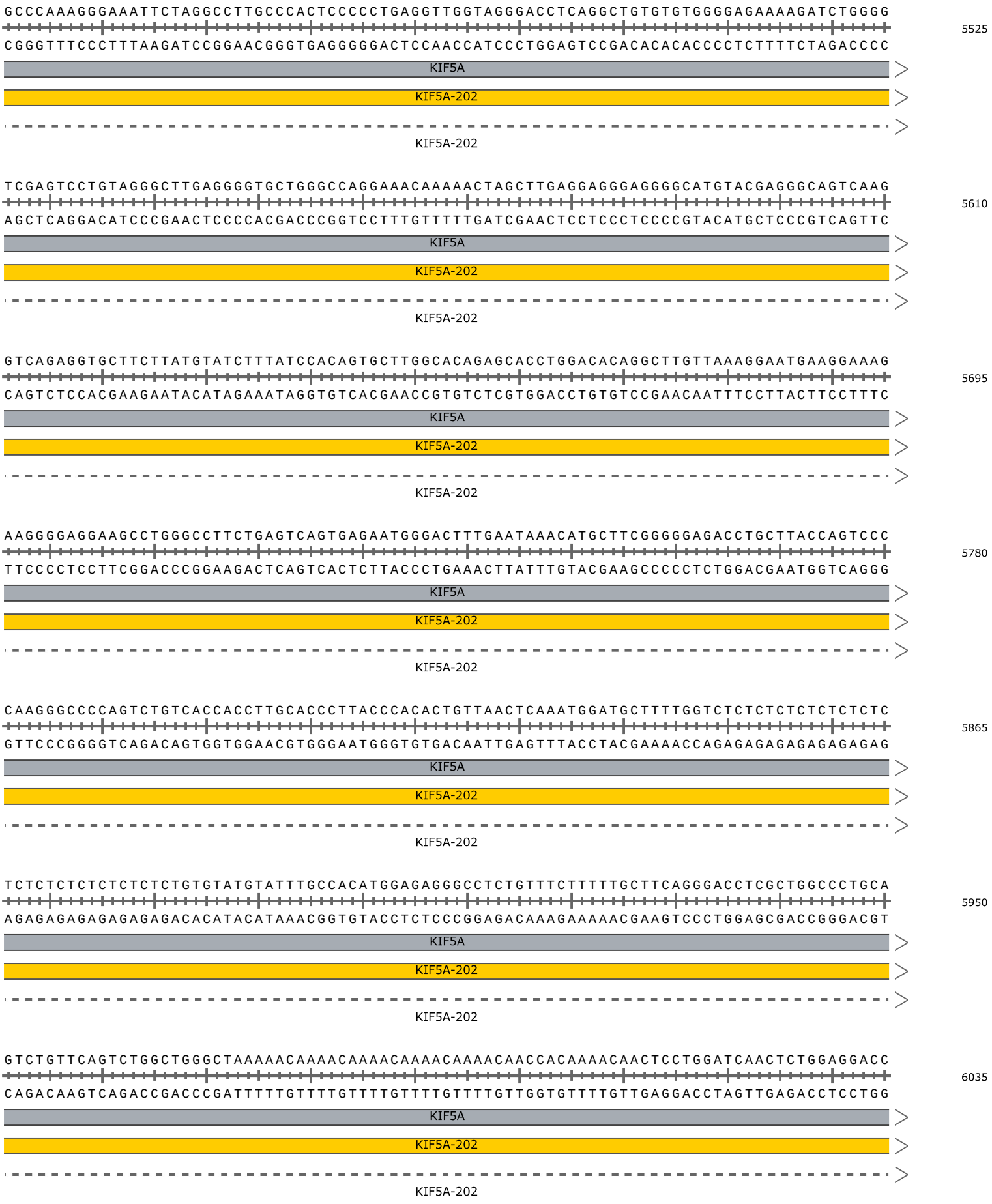
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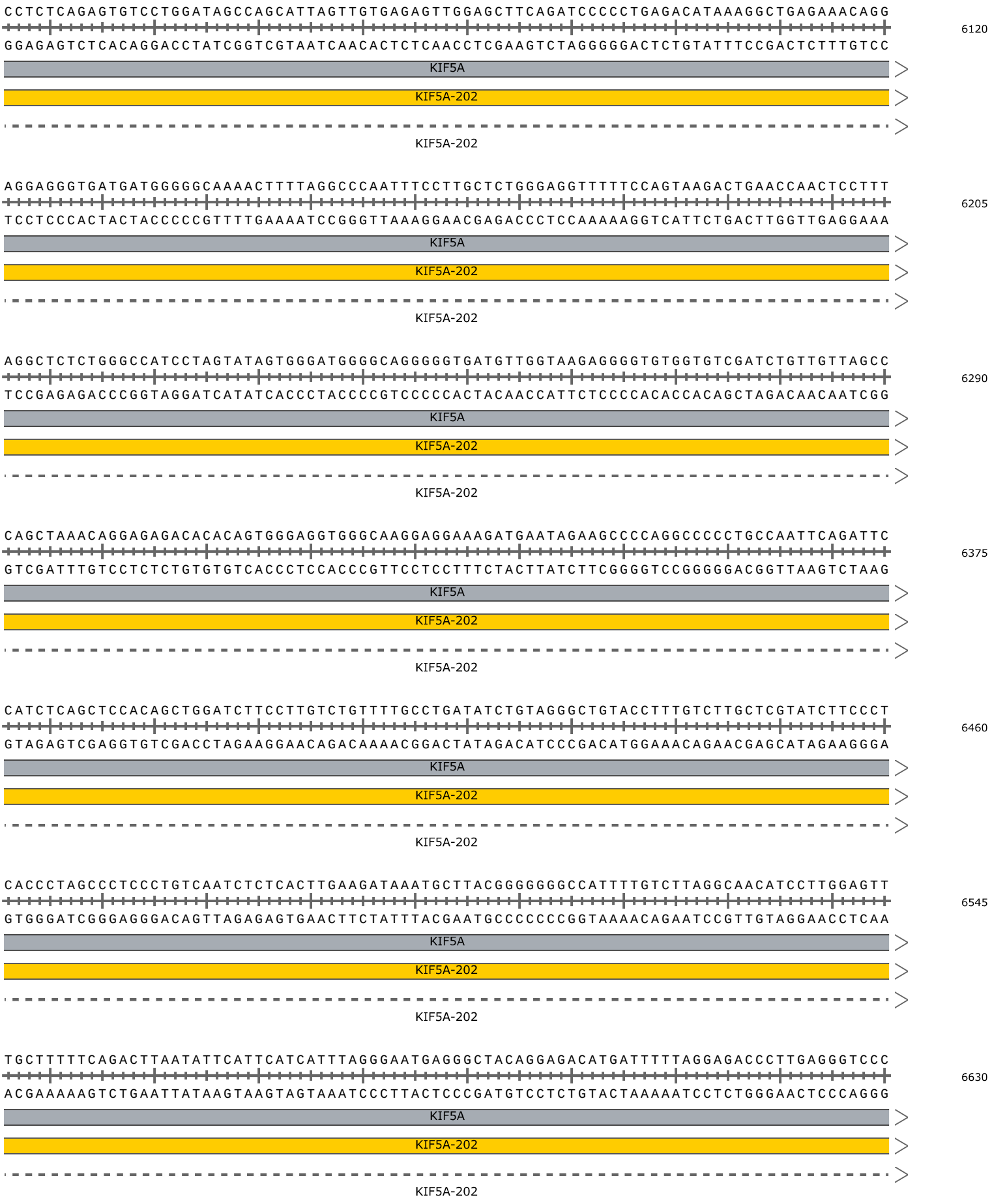
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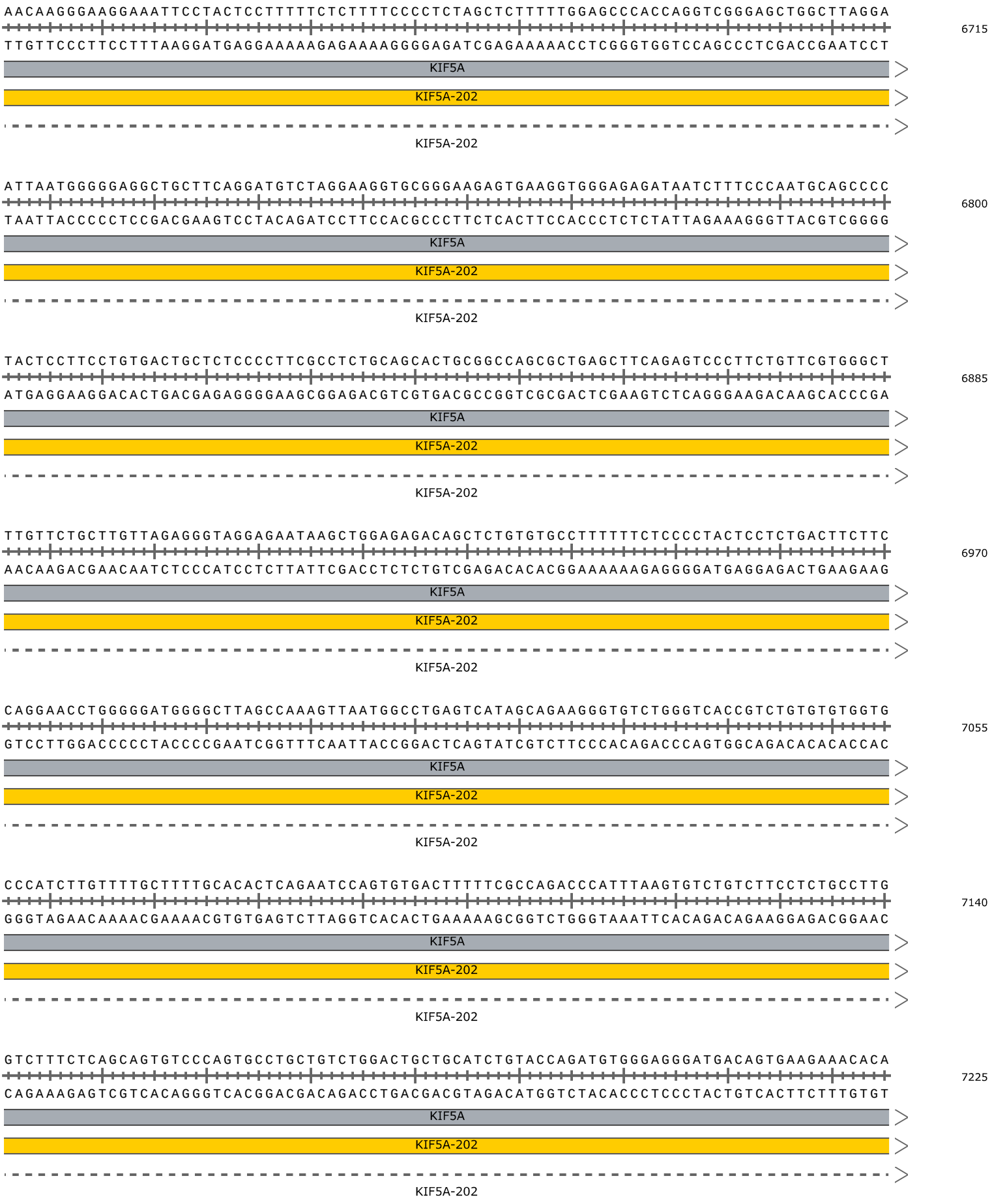
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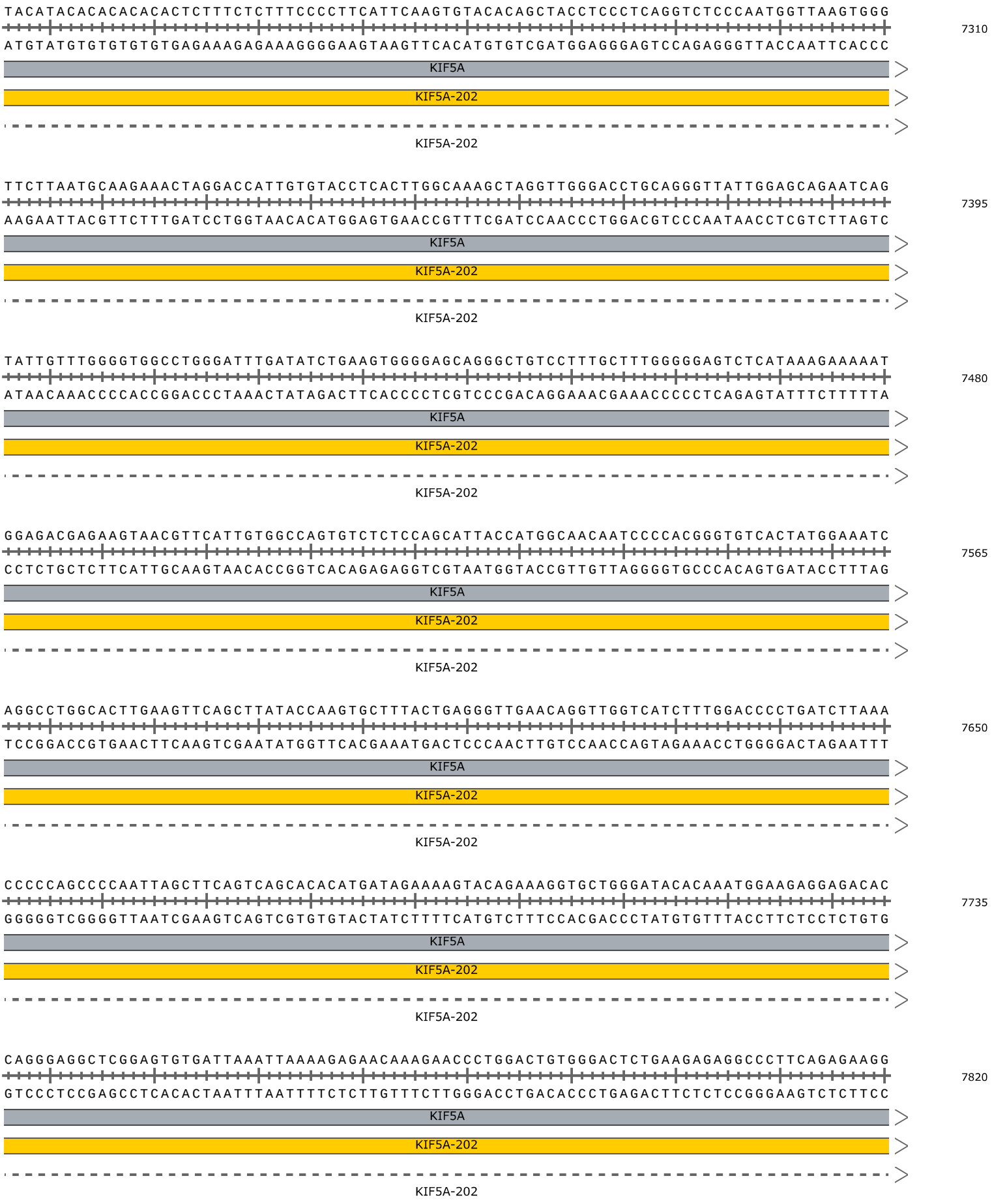
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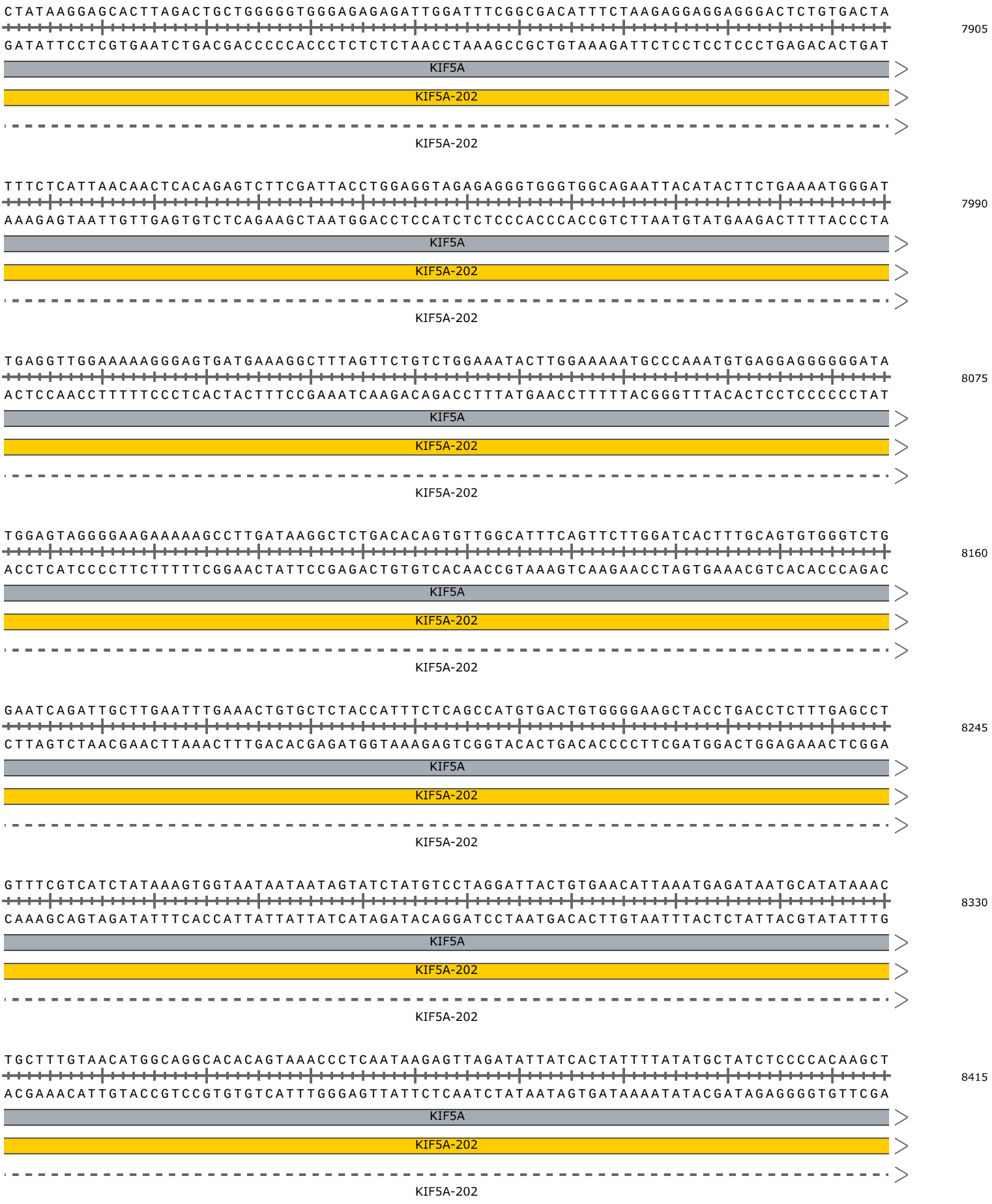
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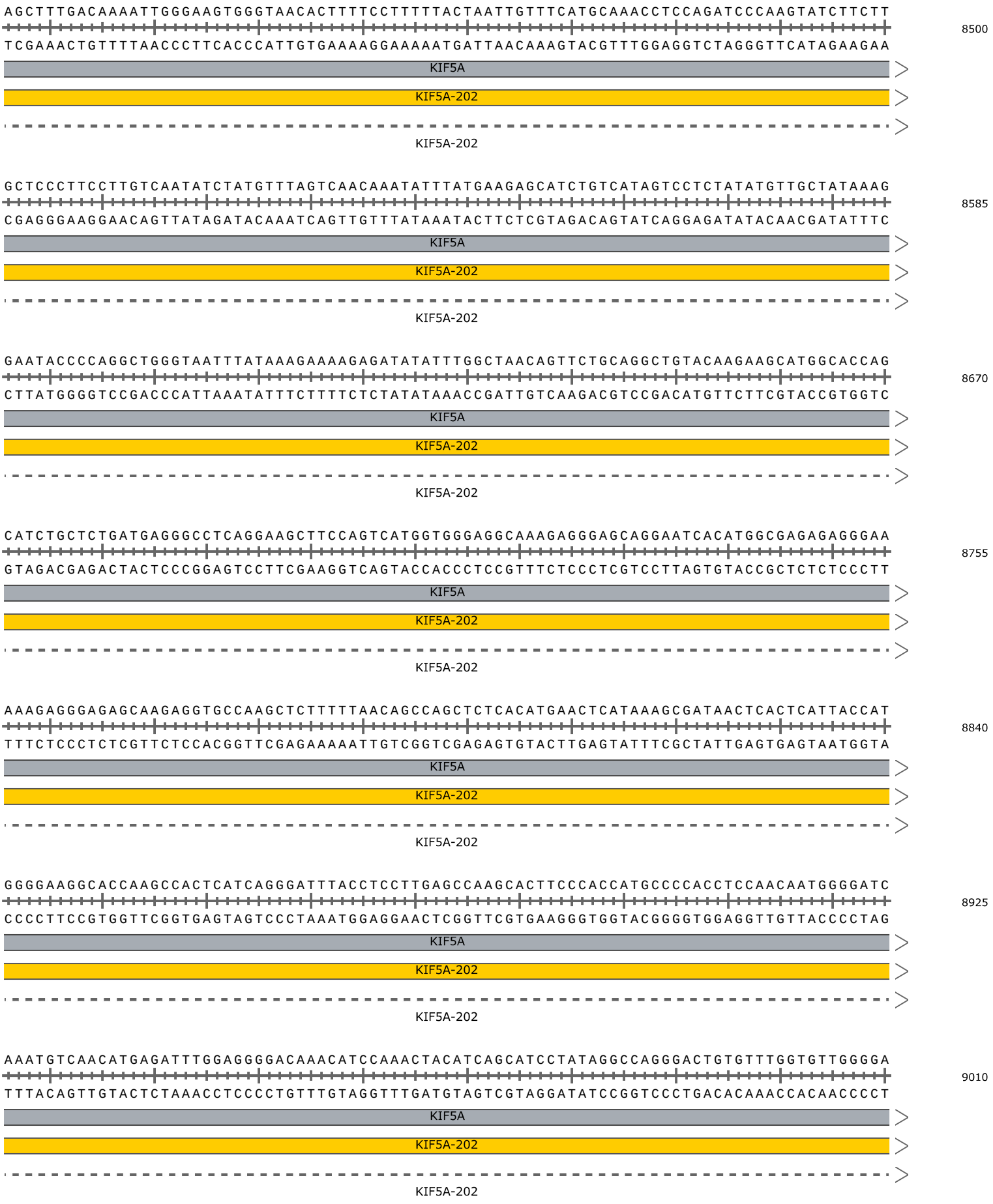
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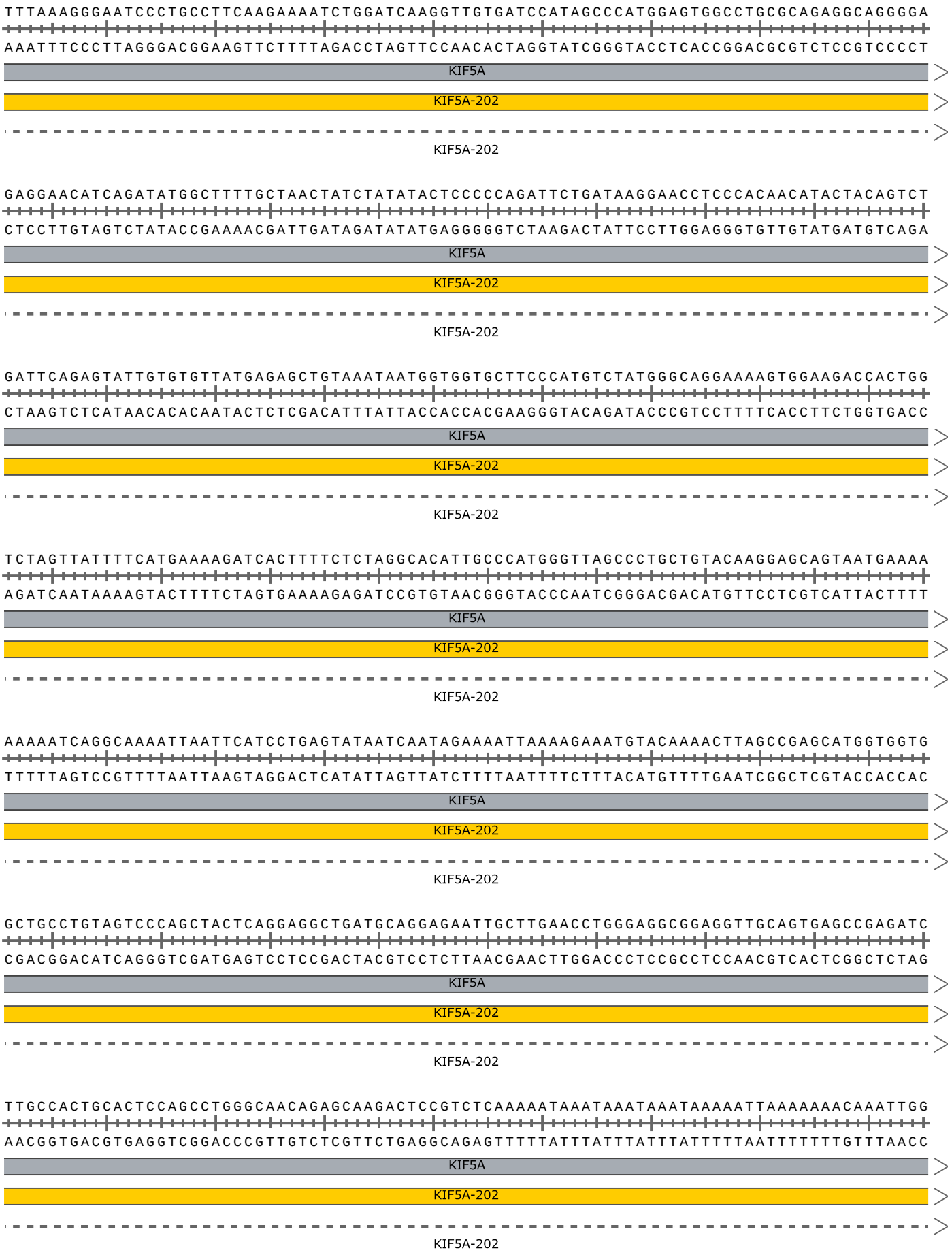
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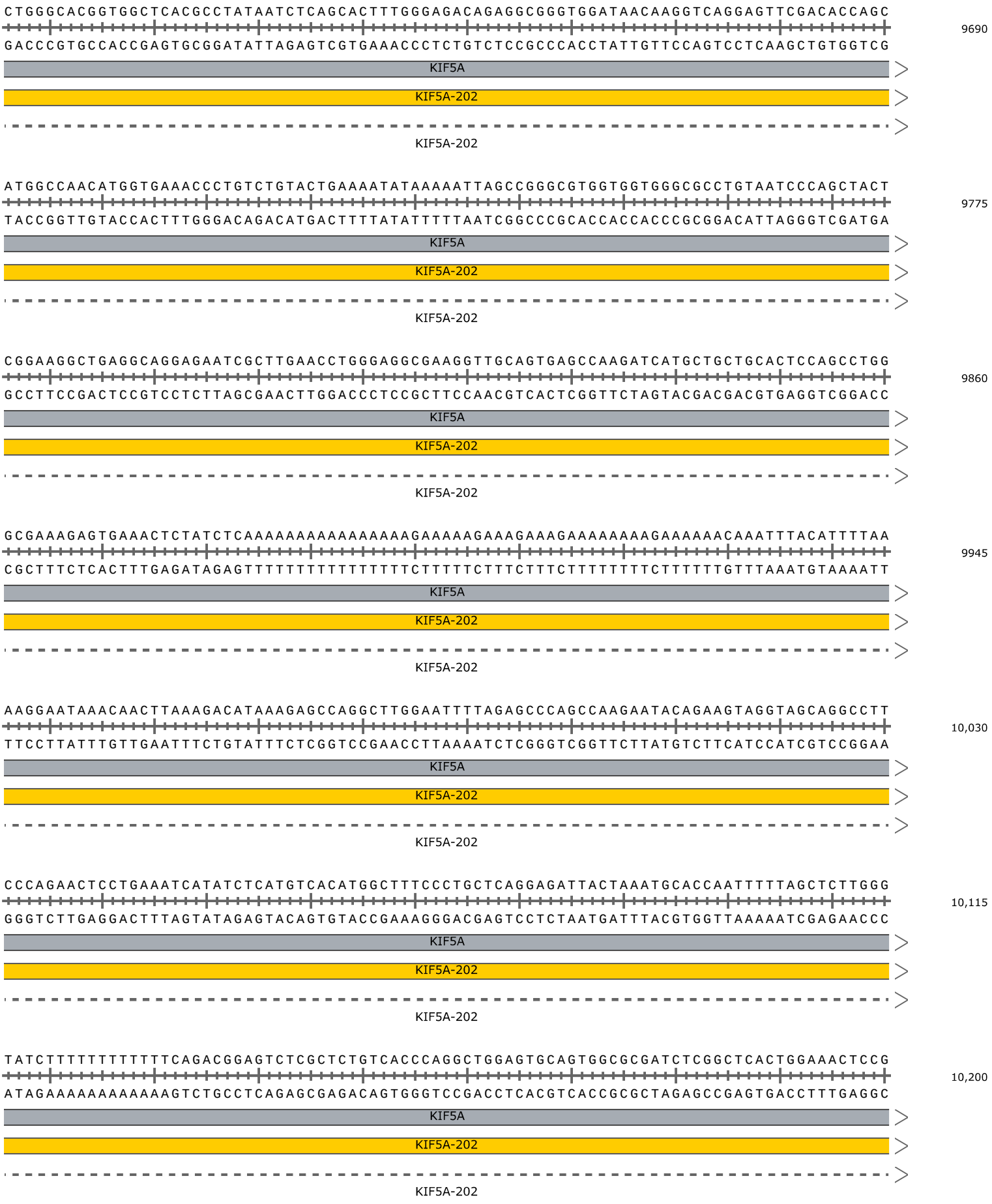
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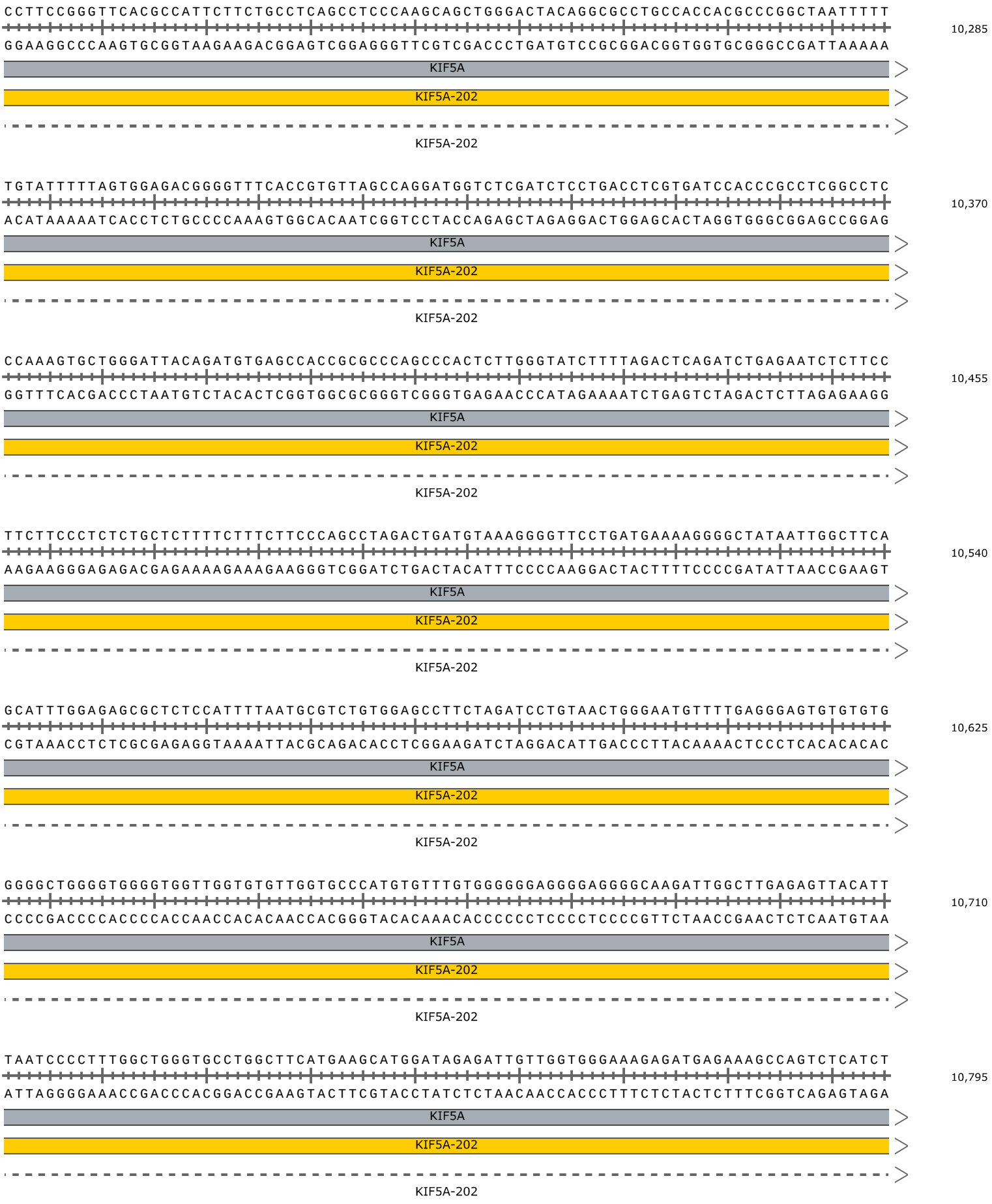
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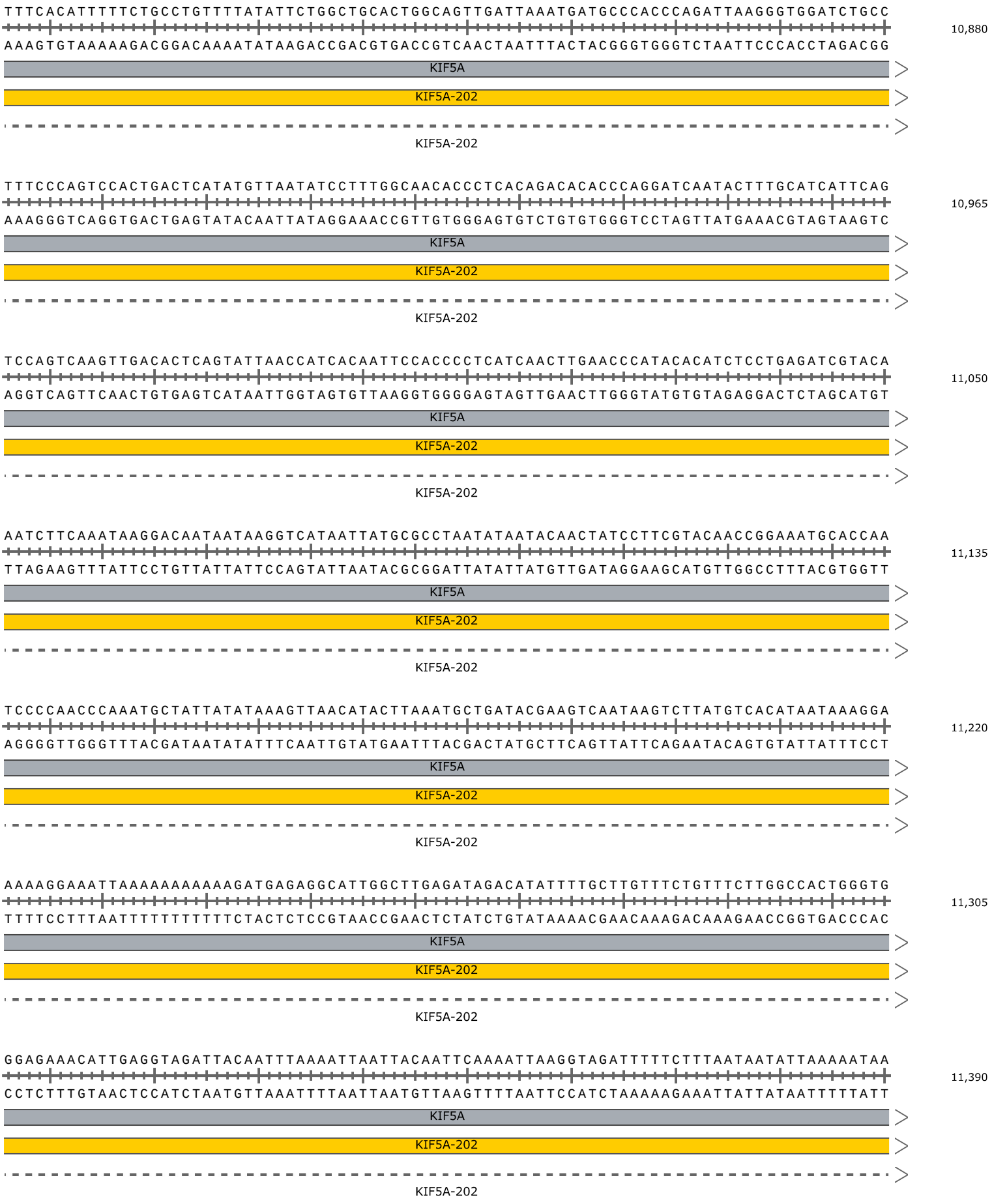
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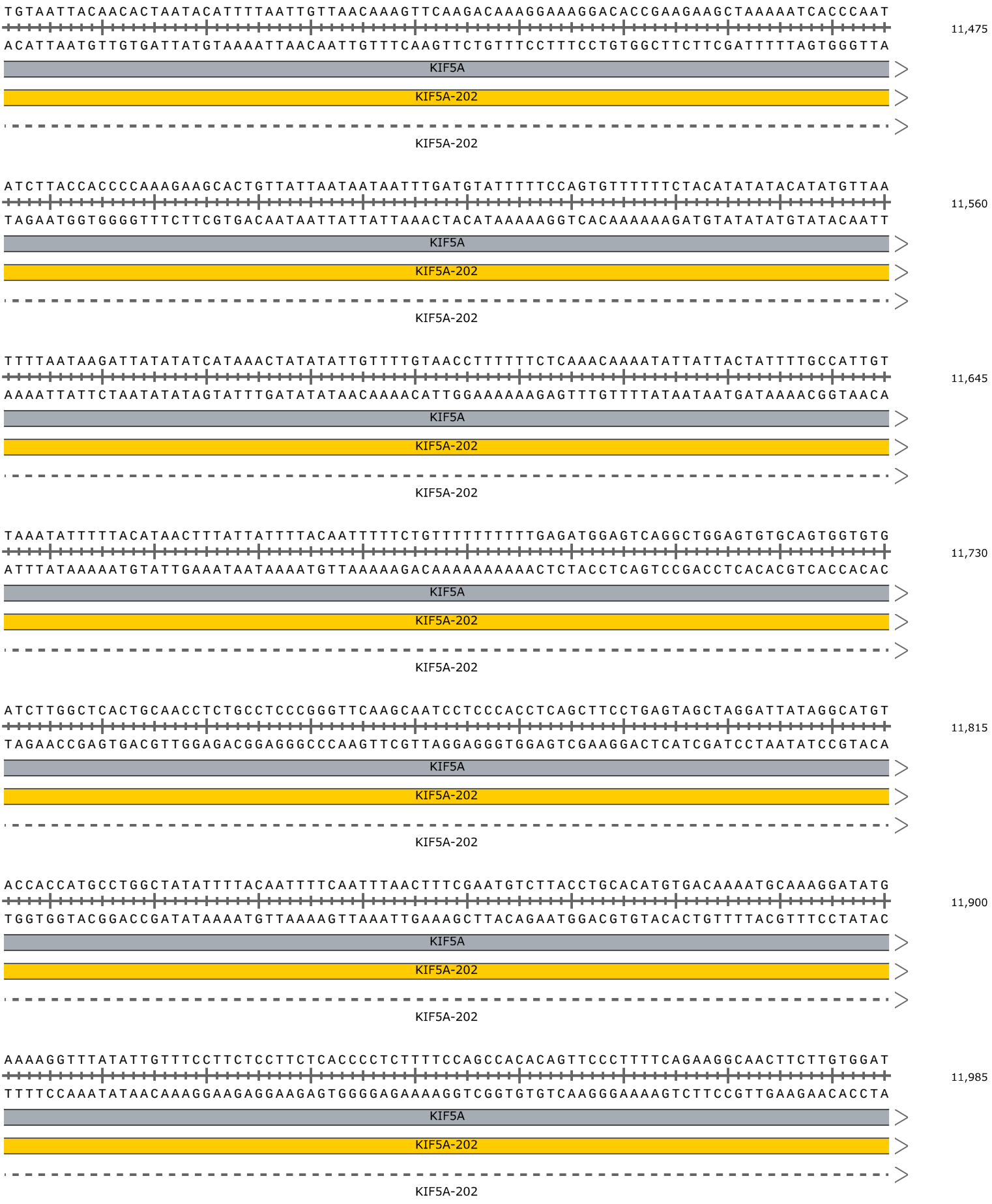
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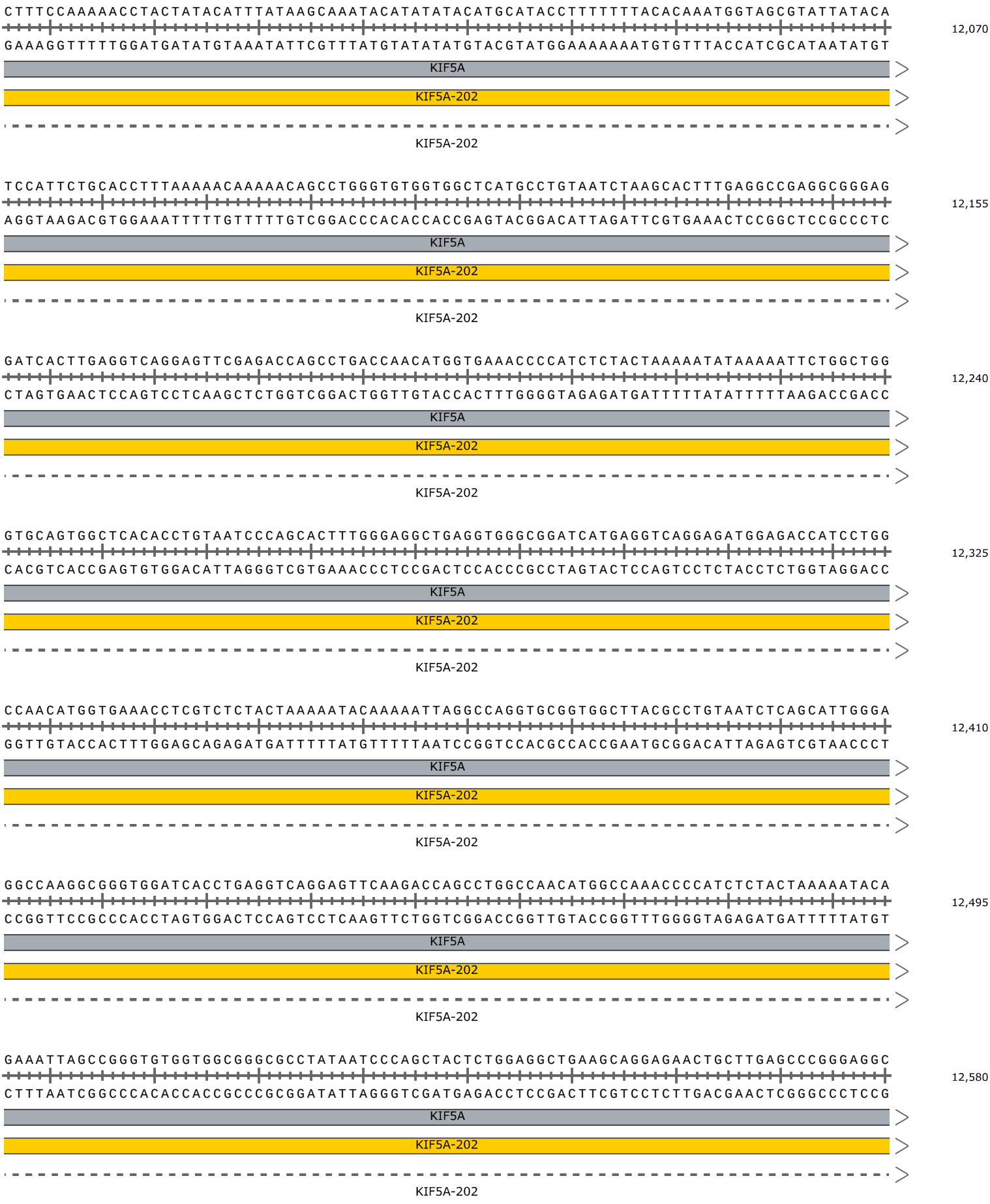
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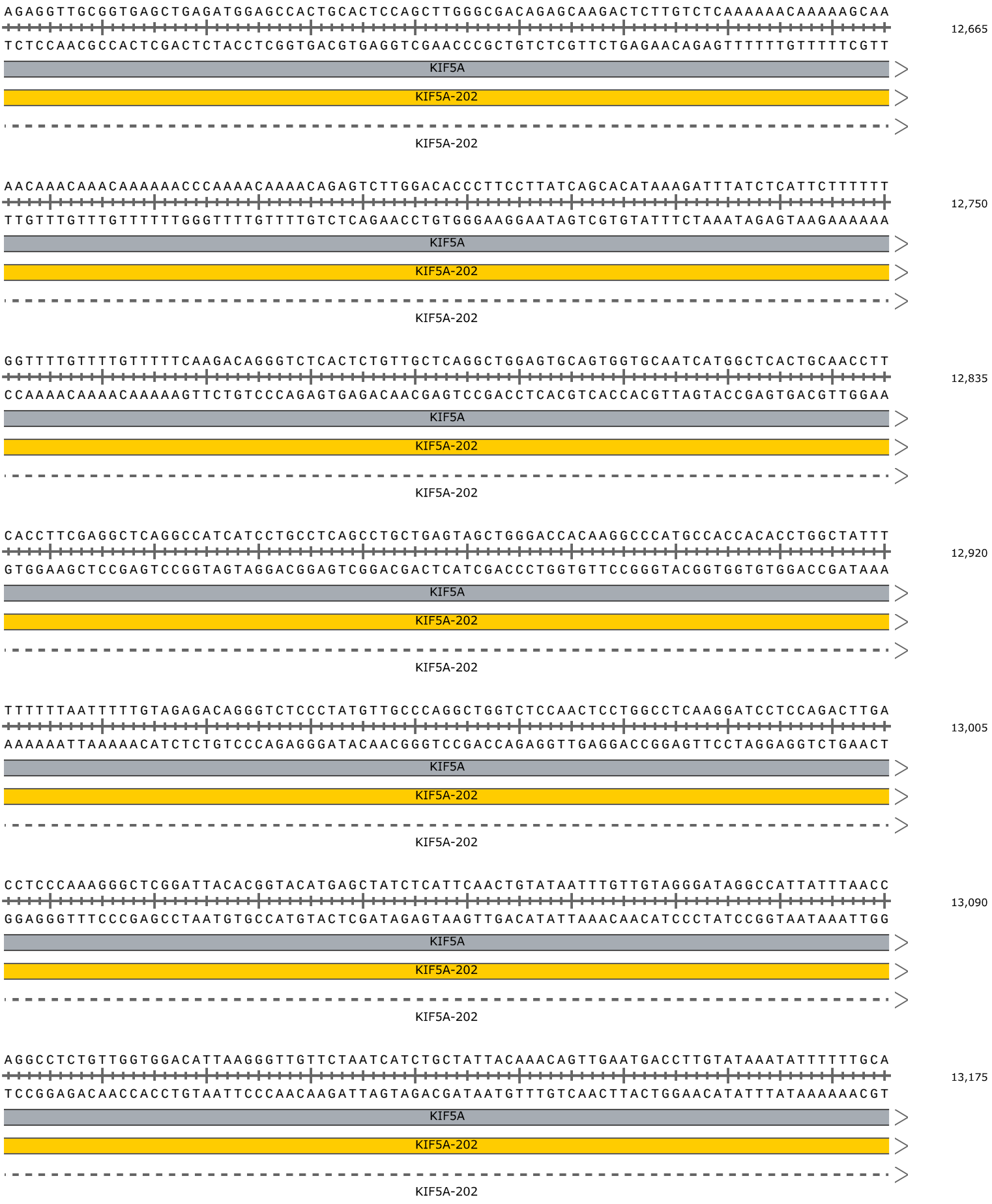
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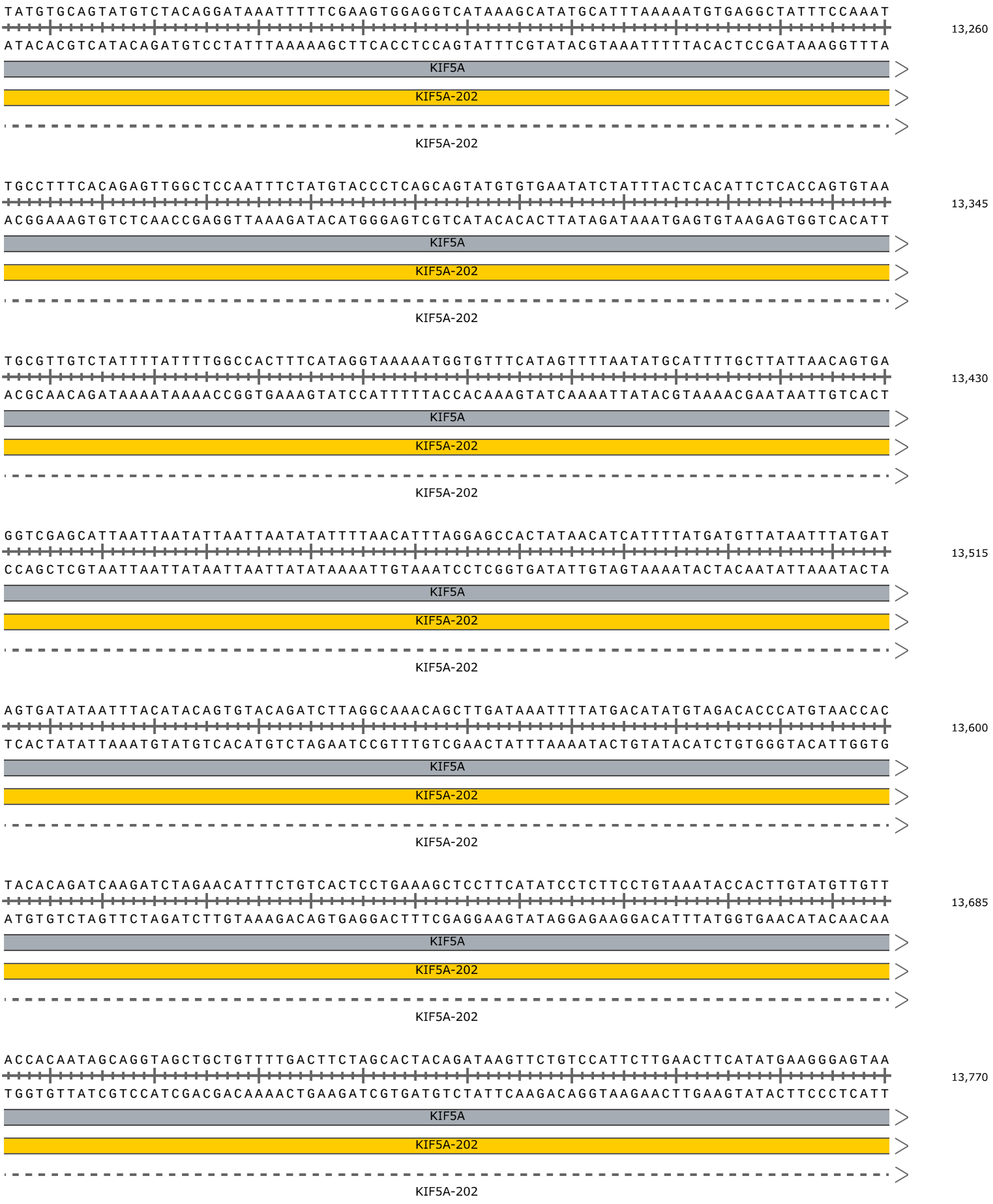
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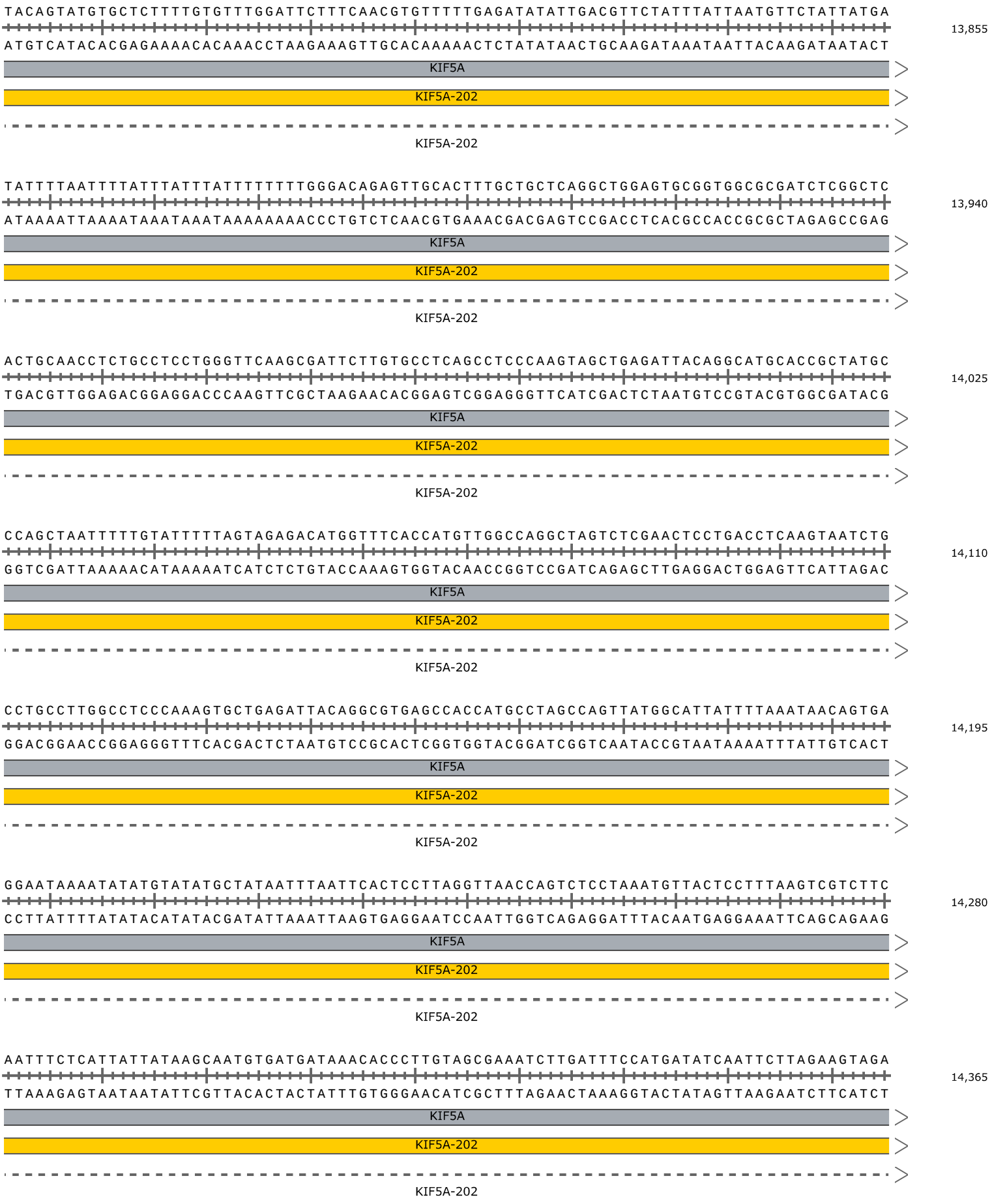
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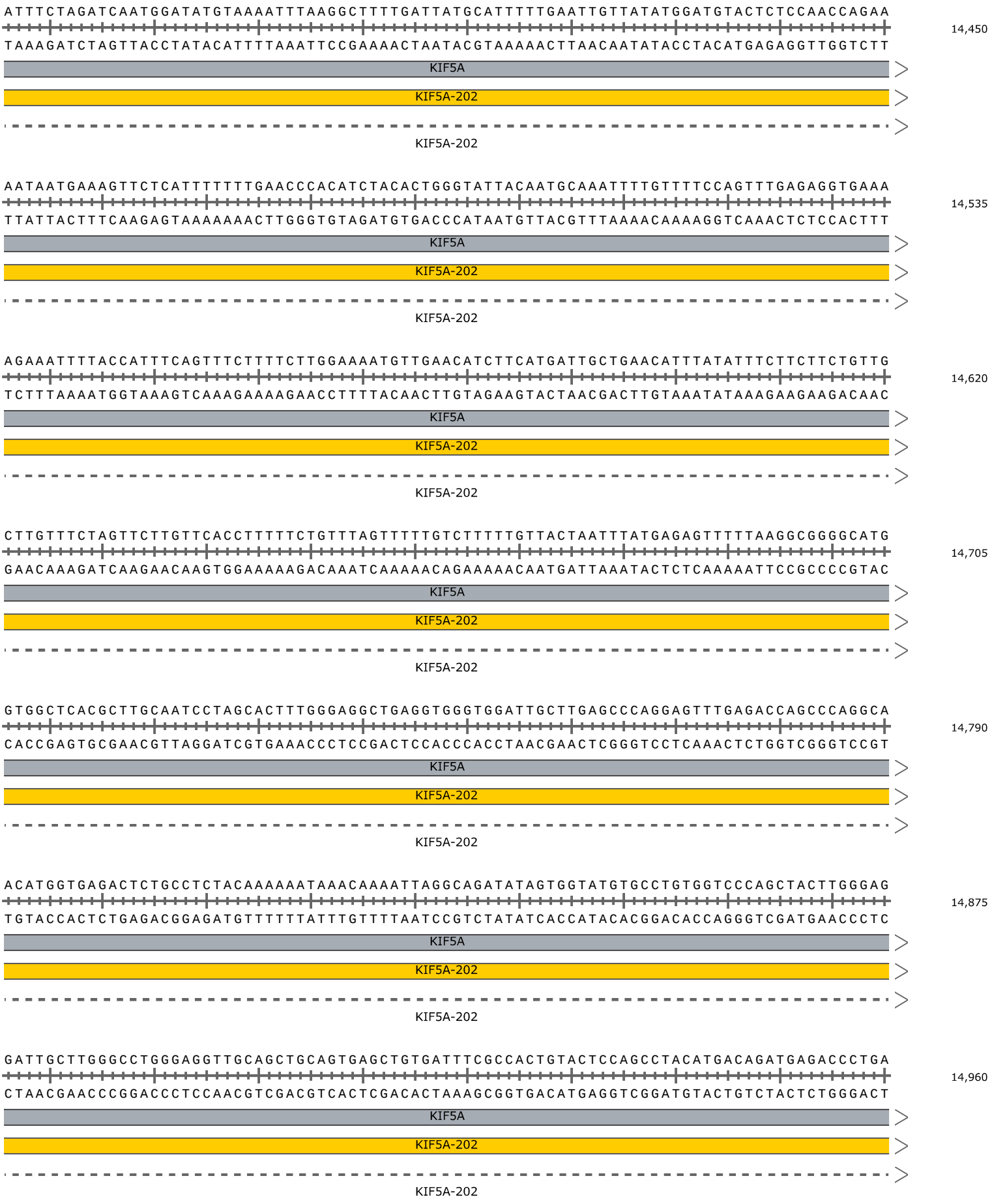
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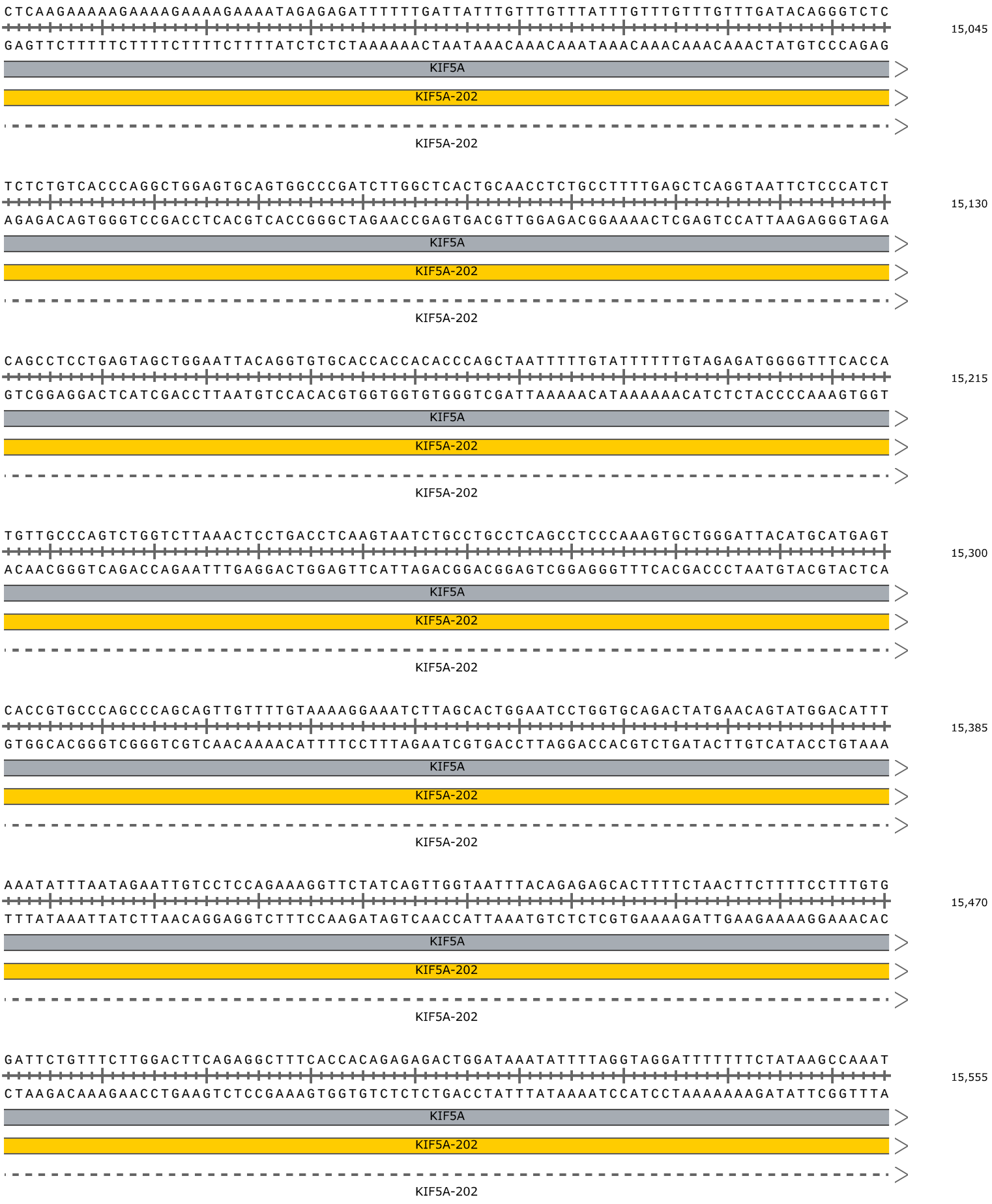
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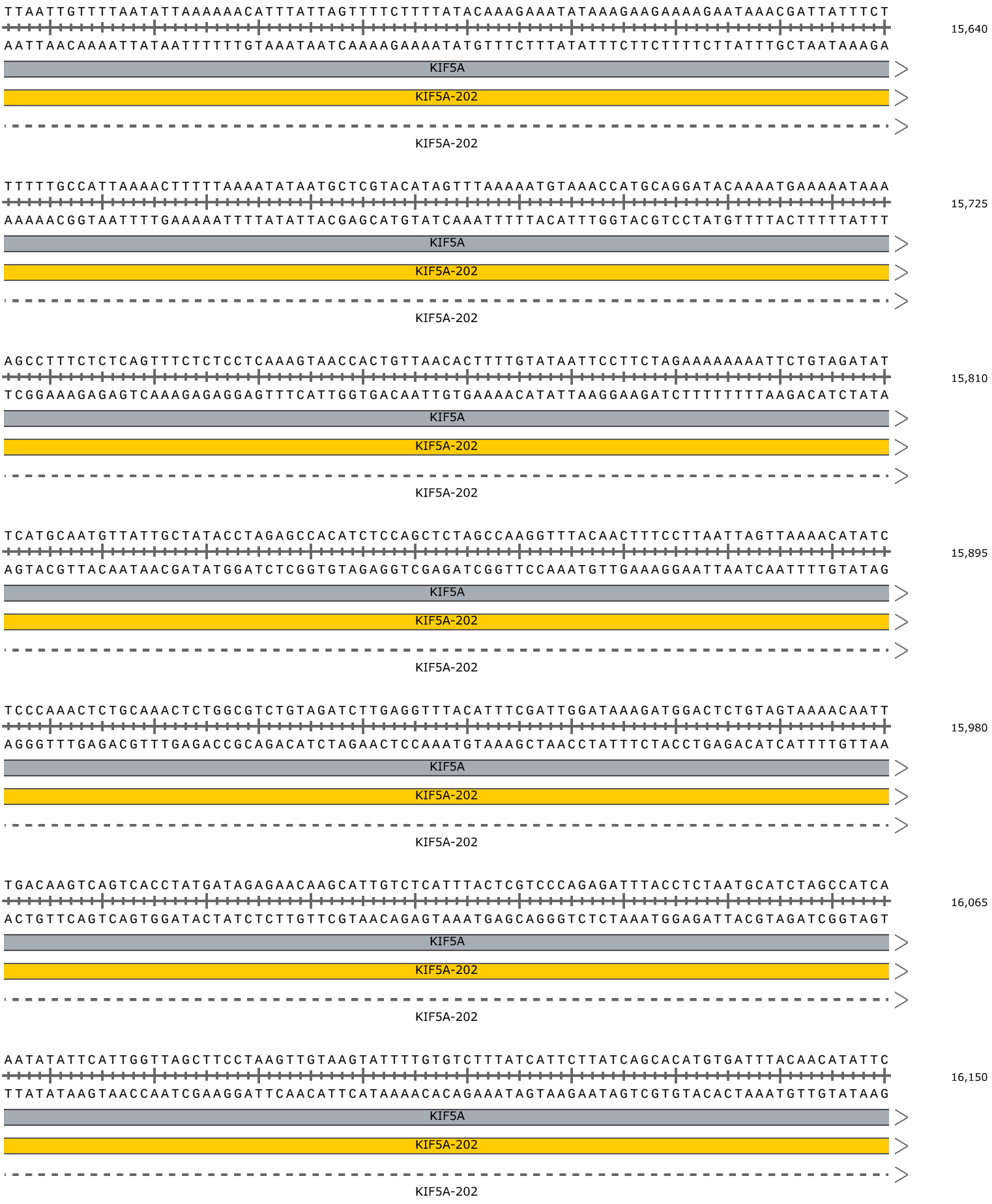
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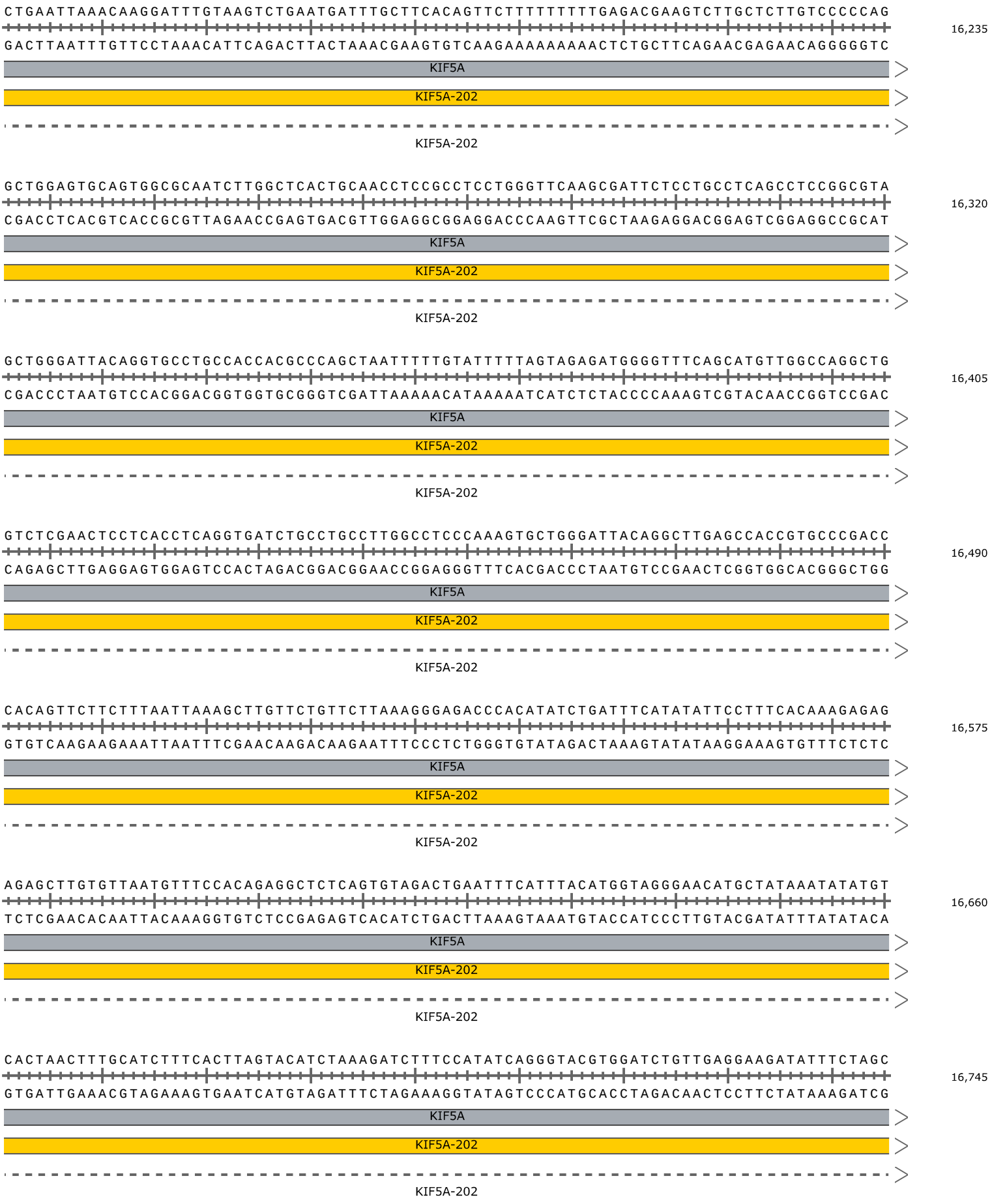
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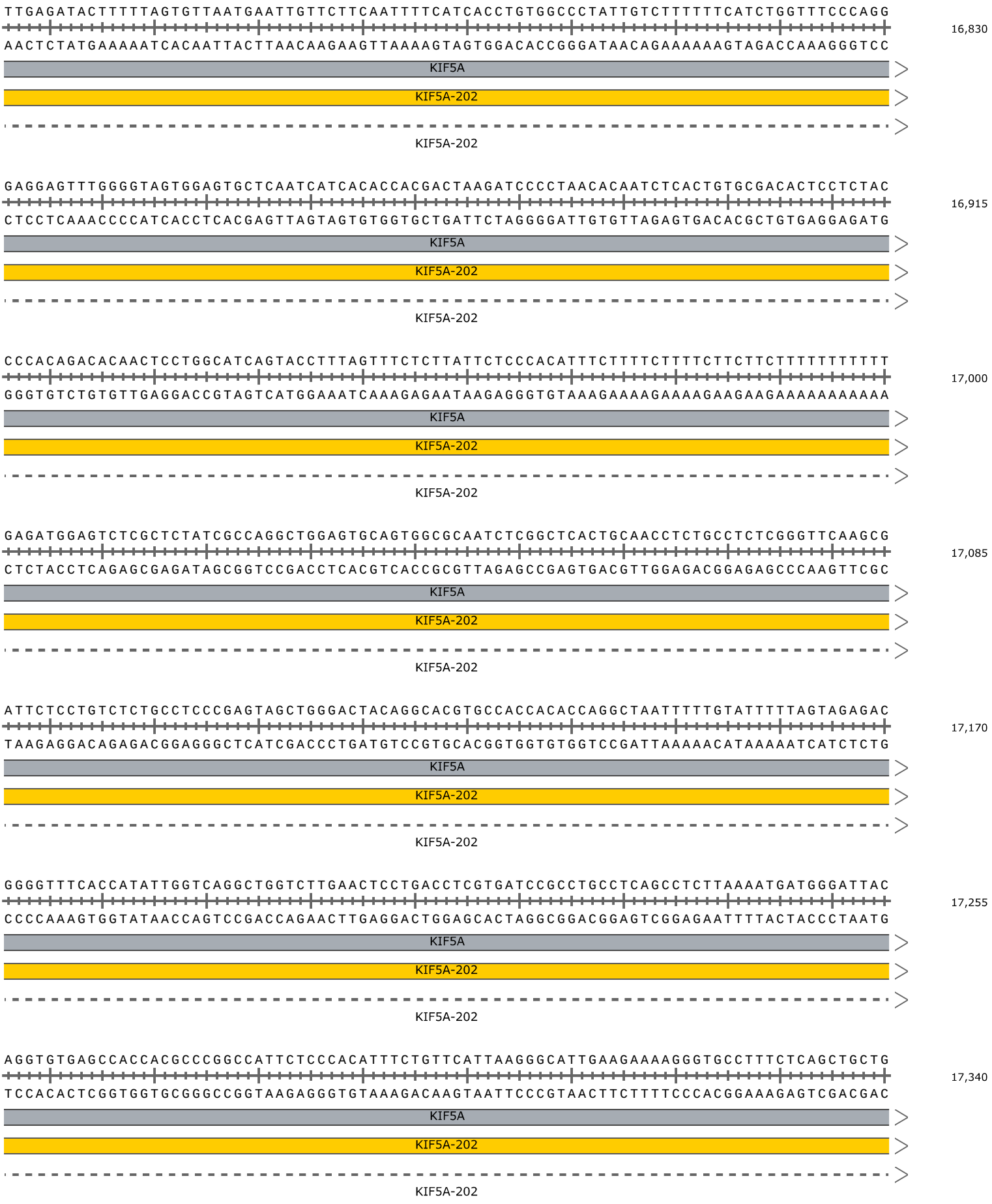
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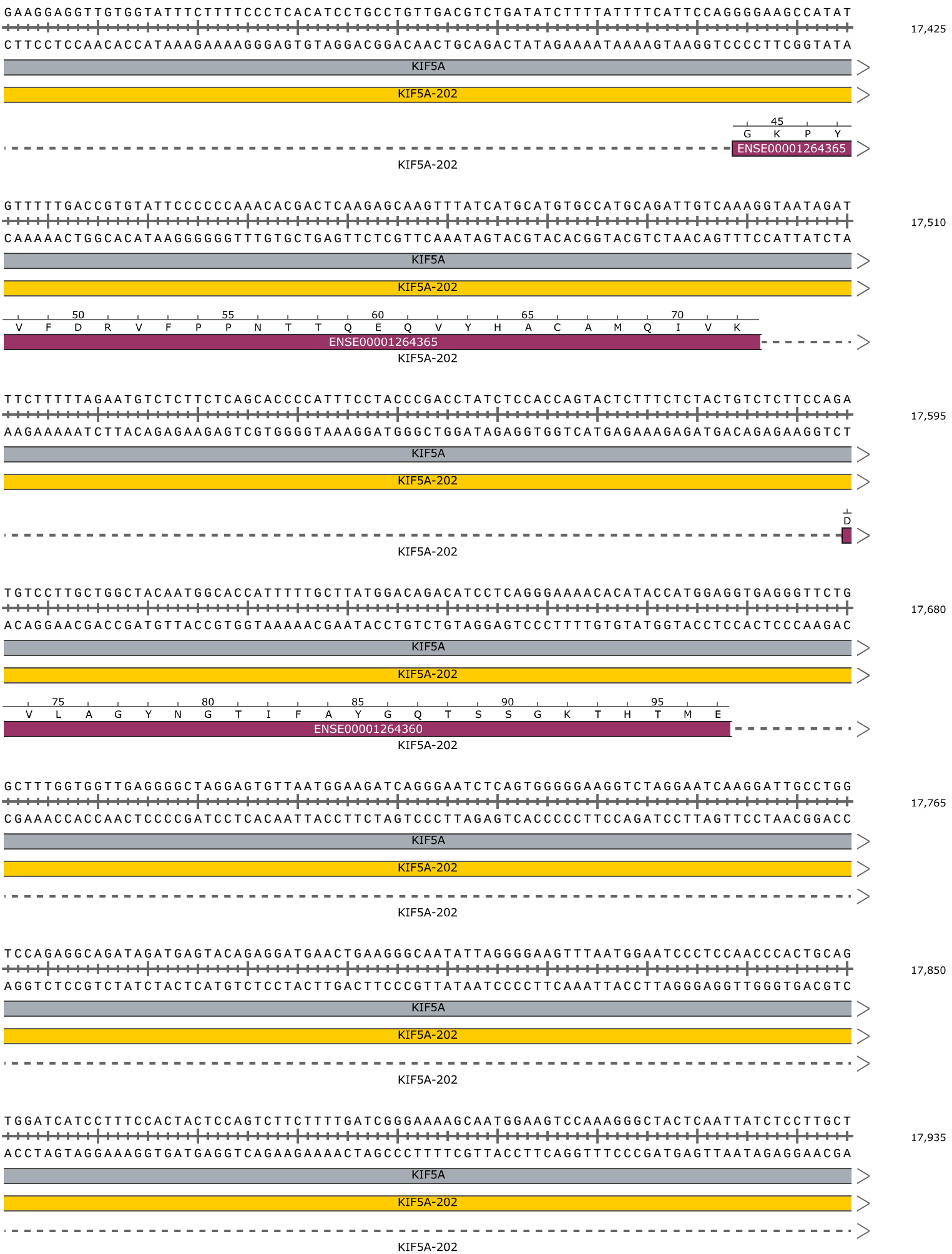
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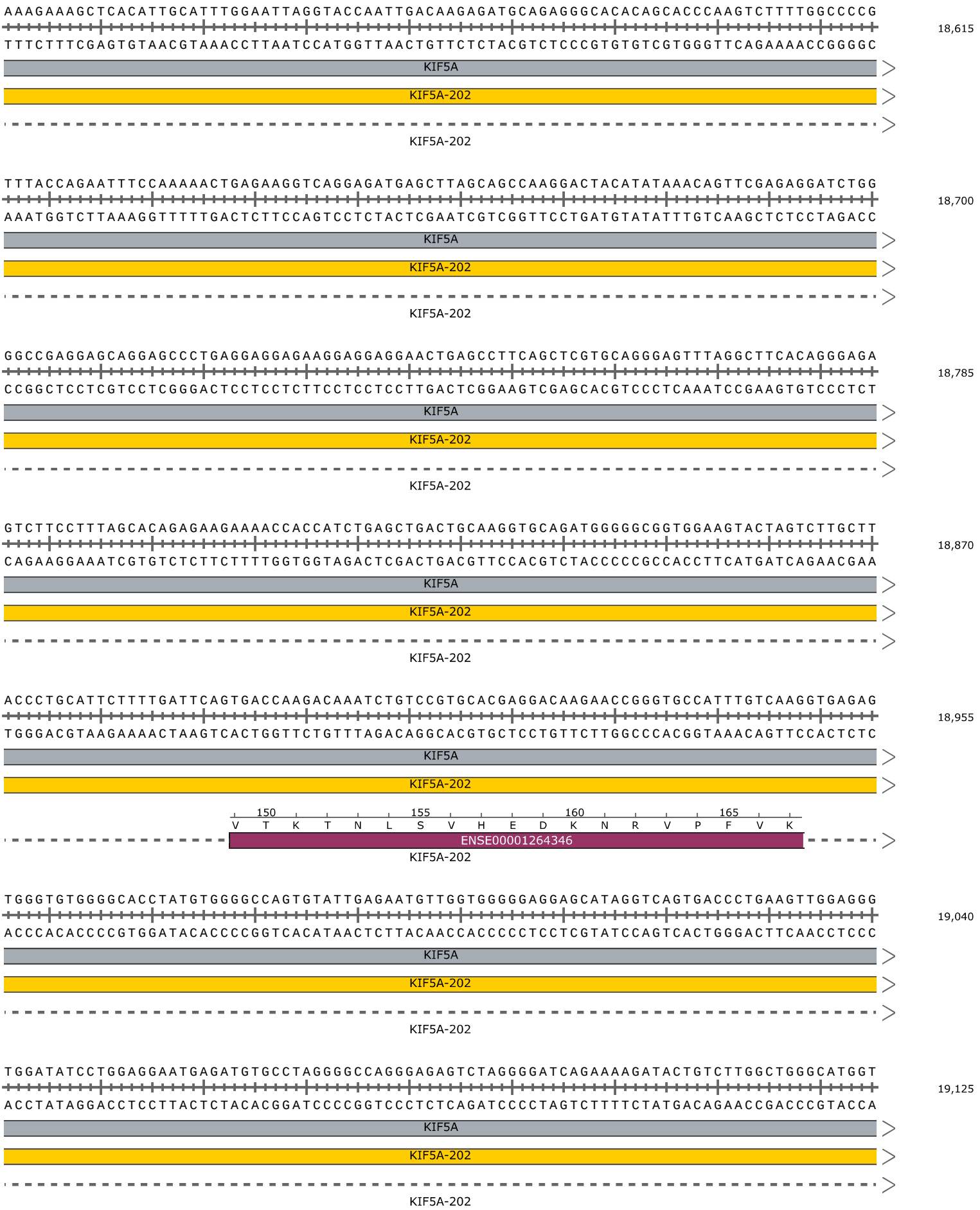
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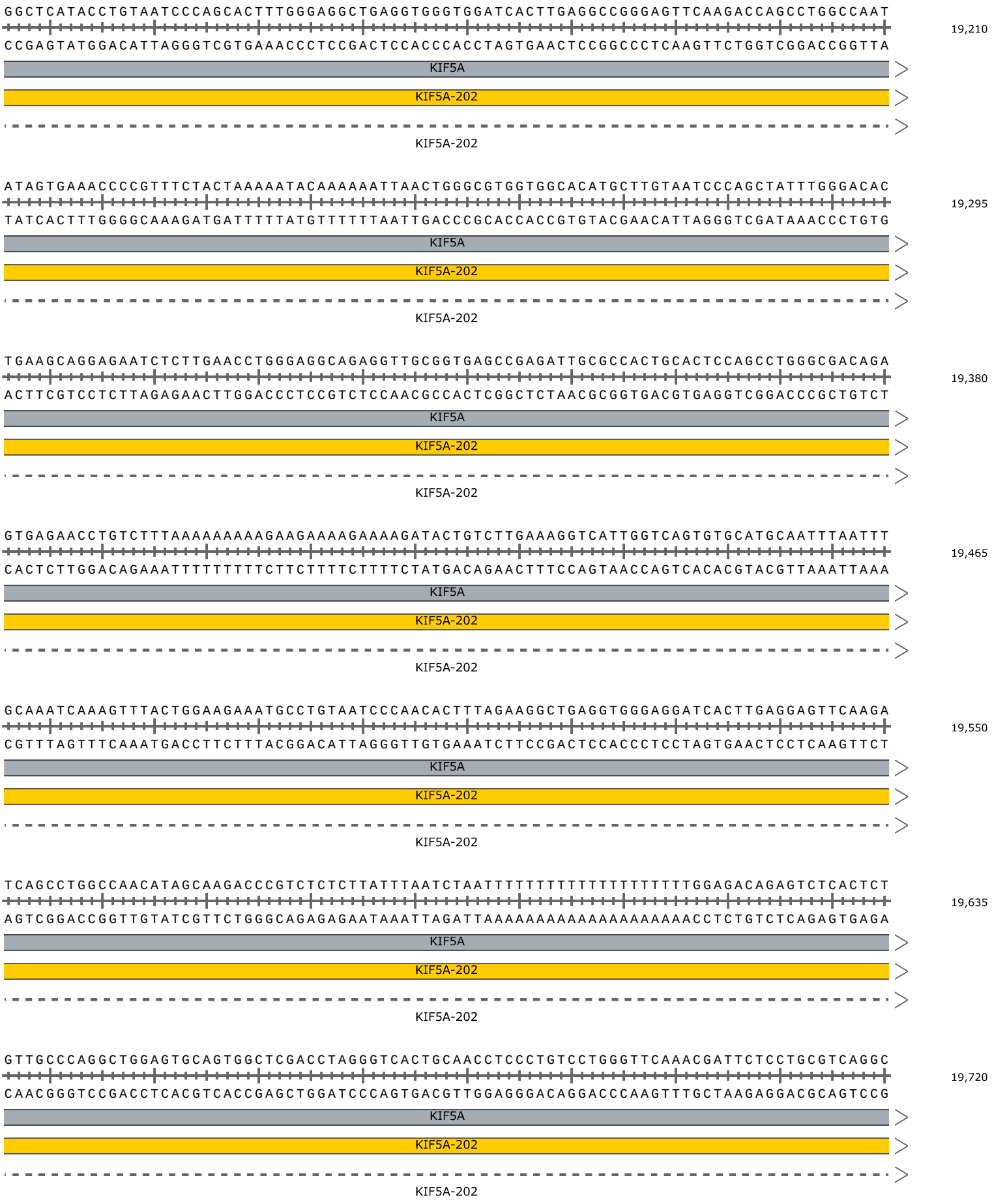
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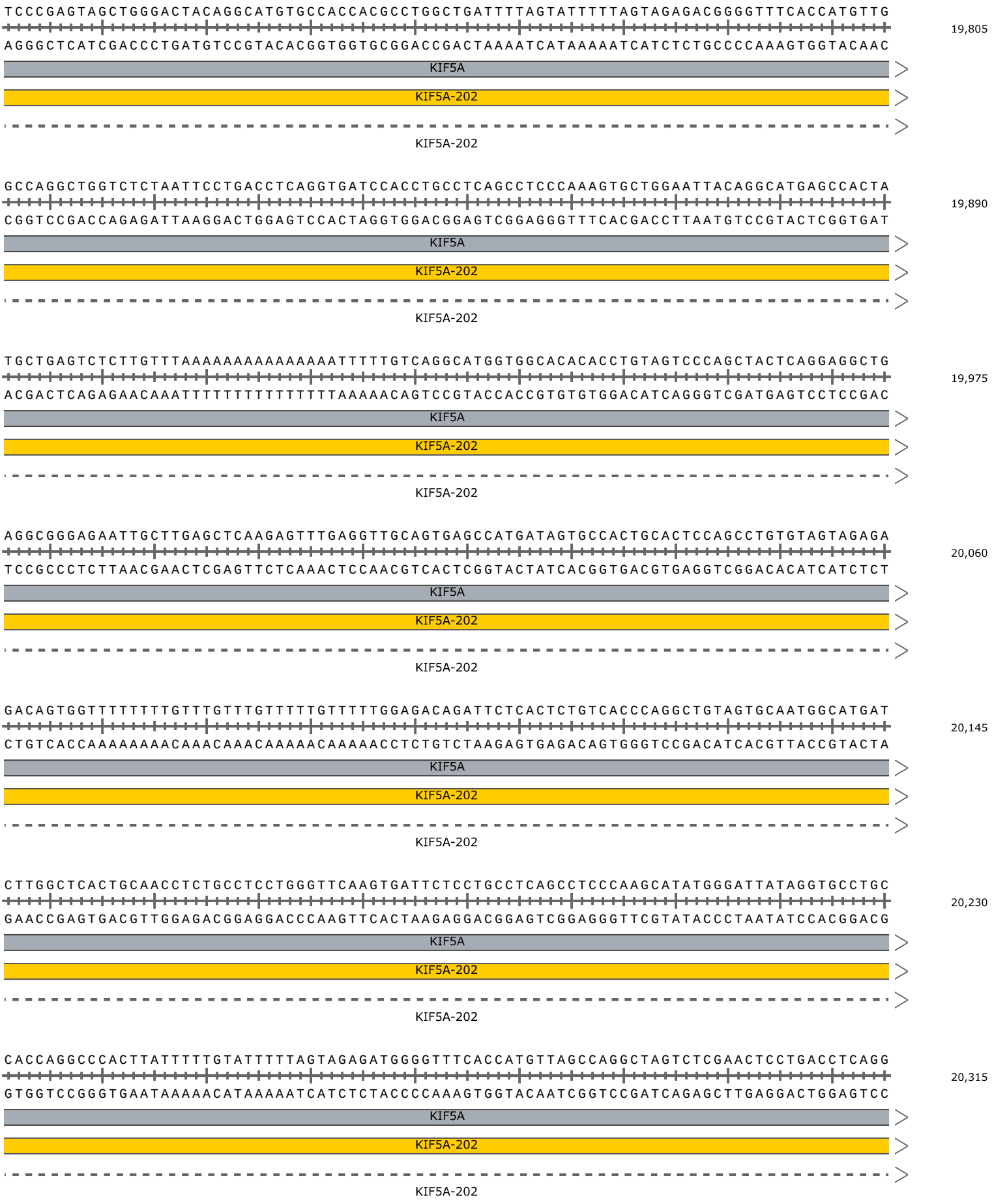
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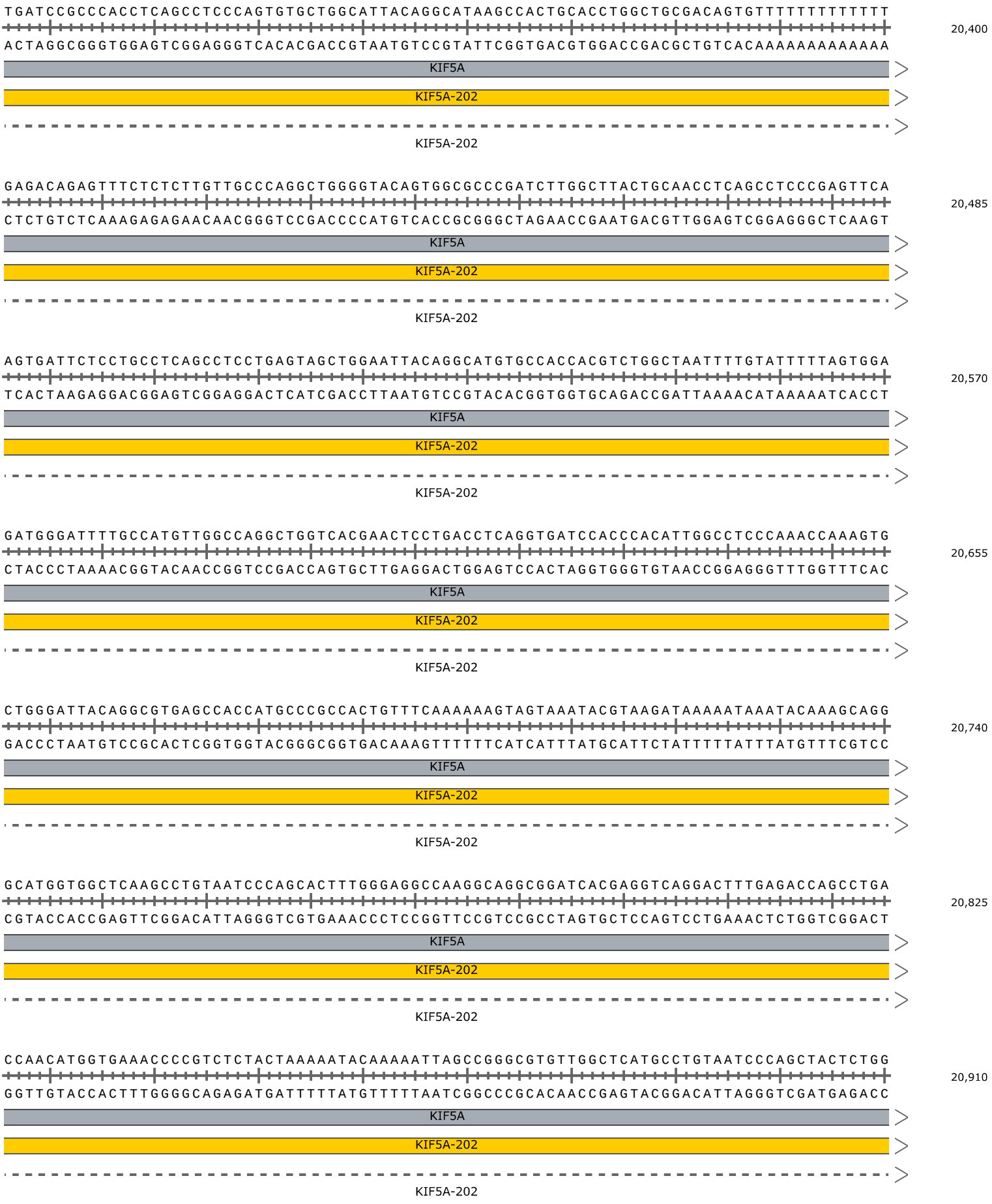
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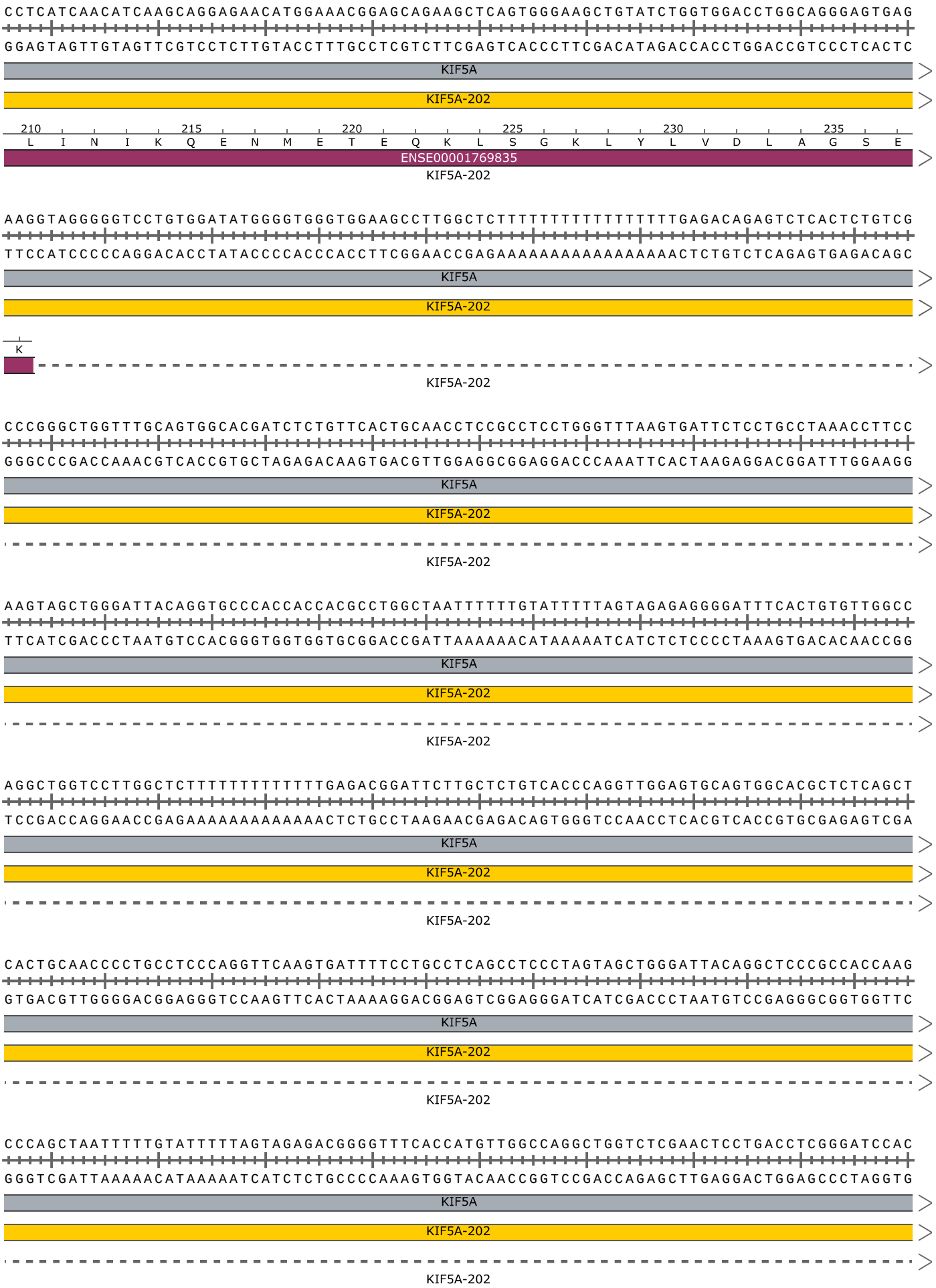
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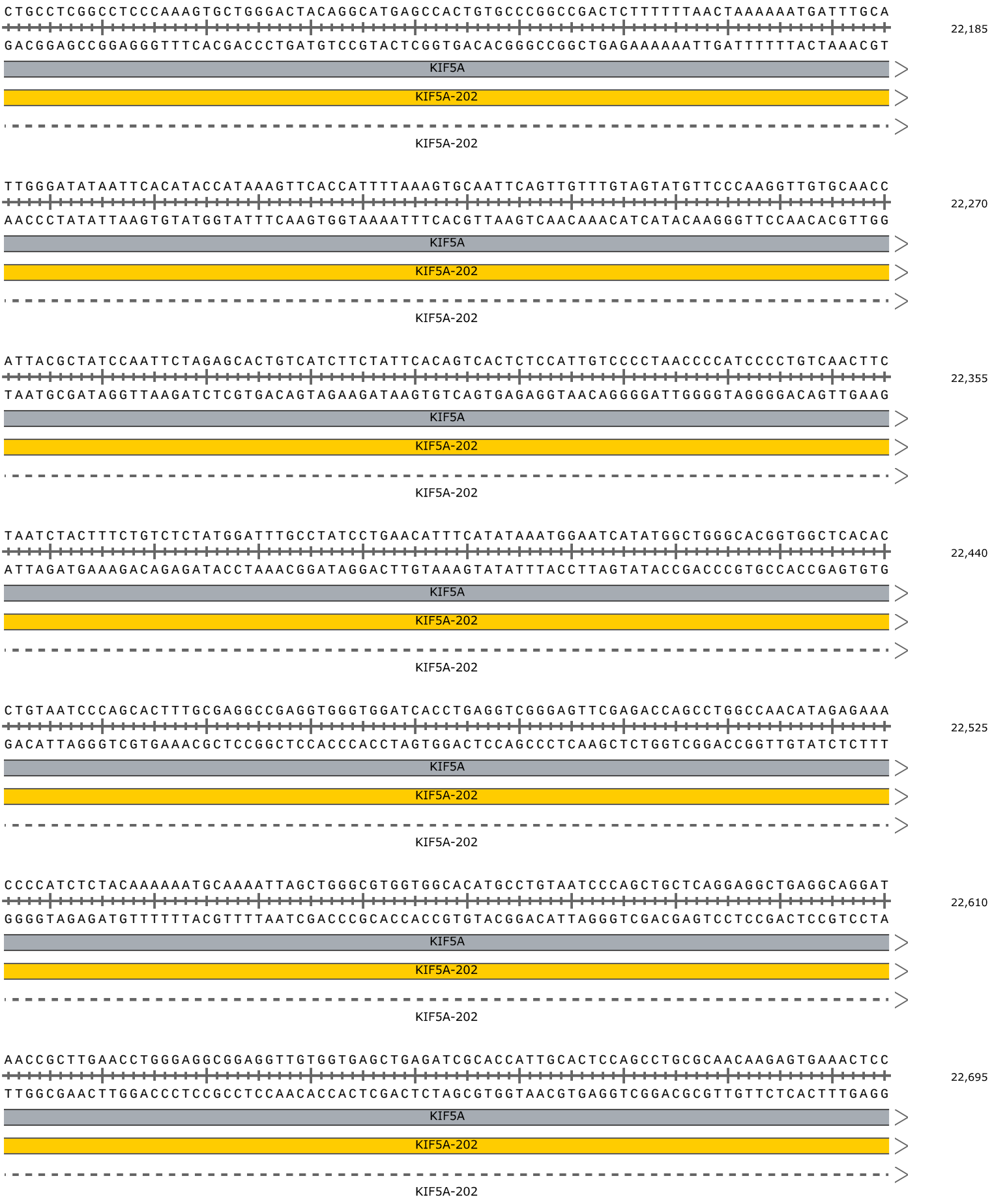
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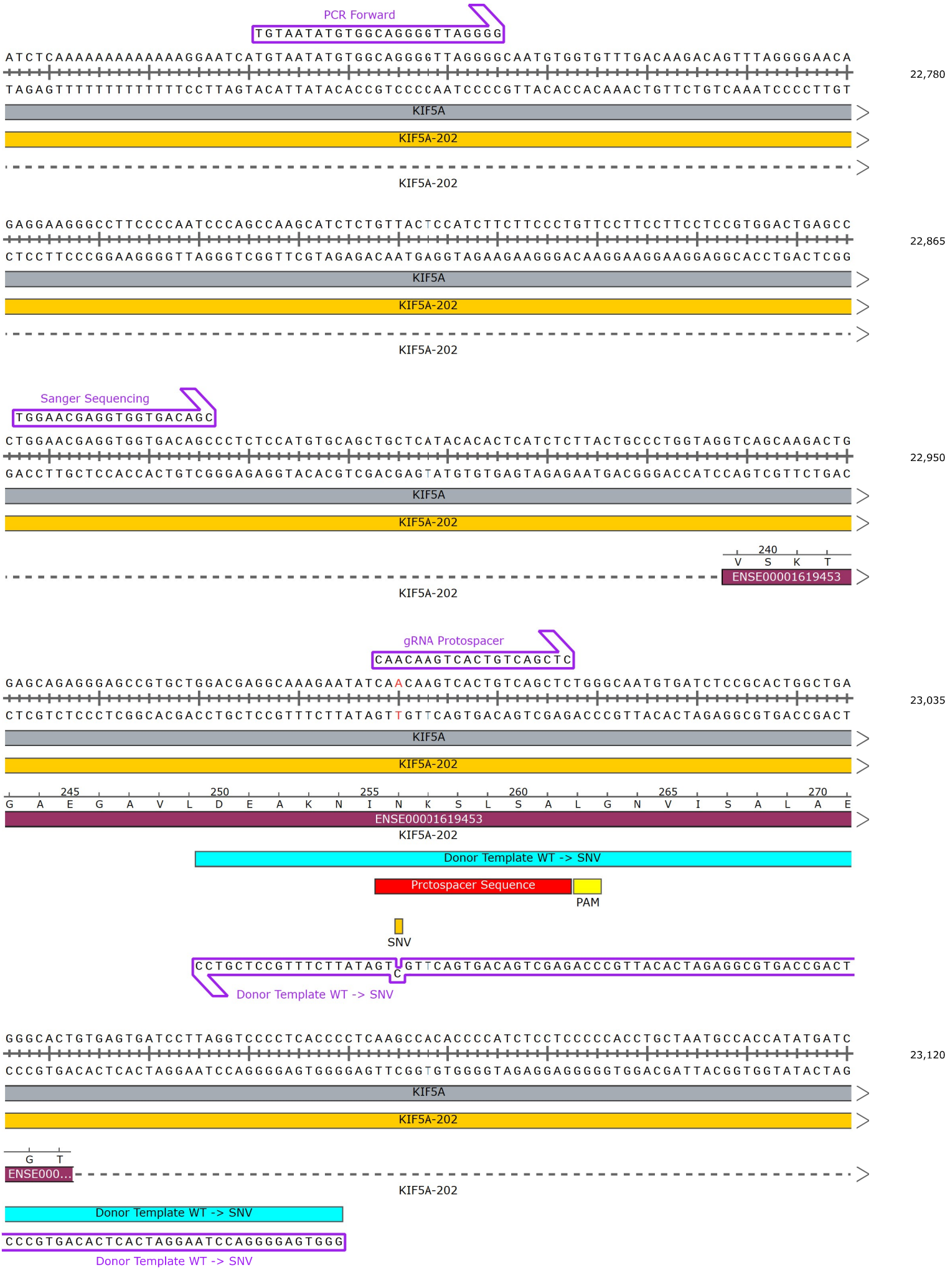
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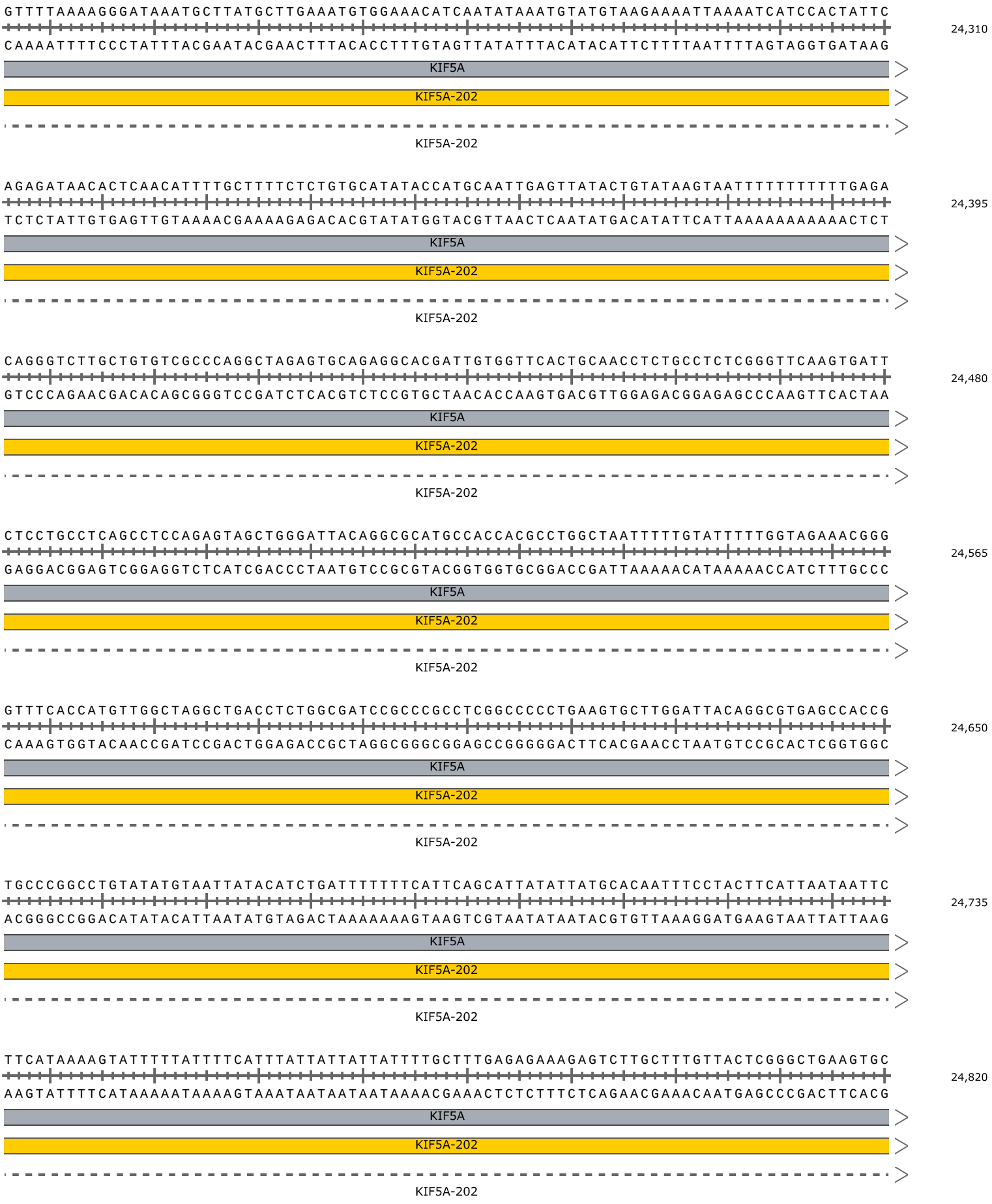
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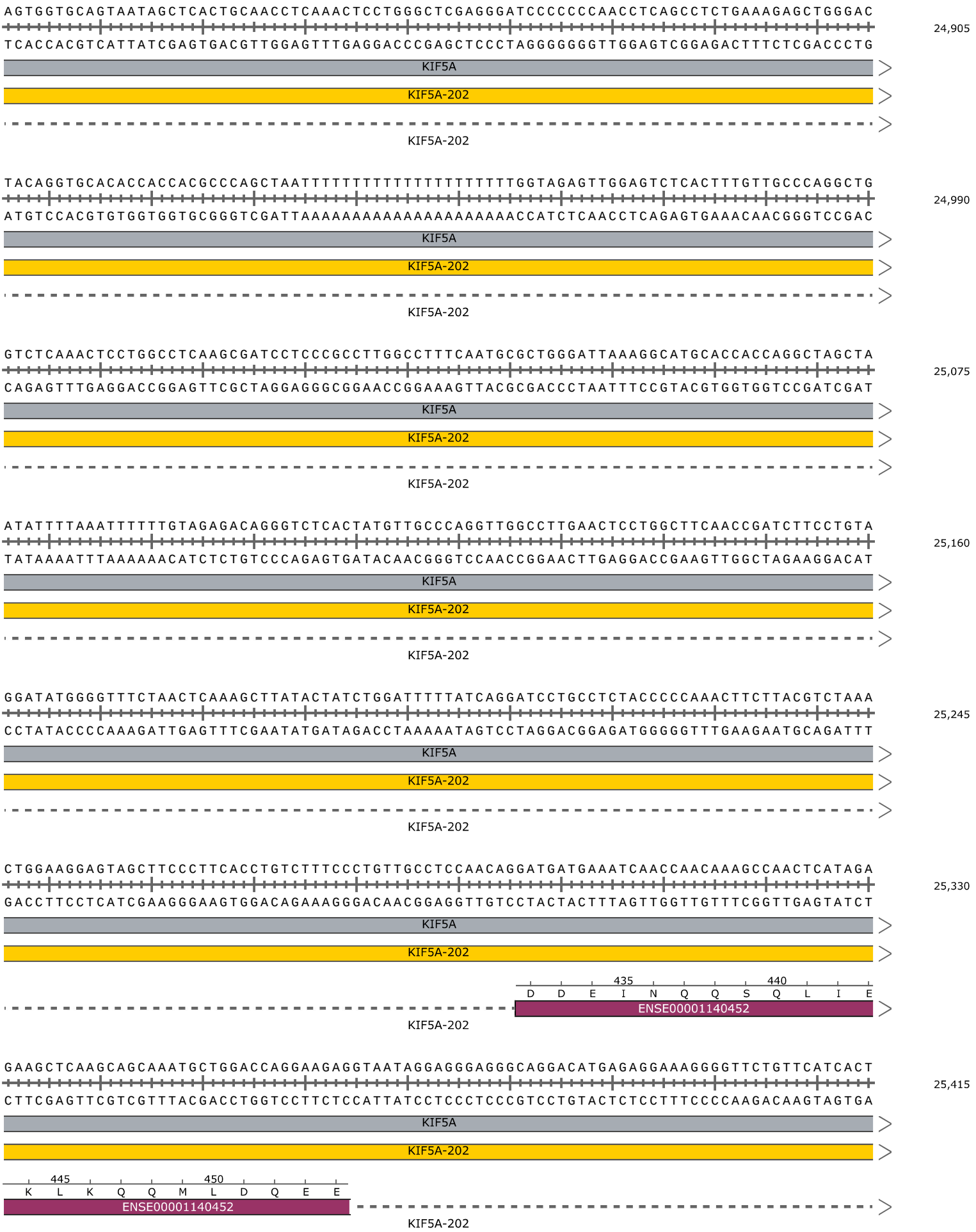
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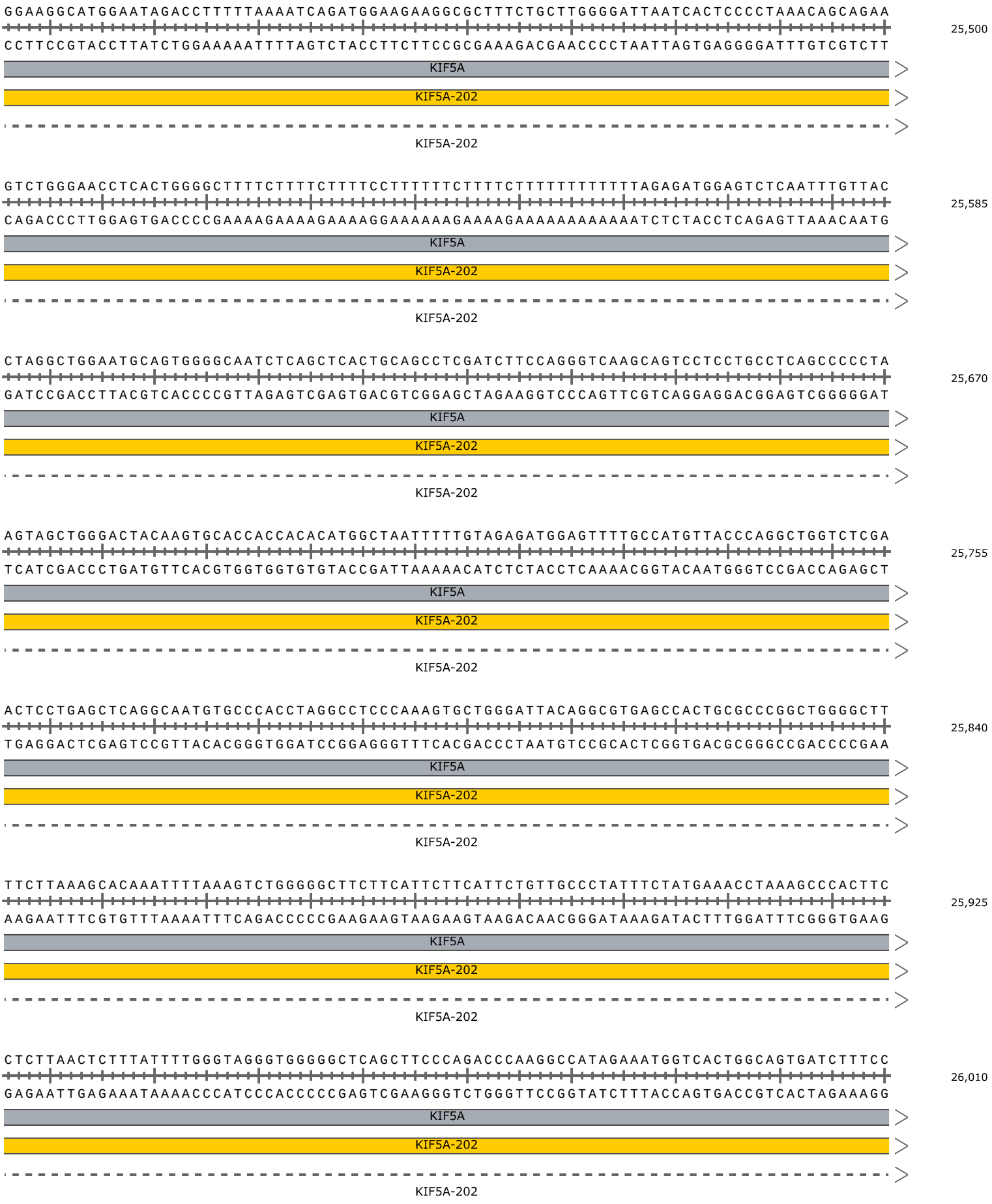
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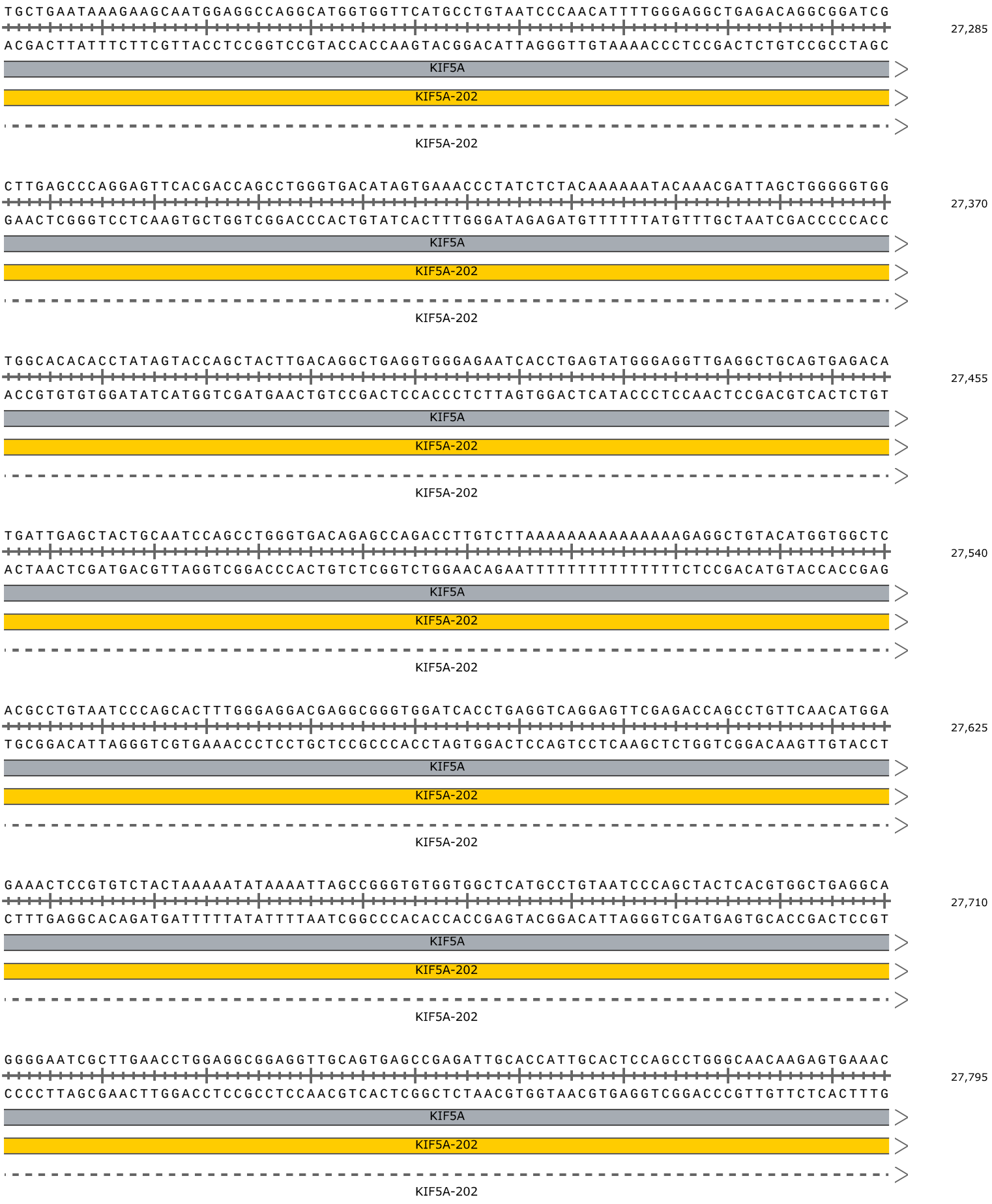
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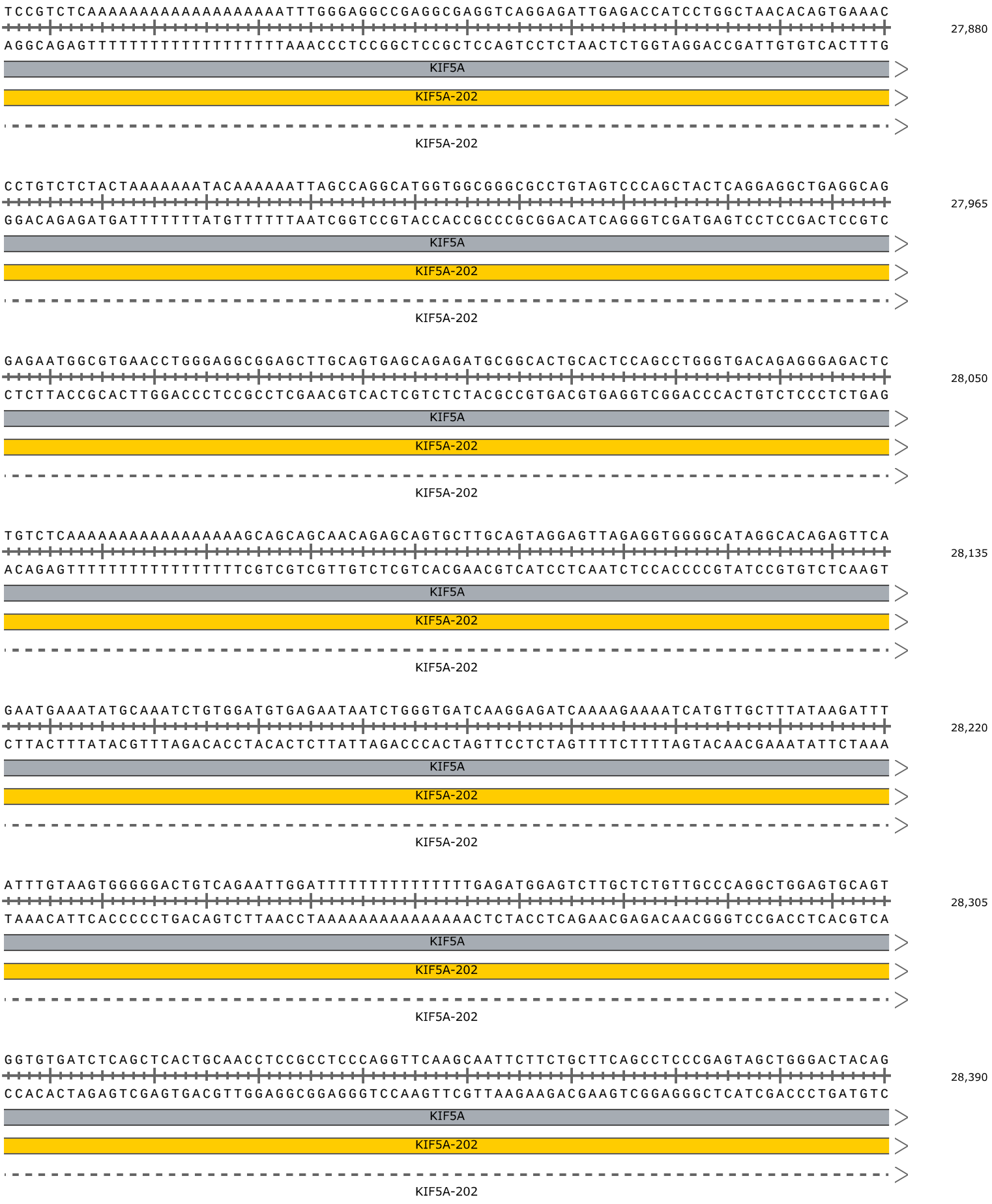
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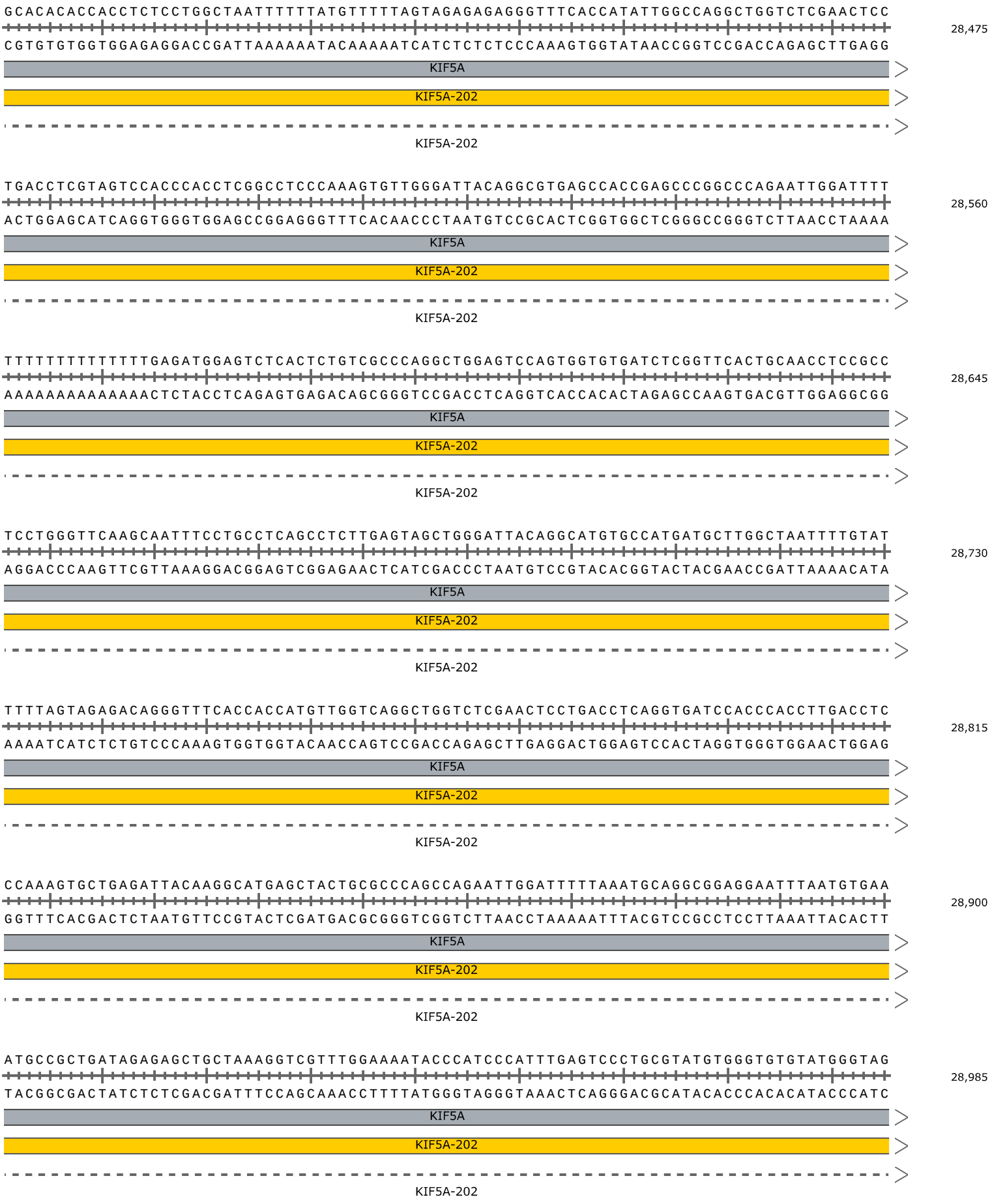
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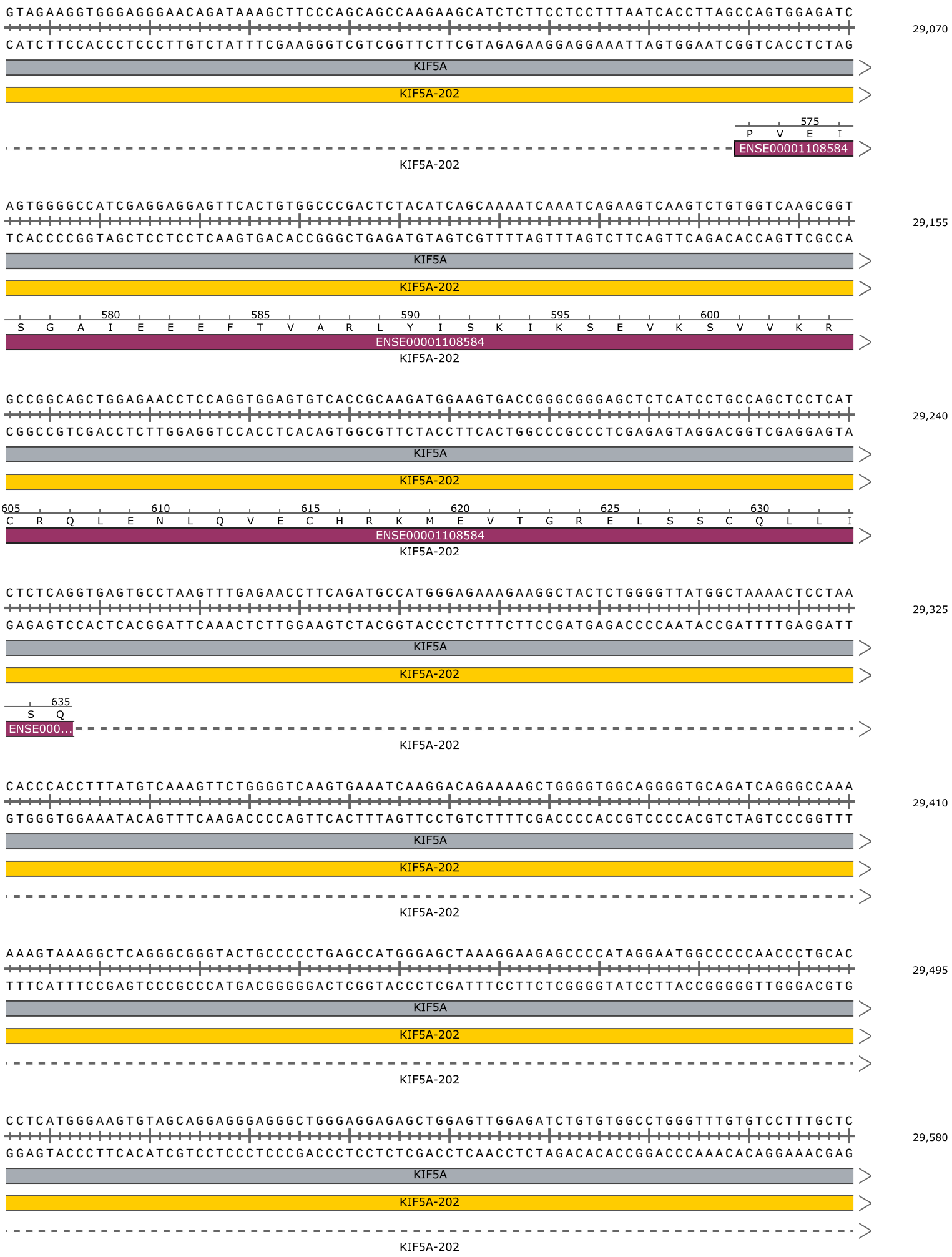
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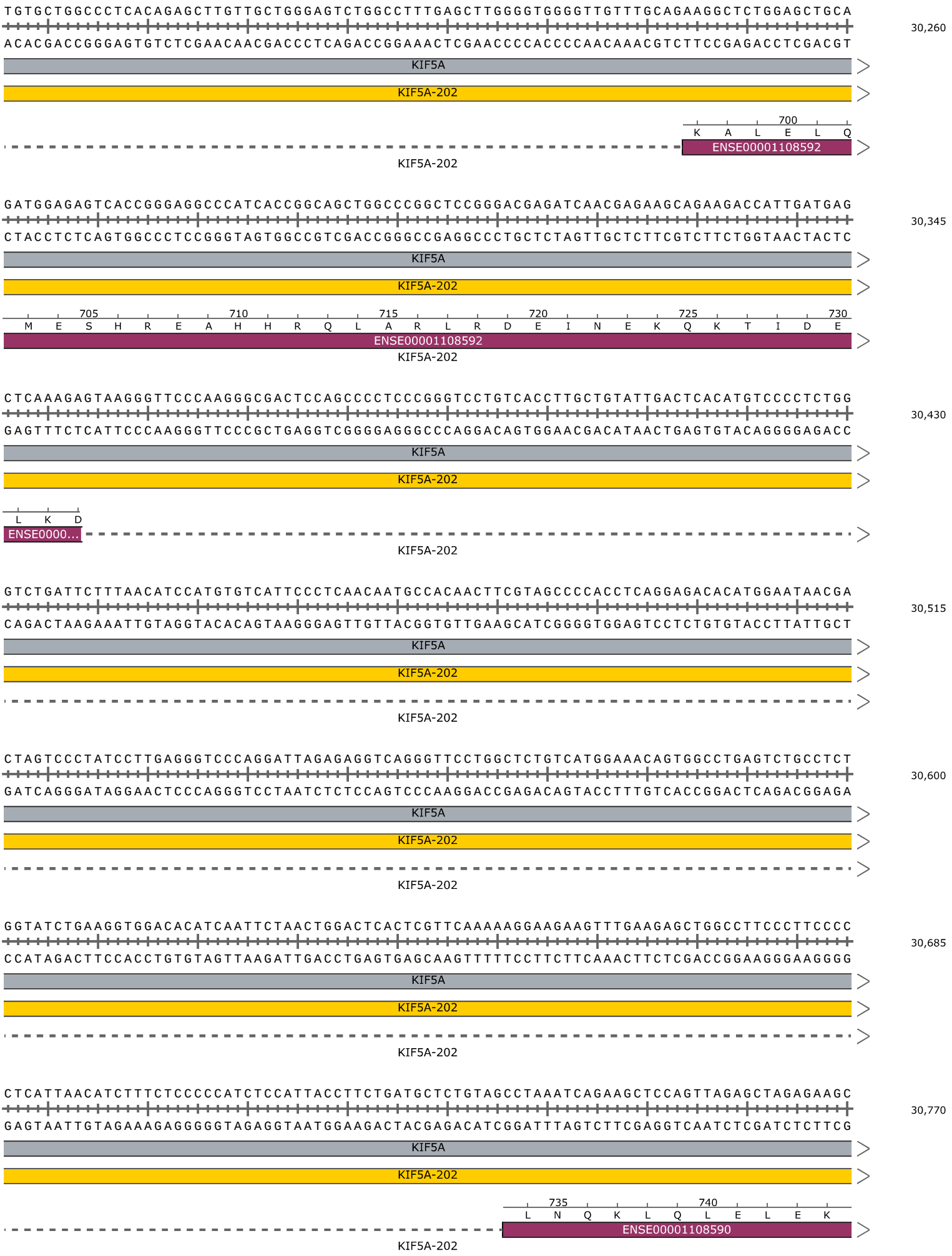
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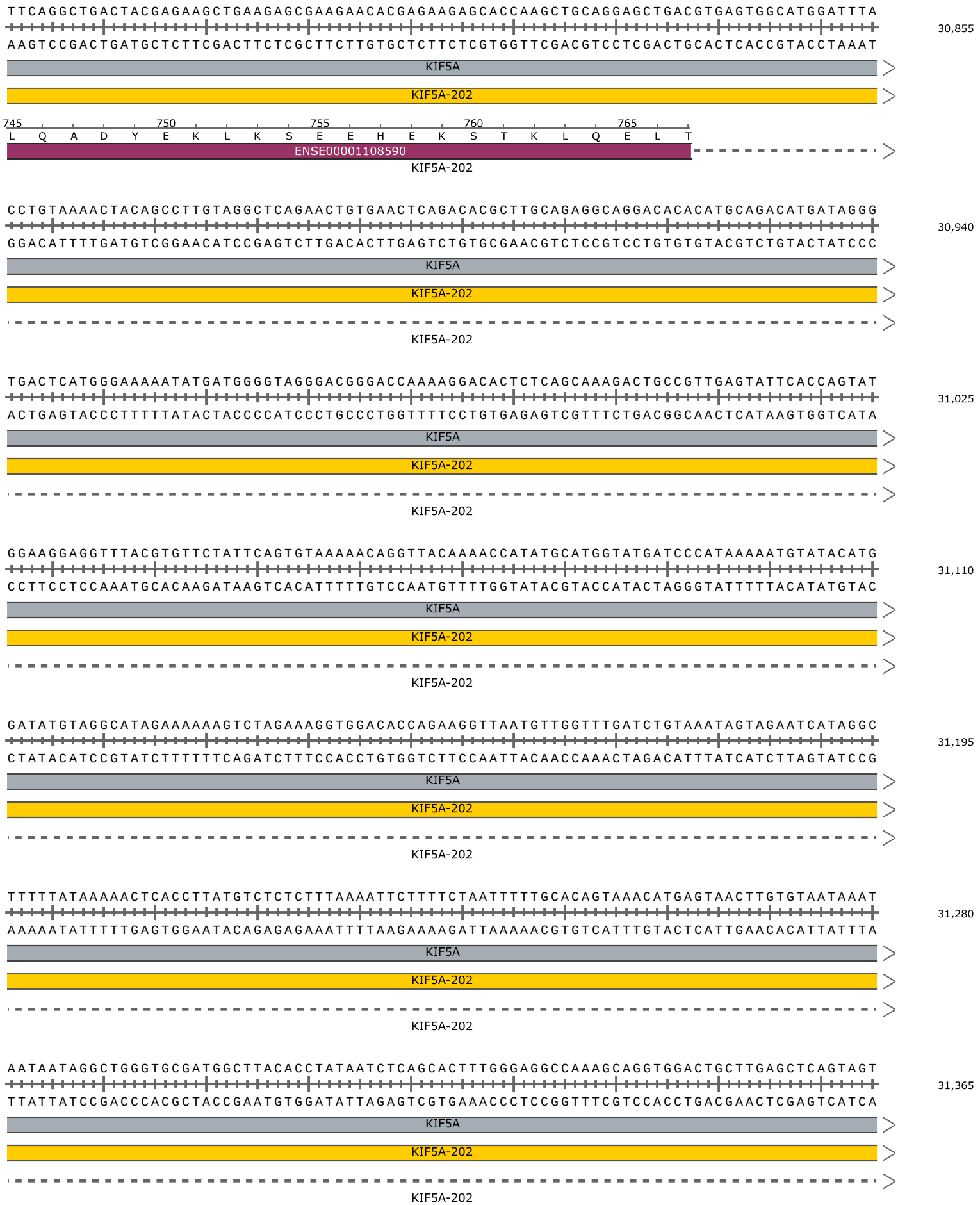
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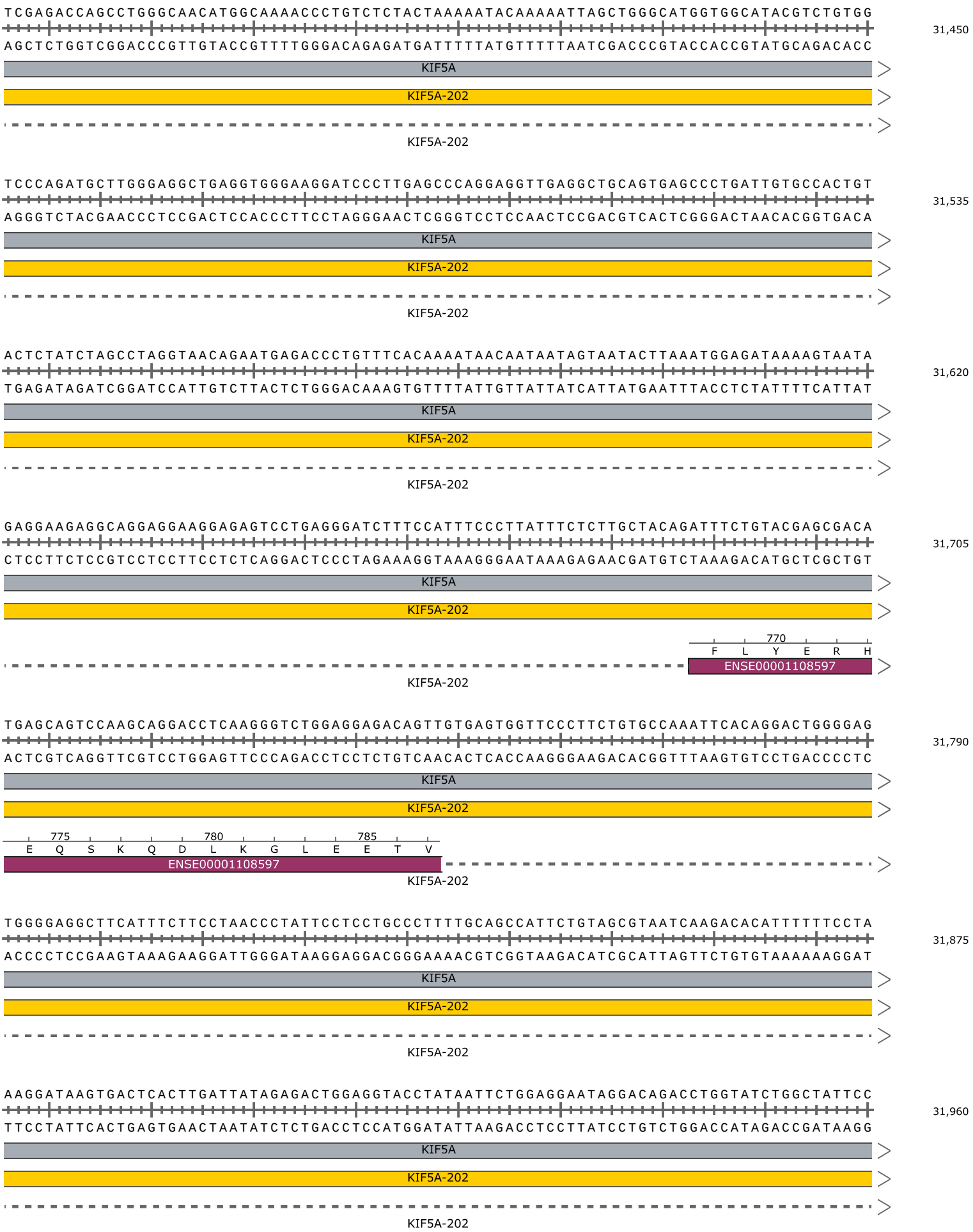
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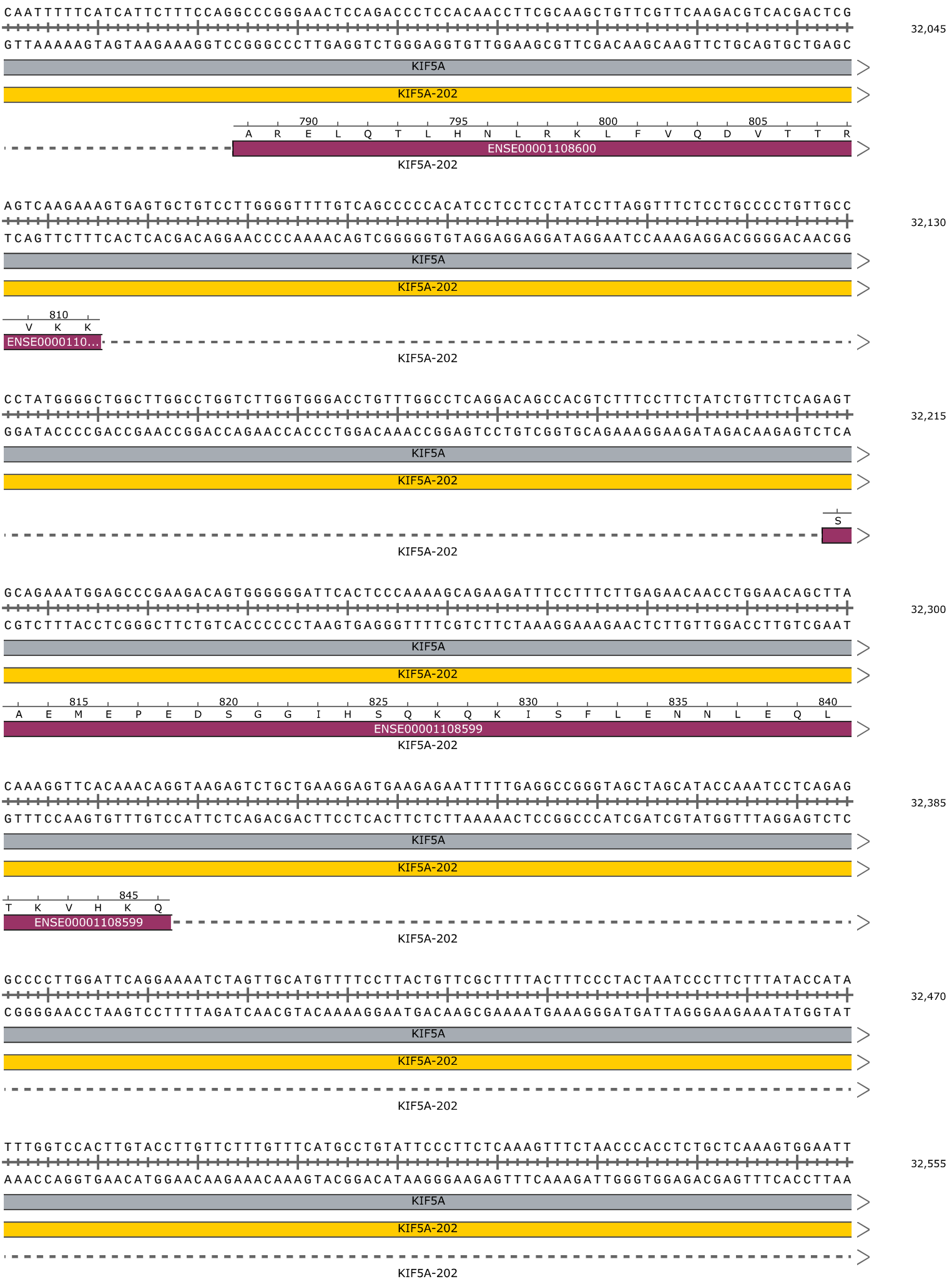
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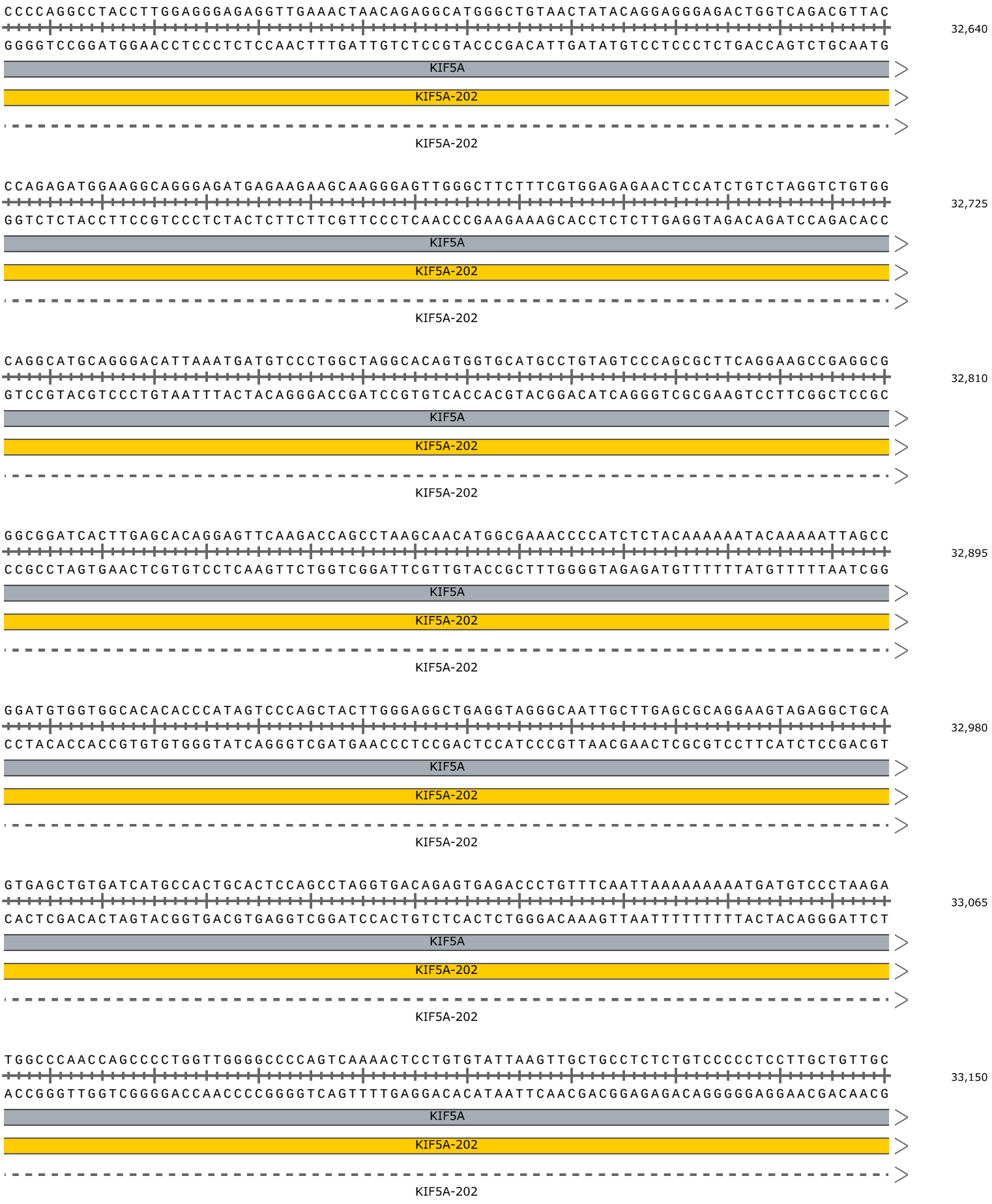
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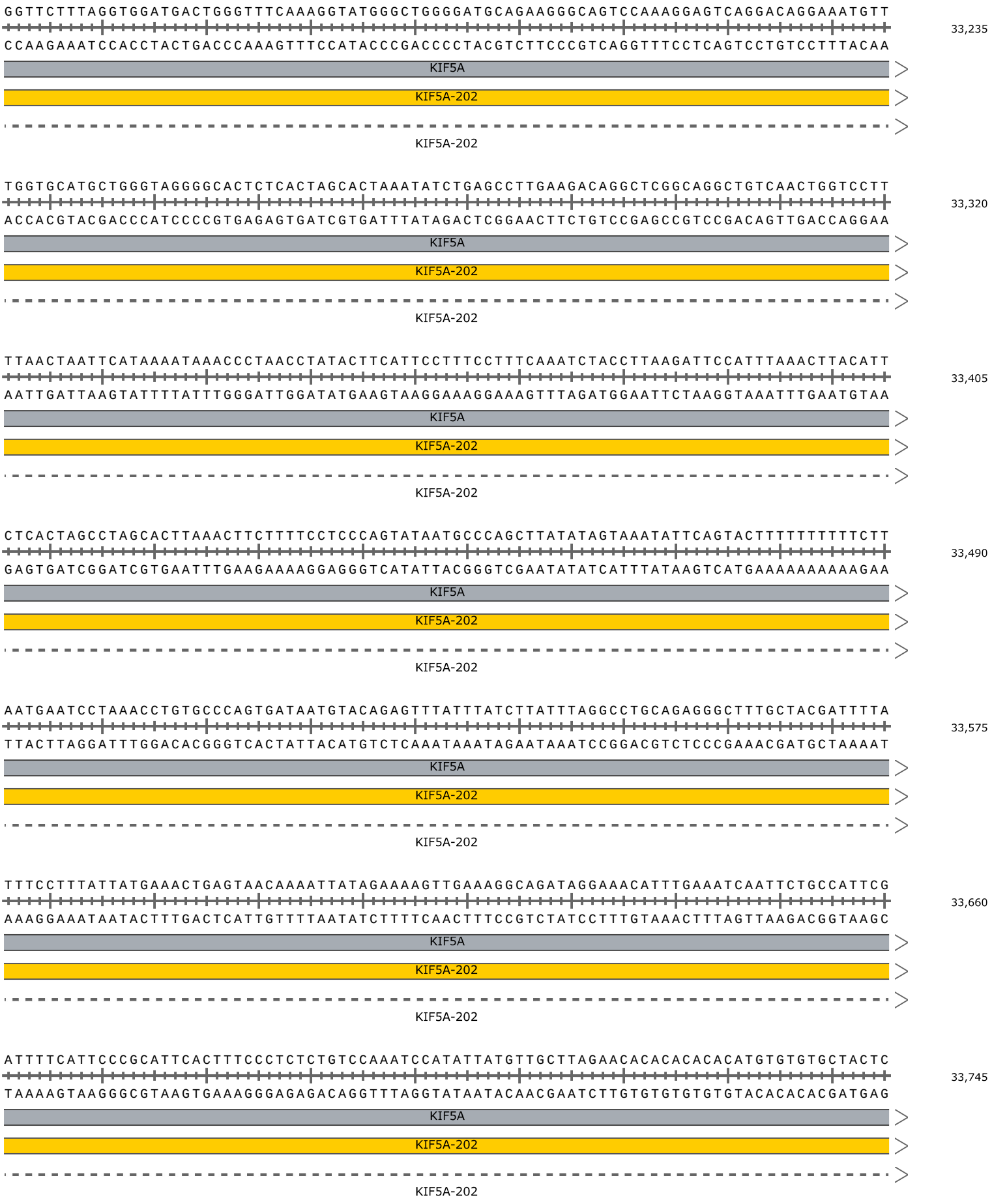
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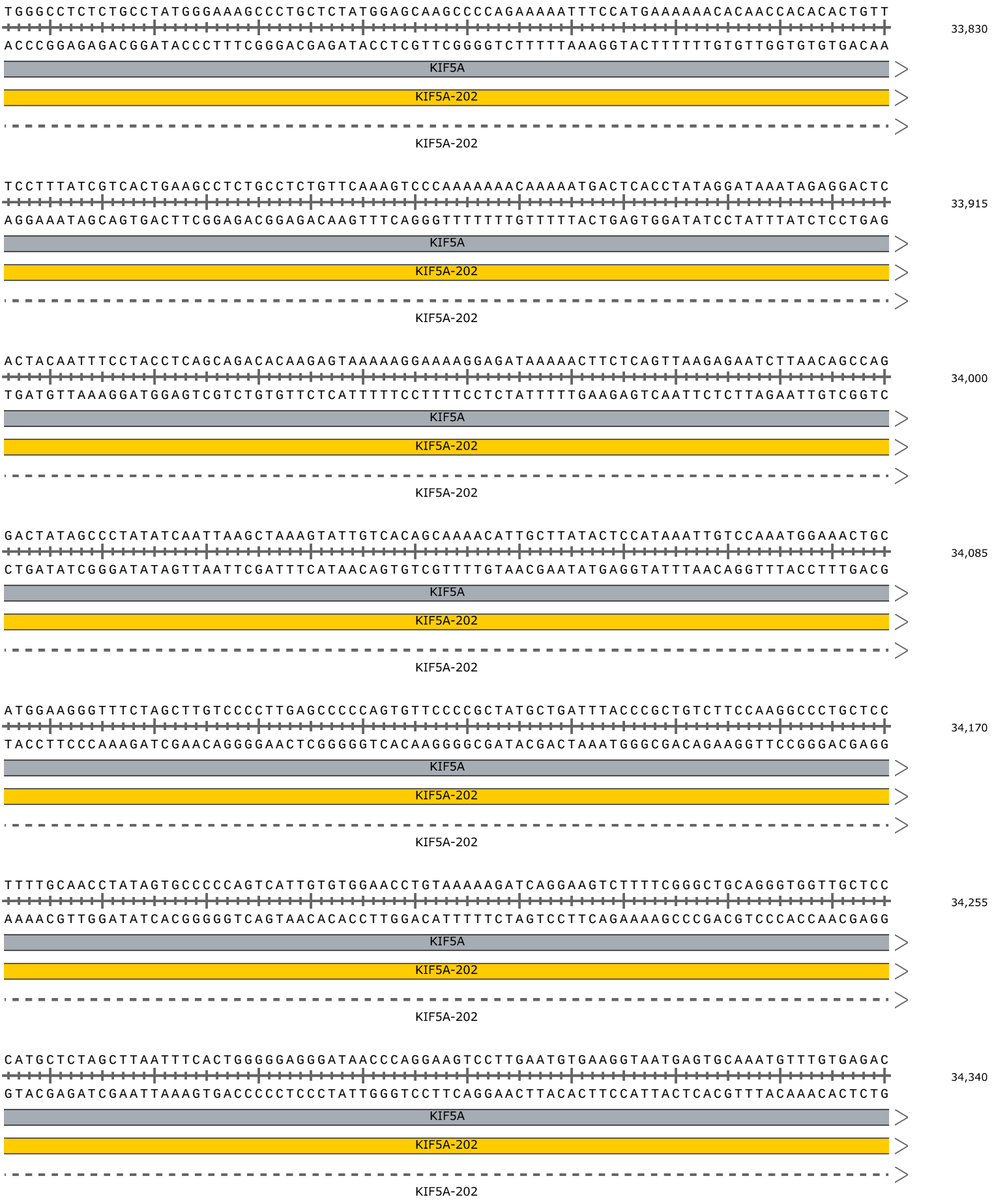
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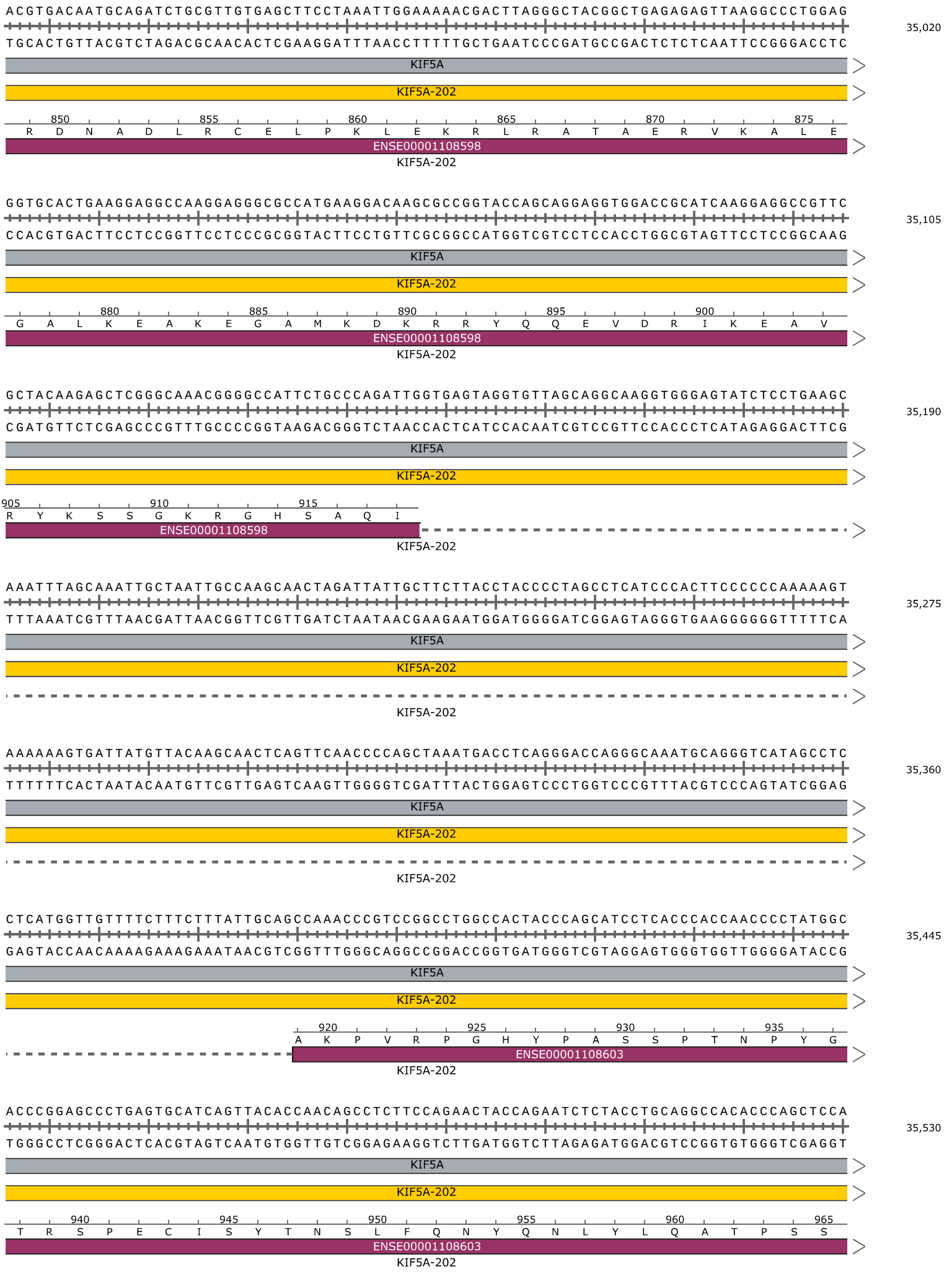
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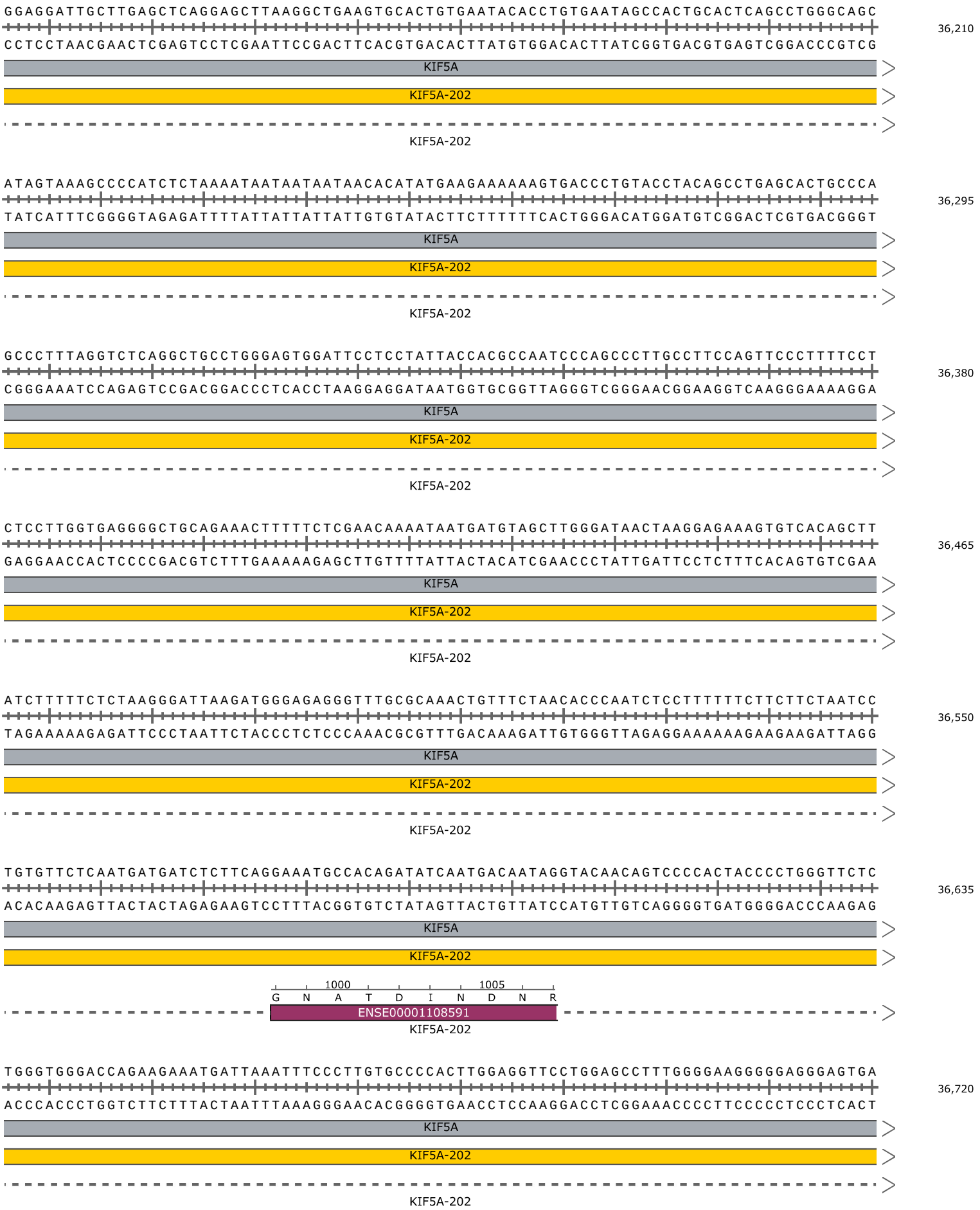
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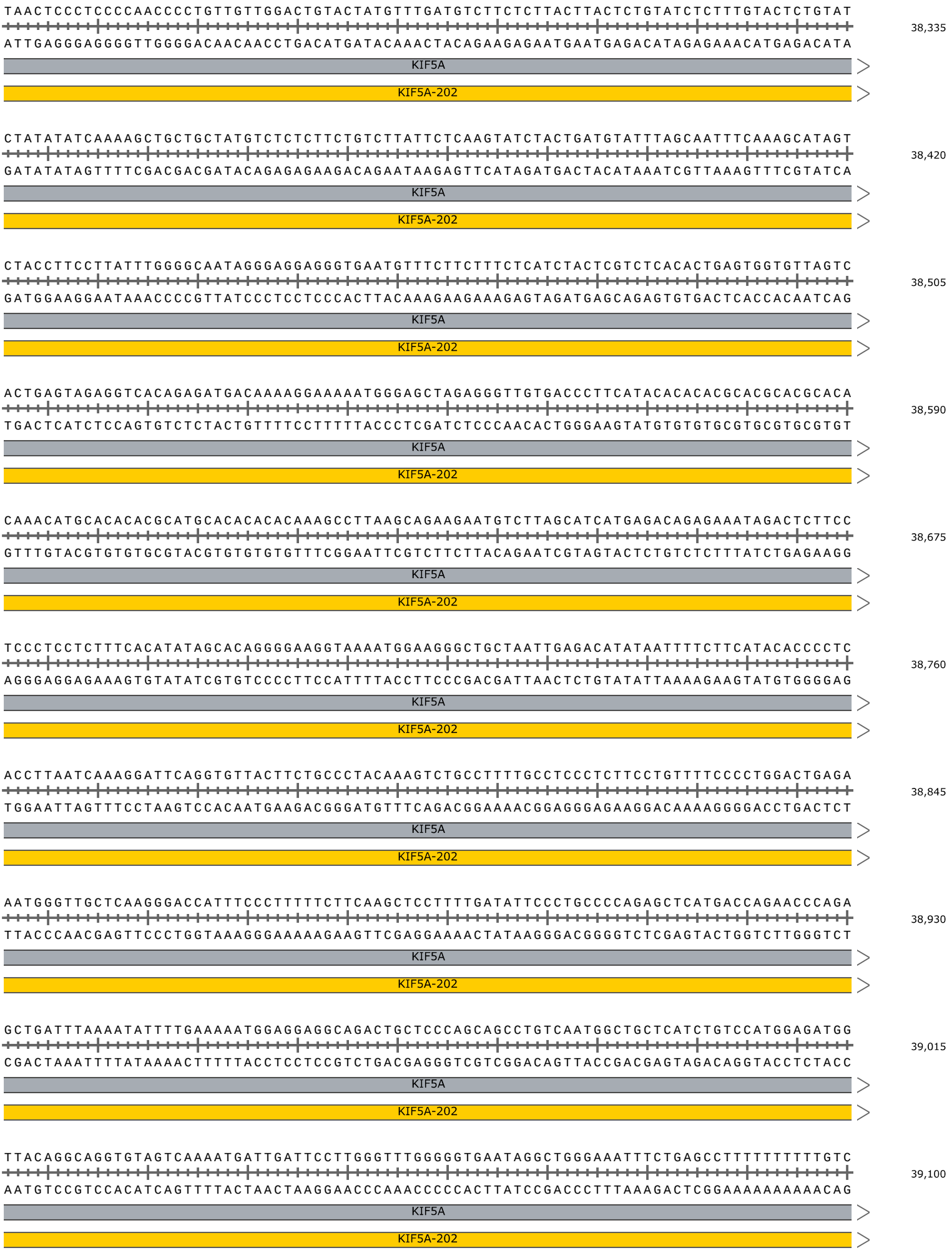
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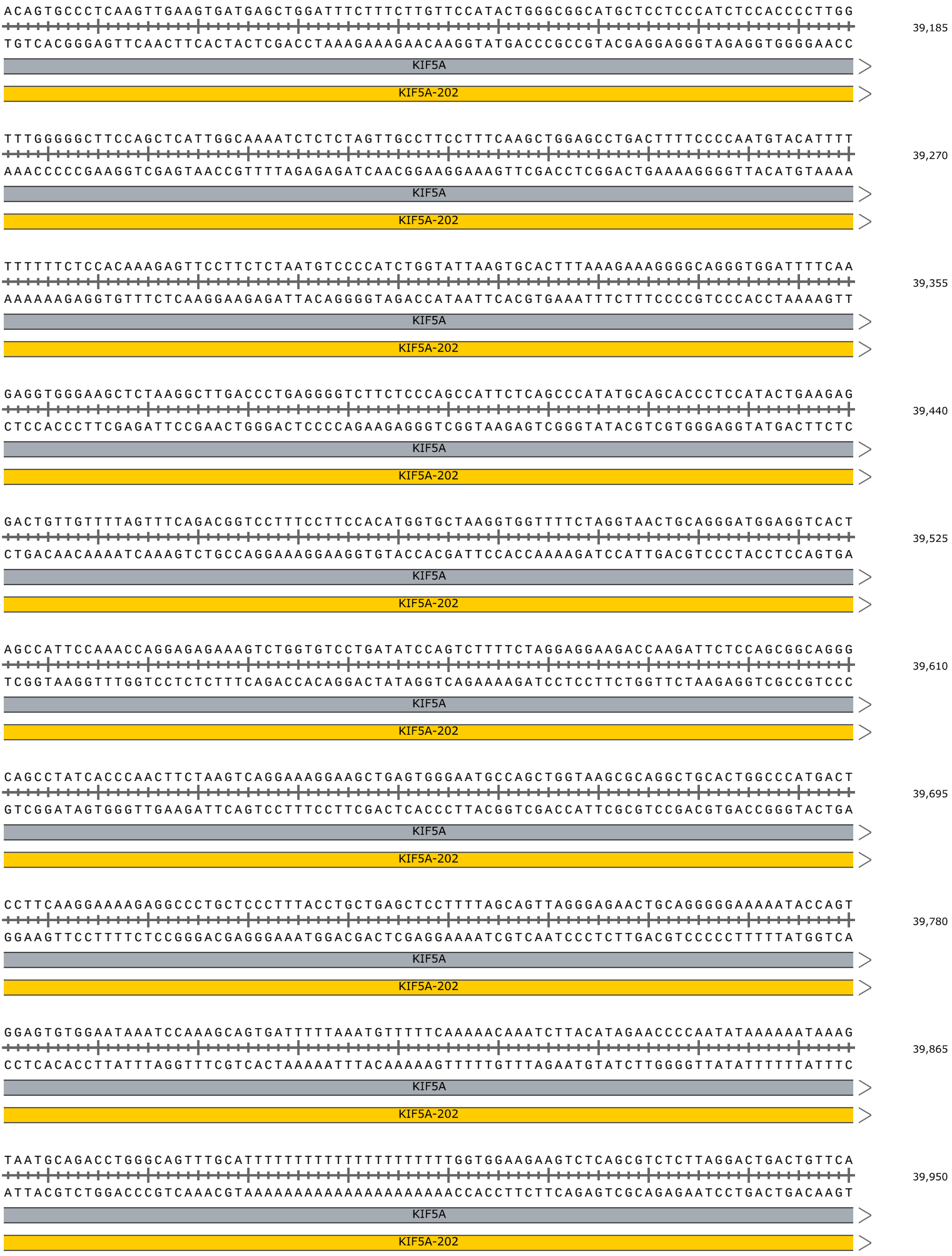
39,100
KIF5A
KIF5A-202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39,185
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KIF5A
KIF5A-202
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39,270
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KIF5A-202
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39,355
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KIF5A
KIF5A-202
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39,440
CTCCACCCTTCGAGATTCCGAACTGGGACTCCCCAGAAGAGGGTCGGTAAGAGTCGGGTATACGTCGTGGGAGGTATGACTTCTC
KIF5A
KIF5A-202
GACTGTTGTTTTAGTTTCAGACGGTCCTTTCCTTCCACATGGTGCTAAGGTGGTTTTCTAGGTAACTGCAGGGATGGAGGTCACT
39,525
CTGACAACAAAATCAAAGTCTGCCAGGAAAGGAAGGTGTACCACGATTCCACCAAAAGATCCATTGACGTCCCTACCTCCAGTGA
KIF5A
KIF5A-202
AGCCATTCCAAACCAGGAGAGAAAGTCTGGTGTCCTGATATCCAGTCTTTTCTAGGAGGAAGACCAAGATTCTCCAGCGGCAGGG
39,610
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KIF5A
KIF5A-202
CAGCCTATCACCCAACTTCTAAGTCAGGAAAGGAAGCTGAGTGGGAATGCCAGCTGGTAAGCGCAGGCTGCACTGGCCCATGACT
39,695
GTCGGATAGTGGGTTGAAGATTCAGTCCTTTCCTTCGACTCACCCTTACGGTCGACCATTCGCGTCCGACGTGACCGGGTACTGA
KIF5A
KIF5A-202
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39,780
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KIF5A
KIF5A-202
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39,865
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KIF5A
KIF5A-202
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39,950
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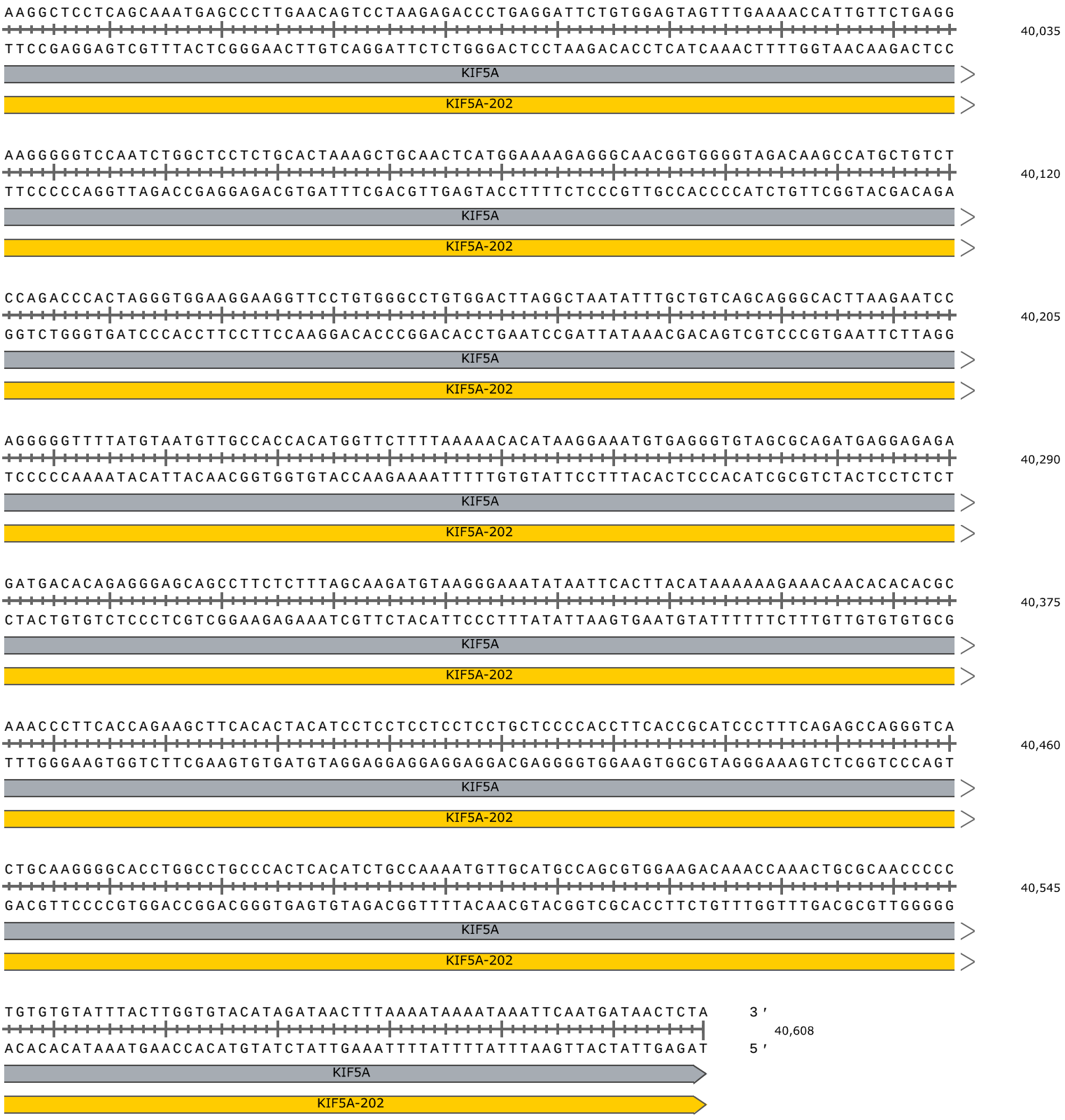
KIF5A
KIF5A-202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40,035
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KIF5A-202
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40,120
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KIF5A-202
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40,205
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KIF5A
KIF5A-202
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40,290
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KIF5A
KIF5A-202
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40,375
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KIF5A
KIF5A-202
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40,460
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KIF5A
KIF5A-202
CTGCAAGGGGCACCTGGCCTGCCCACTCACATCTGCCAAAATGTTGCATGCCAGCGTGGAAGACAAACCAAACTGCGCAACCCCC
40,545
GACGTTCCCCGTGGACCGGACGGGTGAGTGTAGACGGTTTTACAACGTACGGTCGCACCTTCTGTTTGGTTTGACGCGTTGGGGG
KIF5A
KIF5A-202
TGTGTGTATTTACTTGGTGTACATAGATAACTTTAAAATAAAATAAATTCAATGATAACTCTA
3′
40,608
ACACACATAAATGAACCACATGTATCTATTGAAATTTTATTTTATTTAAGTTACTATTGAGAT
5′
KIF5A
KIF5A-202

	Feature		Location		Size		Type
✓	**KIF5A**		1 .. 40,608		40,608 bp	→	gene
	/note	=	gene ENSG00000155980 Protein coding				
	KIF5A-227		1 .. 18,187		18,187 bp	→	prim_transcript
	/note	=	primary transcript ENST00000676250				
	DCTN2-213		3 .. 1149		1147 bp	←	prim_transcript
	/note	=	primary transcript ENST00000549712 protein_coding_CDS_not_defined				
	DCTN2-232		1576 .. 1181		40,214 bp	←	prim_transcript
	/note	=	primary transcript ENST00000678990 Retained intron				
	DCTN2-203		3078 .. 1168		38,699 bp	←	prim_transcript
	/note	=	primary transcript ENST00000546559 protein_coding_CDS_not_defined				
	KIF5A-204		4002 .. 40,605		36,604 bp	→	prim_transcript
	/note	=	primary transcript ENST00000674619				
✓	**KIF5A-202**		4019 .. 40,608		36,590 bp	→	prim_transcript
	/note	=	primary transcript ENST00000455537				
	KIF5A-201		4019 .. 38,623		34,605 bp	→	prim_transcript
	/note	=	primary transcript ENST00000286452				
	KIF5A-230		4019 .. 18,187		14,169 bp	→	prim_transcript
	/note	=	primary transcript ENST00000676359				
	KIF5A-211		4019 .. 17,668		13,650 bp	→	prim_transcript
	/note	=	primary transcript ENST00000675216 Nonsense mediated decay				
	KIF5A-209		4019 .. 17,501		13,483 bp	→	prim_transcript
	/note	=	primary transcript ENST00000675023 Nonsense mediated decay				
	KIF5A-232		4080 .. 40,567		36,488 bp	→	prim_transcript
	/note	=	primary transcript ENST00000676457				
	KIF5A-201		4247 .. 37,154		32,908 bp	→	CDS
	▸ 25 segments = 2832 bp						
	/note	=	coding sequence ENSP00000286452				
	/translation	=	MAETNNECSIKVLCRFRPLNQAEILRGDKFIPIFQGDDSVVIG,,VSYFEIYLDKIRDLLD,,VTKTNLSVHEDKNRVPFVK,,GCTERFVSSPEEILDVI DEGKSNRHVAVT,,NMNEHSSRSHSIFLINIKQENMETEQKLSGKLYLVDLAGSEK,,VSKTGAEGAVLDEAKNINKSLSALGNVISALAEGT,,KSYV PYRDSKMTRILQDSLGGNCRTTMFICCSPSSYNDAETKSTLMFGQR,,AKTIKNTASVNLELTAEQWKKKYEKEKEKTKAQKETIAKLEAELSRWRN ,,GENVPETERLAGEEAALGAELCEETPVNDNSSIVVRIAPEERQKYEEEIRRLYKQLDDK,,DDEINQQSQLIEKLKQQMLDQEE,,LLVSTRGDNE KVQRELSHLQSENDAAKDEVKEVLQALEELAVNYDQKSQEVEEKSQQNQLLVDELSQKV,,ATMLSLESELQRLQEVSGHQRKRIAEVLNGLMK DLSEFSVIVGNGEIKL,,PVEISGAIEEEFTVARLYISKIKSEVKSVVKRCRQLENLQVECHRKMEVTGRELSSCQLLISQ,,HEAKIRSLTEYMQSVE LKKRHLEESYDSLSDELAKLQAQ,,ETVHEVALKDKEPDTQDADEVK,,KALELQMESHREAHHRQLARLRDEINEKQKTIDELKD,,LNQKLQLELE KLQADYEKLKSEEHEKSTKLQELT,,FLYERHEQSKQDLKGLEETV,,ARELQTLHNLRKLFVQDVTTRVKK,,SAEMEPEDSGGIHSQKQKISFLENNL EQLTKVHKQ,,LVRDNADLRCELPKLEKRLRATAERVKALEGALKEAKEGAMKDKRRYQQEVDRIKEAVRYKSSGKRGHSAQI,,AKPVRPGHYPAS SPTNRYGTRSPFCISYTNSLFQNYQNLYLQATPSSTSDMY,,FANSCTSSGATSSGGPLASYQKANMDN,,GNATDINDNR,,SDLPCGYEAEDQAK LFPLHQETAAS*				
	943 amino acids = 107.3 kDa						
✓	**KIF5A-202**		4247 .. 37,154		32,908 bp	→	CDS
	▸ 28 segments = 3099 bp						
	/note	=	coding sequence ENSP00000408979				
	/translation	=	MAETNNECSIKVLCRFRPLNQAEILRGDKFIPIFQGDDSVVIG,,GKPYVFDRVFPPNTTQEQVYHACAMQIVK,,DVLAGYNGTIFAYGQTSSGKT HTME,,GKLHDPQLMGIIPRIARDIFNHIYSMDENLEFHIK,,VSYFEIYLDKIRDLLD,,VTKTNLSVHEDKNRVPFVK,,GCTERFVSSPEEILDVIDEG KSNRHVAVT,,NMNEHSSRSHSIFLINIKQENMETEQKLSGKLYLVDLAGSEK,,VSKTGAEGAVLDEAKNINKSLSALGNVISALAEGT,,KSYVPYR DSKMTRILQDSLGGNCRTTMFICCSPSSYNDAETKSTLMFGQR,,AKTIKNTASVNLELTAEQWKKKYEKEKEKTKAQKETIAKLEAELSRWRN,,GE NVPETERLAGEEAALGAELCEETPVNDNSSIVVRIAPEERQKYEEEIRRLYKQLDDK,,DDEINQQSQLIEKLKQQMLDQEE,,LLVSTRGDNEKVQ RELSHLQSENDAAKDEVKEVLQALEELAVNYDQKSQEVEEKSQQNQLLVDELSQKV,,ATMLSLESELQRLQEVSGHQRKRIAEVLNGLMKDLSE FSVIVGNGEIKL,,PVEISGAIEEEFTVARLYISKIKSEVKSVVKRCRQLENLQVECHRKMEVTGRELSSCQLLISQ,,HEAKIRSLTEYMQSVELKKR HLEESYDSLSDELAKLQAQ,,ETVHEVALKDKEPDTQDADEVK,,KALELQMESHREAHHRQLARLRDEINEKQKTIDELKD,,LNQKLQLELEKLQA DYEKLKSEEHEKSTKLQELT,,FLYERHEQSKQDLKGLEETV,,ARELQTLHNLRKLFVQDVTTRVKK,,SAEMEPEDSGGIHSQKQKISFLENNLEQLT KVHKQ,,LVRDNADLRCELPKLEKRLRATAERVKALEGALKEAKEGAMKDKRRYQQEVDRIKEAVRYKSSGKRGHSAQI,,AKPVRPGHYPASSPT NRYGTRSPFCISYTNSLFQNYQNLYLQATPSSTSDMY,,FANSCTSSGATSSGGPLASYQKANMDN,,GNATDINDNR,,SDLPCGYEAEDQAKLFPL HQETAAS*				
	1032 amino acids = 117.4 kDa						

Feature	Location	Size		Type
KIF5A-204	4247 .. 37,154	32,908 bp	→	CDS

▸ 29 segments = 3120 bp

/note = coding sequence ENSP00000502270

/translation = MAETNNECSIKVLCRFRPLNQAEILRGDKFIPIFQGDDSVVIG,,GKPYVFDRVFPPNTTQEQVYHACAMQIVK,,DVLAGYNGTIFAYGQTSSGKT
HTME,,GKLHDPQLMGIIPRIARDIFNHIYSMDENLEFHIK,,VSYFEIYLDKIRDLLD,,VTKTNLSVHEDKNRVPFVK,,GCTERFVSSPEEILDVIDEG
KSNRHVAVT,,NMNEHSSRSHSIFLINIKQENMETEQKLSGKLYLVDLAGSEK,,VSKTGAEGAVLDEAKNINKSLSALGNVISALAEGT,,KSYVPYR
DSKMTRILQDSLGGNCRTTMFICCSPSSYNDAETKSTLMFGQR,,AKTIKNTASVNLELTAEQWKKKYEKEKEKTKAQKETIAKLEAELSRWRN,,GE
NVPETERLAGEEAALGAELCEETPVNDNSSIVVRIAPEERQKYEEEIRRLYKQLDDK,,DDEINQQSQLIEKLKQQMLDQEE,,LLVSTRGDNEKVQ
RELSHLQSENDAAKDEVKEVLQALEELAVNYDQKSQEVEEKSQQNQLLVDELSQKV,,ATMLSLESELQRLQEVSGHQRKRIAEVLNGLMKDLSE
FSVIVGNGEIKL,,PVEISGAIEEEFTVARLYISKIKSEVKSVVKRCRQLENLQVECHRKMEVTGRELSSCQLLISQ,,HEAKIRSLTEYMQSVELKKR
HLEESYDSLSDELAKLQAQ,,ETVHEVALKDKEPDTQDADEVK,,KALELQMESHREAHHRQLARLRDEINEKQKTIDELKD,,LNQKLQLELEKLQA
DYEKLKSEEHEKSTKLQELT,,FLYERHEQSKQDLKGLEETV,,ARELQTLHNLRKLFVQDVTTRVKK,,SAEMEPEDSGGIHSQKQKISFLENNLEQLT
KVHKQ,,VDDWVSK,,LVRDNADLRCELPKLEKRLRATAERVKALEGALKEAKEGAMKDKRRYQQEVDRIKEAVRYKSSGKRGHSAQI,,AKPVRPG
HYPASSPTNPYGTRSPECISYTNSLFQNYQNLYLQATPSSTSDMY,,FANSCTSSGATSSGGPLASYQKANMDN,,GNATDINDNR,,SDLPCGYEAE
DQAKLFPLHQETAAS*

1039 amino acids = 116.2 kDa

KIF5A-232	4247 .. 37,154	32,908 bp	→	CDS

▸ 27 segments = 2994 bp

/note = coding sequence ENSP00000501588

/translation = MAETNNECSIKVLCRFRPLNQAEILRGDKFIPIFQGDDSVVIG,,GKPYVFDRVFPPNTTQEQVYHACAMQIVK,,DVLAGYNGTIFAYGQTSSGKT
HTME,,VSYFEIYLDKIRDLLD,,VTKTNLSVHEDKNRVPFVK,,GCTERFVSSPEEILDVIDEGKSNRHVAVT,,NMNEHSSRSHSIFLINIKQENMETE
QKLSGKLYLVDLAGSEK,,VSKTGAEGAVLDEAKNINKSLSALGNVISALAEGT,,KSYVPYRDSKMTRILQDSLGGNCRTTMFICCSPSSYNDAETK
STLMFGQR,,AKTIKNTASVNLELTAEQWKKKYEKEKEKTKAQKETIAKLEAELSRWRN,,GENVPETERLAGEEAALGAELCEETPVNDNSSIVVRI
APEERQKYEEEIRRLYKQLDDK,,DDEINQQSQLIEKLKQQMLDQEE,,LLVSTRGDNEKVQRELSHLQSENDAAKDEVKEVLQALEELAVNYDQK
SQEVEEKSQQNQLLVDELSQKV,,ATMLSLESELQRLQEVSGHQRKRIAEVLNGLMKDLSEFSVIVGNGEIKL,,PVEISGAIEEEFTVARLYISKIKS
EVKSVVKRCRQLENLQVECHRKMEVTGRELSSCQLLISQ,,HEAKIRSLTEYMQSVELKKRHLEESYDSLSDELAKLQAQ,,ETVHEVALKDKEPDT
QDADEVK,,KALELQMESHREAHHRQLARLRDEINEKQKTIDELKD,,LNQKLQLELEKLQADYEKLKSEEHEKSTKLQELT,,FLYERHEQSKQDLKG
LEETV,,ARELQTLHNLRKLFVQDVTTRVKK,,SAEMEPEDSGGIHSQKQKISFLENNLEQLTKVHKQ,,LVRDNADLRCELPKLEKRLRATAERVKAL
EGALKEAKEGAMKDKRRYQQEVDRIKEAVRYKSSGKRGHSAQI,,AKPVRPGHYPASSPTNPYGTRSPECISYTNSLFQNYQNLYLQATPSSTSD
MY,,FANSCTSSGATSSGGPLASYQKANMDN,,GNATDINDNR,,SDLPCGYEAEDQAKLFPLHQETAAS*

997 amino acids = 113.2 kDa

KIF5A-230	4247 .. 18,187	13,941 bp	→	CDS

▸ 2 segments = 234 bp

/note = coding sequence ENSP00000502609

/translation = MAETNNECSIKVLCRFRPLNQAEILRGDKFIPIFQGDDSVVIG,,GKLHDPQLMGIIPRIARDIFNHIYSMDENLEFHIK

78 amino acids = 9.0 kDa

DCTN2-208	10,530 .. 1181	31,260 bp	←	prim_transcript

/note = primary transcript ENST00000547480
Retained intron

DCTN2-207	11,047 .. 1163	30,725 bp	←	prim_transcript

/note = primary transcript ENST00000547345
Retained intron

DCTN2-204	13,031 .. 1160	28,738 bp	←	prim_transcript

/note = primary transcript ENST00000546670
Protein coding

DCTN2-218	13,232 .. 1096	28,473 bp	←	prim_transcript

/note = primary transcript ENST00000550954
Protein coding

DCTN2-217	14,010 .. 1197	27,796 bp	←	prim_transcript

/note = primary transcript ENST00000550750
Nonsense mediated decay

DCTN2-222	14,010 .. 1054	27,653 bp	←	prim_transcript

/note = primary transcript ENST00000551611
Nonsense mediated decay

DCTN2-212	15,408 .. 1095	26,296 bp	←	prim_transcript

/note = primary transcript ENST00000549394
Nonsense mediated decay

DCTN2-215	15,671 .. 1127	26,065 bp	←	prim_transcript

/note = primary transcript ENST00000550201
Nonsense mediated decay

DCTN2-201	15,714 .. 1116	26,011 bp	←	prim_transcript

/note = primary transcript ENST00000434715
Protein coding

DCTN2-228	15,715 .. 1199	26,093 bp	←	prim_transcript

/note = primary transcript ENST00000678322
Protein coding

Feature			Location			Size			Type
DCTN2-202			15,715	..	1152	26,046 bp		←	prim_transcript
/note	=	primary transcript ENST00000543672 Protein coding							
DCTN2-231			15,715	..	666	25,560 bp		←	prim_transcript
/note	=	primary transcript ENST00000678653 Protein coding							
DCTN2-230			15,872	..	1197	25,934 bp		←	prim_transcript
/note	=	primary transcript ENST00000678521 Nonsense mediated decay							
DCTN2-224			15,946	..	1152	25,815 bp		←	prim_transcript
/note	=	primary transcript ENST00000552390 Retained intron							
DCTN2-229			15,951	..	1152	25,810 bp		←	prim_transcript
/note	=	primary transcript ENST00000678505 Protein coding							
DCTN2-209			15,974	..	1167	25,802 bp		←	prim_transcript
/note	=	primary transcript ENST00000548249 Protein coding							
DCTN2			16,392	..	1199	25,416 bp		←	gene
/note	=	gene ENSG00000175203 Protein coding							
KIF5A-227			18,107	..	18,187	81 bp		→	CDS
/note	=	coding sequence ENSP00000501749							
/translation	=	MGIIPRIARDIFNHIYSMDENLEFHIK 27 amino acids = 3.3 kDa							
✓ **Donor Template WT -> SNV**			22,970	..	23,069	100 bp		⊢	misc_feature
✓ **Protospacer Sequence**			22,988	..	23,007	20 bp		⊢	misc_feature
✓ **SNV**			22,990	..	22,990	1 bp		⊢	misc_feature
/note	=	WT = A SNV = G							
✓ **PAM**			23,008	..	23,010	3 bp		⊢	misc_feature
KIF5A-225			23,266	..	33,860	10,595 bp		→	prim_transcript
/note	=	primary transcript ENST00000676081 Retained intron							
KIF5A-220			23,555	..	40,399	16,845 bp		→	prim_transcript
/note	=	primary transcript ENST00000675882 Retained intron							
KIF5A-205			25,296	..	25,584	289 bp		→	prim_transcript
/note	=	primary transcript ENST00000674653 protein_coding_CDS_not_defined							
KIF5A-223			25,744	..	33,822	8079 bp		→	prim_transcript
/note	=	primary transcript ENST00000675984 Retained intron							
KIF5A-229			26,036	..	29,247	3212 bp		→	CDS
▶ 2 segments = 396 bp									
/note	=	coding sequence ENSP00000501978							
/translation	=	LLVSTRGDNEKVQRELSHLQSENDAAKDEVKEVLQALEELAVNYDQKSQEVEEKSQQNQLLVDELSQKV,,PVEISGAIEEEFTVARLYISKIKSEVKSVVKRCRQLENLQVECHRKMEVTGRELSSCQLLISQ 132 amino acids = 15.1 kDa							
KIF5A-229			26,036	..	29,247	3212 bp		→	prim_transcript
/note	=	primary transcript ENST00000676352							
KIF5A-226			26,036	..	26,701	666 bp		→	prim_transcript
/note	=	primary transcript ENST00000676242 protein_coding_CDS_not_defined							
KIF5A-222			26,116	..	39,314	13,199 bp		→	prim_transcript
/note	=	primary transcript ENST00000675929 Retained intron							

Feature	Location	Size		Type
KIF5A-215	26,555 .. 29,247	2693 bp	→	CDS

▸ 2 segments = 234 bp

/note = coding sequence ENSP00000502531

/translation = ATMLSLESELQRLQE,,PVEISGAIEEEFTVARLYISKIKSEVKSVVKRCRQLENLQVECHRKMEVTGRELSSCQLLISQ
78 amino acids = 9.0 kDa

KIF5A-215	26,555 .. 29,247	2693 bp	→	prim_transcript

/note = primary transcript ENST00000675629

KIF5A-212	29,059 .. 30,837	1779 bp	→	prim_transcript

/note = primary transcript ENST00000675299
Nonsense mediated decay

KIF5A-213	30,768 .. 33,409	2642 bp	→	prim_transcript

/note = primary transcript ENST00000675397
protein_coding_CDS_not_defined

KIF5A-206	32,213 .. 35,543	3331 bp	→	prim_transcript

/note = primary transcript ENST00000674776
Nonsense mediated decay

KIF5A-221	32,213 .. 35,147	2935 bp	→	CDS

▸ 2 segments = 310 bp

/note = coding sequence ENSP00000502360

/translation = SAEMEPEDSGGIHSQKQKISFLENNLEQLTK,,LVRDNADLRCELPKLEKRLRATAERVKALEGALKEAKEGAMKDKRRYQQEVDRIKEAVRYKSS
GKRGHSAQI
103 amino acids = 11.8 kDa

KIF5A-221	32,213 .. 35,147	2935 bp	→	prim_transcript

/note = primary transcript ENST00000675907

KIF5A-216	34,931 .. 35,543	613 bp	→	CDS

▸ 2 segments = 404 bp

/note = coding sequence ENSP00000502231

/translation = LVRDNADLRCELPKLEKRLRATAERVKALEGALKEAKEGAMKDKRRYQQEVDRIKEAVRYKSSGKRGHSAQI,,ASSWLFSFFIAAKPVRPGHYPA
SSPTNPYGTRSPECISYTNSLFQNYQNLYLQATPSSTSDM
134 amino acids = 15.2 kDa

KIF5A-216	34,931 .. 35,543	613 bp	→	prim_transcript

/note = primary transcript ENST00000675634

KIF5A-218	34,989 .. 39,831	4843 bp	→	prim_transcript

/note = primary transcript ENST00000675737
Retained intron

KIF5A-203	35,653 .. 36,849	1197 bp	→	prim_transcript

/note = primary transcript ENST00000552227
Retained intron

KIF5A-217	35,845 .. 38,623	2779 bp	→	prim_transcript

/note = primary transcript ENST00000675697

KIF5A-217	35,845 .. 38,199	2355 bp	→	CDS

▸ 3 segments = 205 bp

/note = coding sequence ENSP00000501809

/translation = LCKLLYQQWSHIFWRPLGFLPEGQHGQW,,SDLPCGYEAEDQAKLFPLHQETAAS*SPTPTAAYLHFQ,,FL
68 codons (1 internal stop codon)

KIF5A-224	35,845 .. 36,604	760 bp	→	CDS

▸ 2 segments = 99 bp

/note = coding sequence ENSP00000501739

/translation = LCKLLYQQWSHIFWRPLGFLPEGQHGQ*,,YQ*Q*
33 codons (2 internal stop codons)

KIF5A-224	35,845 .. 36,604	760 bp	→	prim_transcript

/note = primary transcript ENST00000676055

KIF5A-231	35,911 .. 39,873	3963 bp	→	prim_transcript

/note = primary transcript ENST00000676437

Feature	Location	Size		Type
KIF5A-231	35,911 .. 36,902	992 bp	→	CDS

▸ 2 segments = 343 bp

/note = coding sequence ENSP00000502358
/translation = GQHGQW,,KCHRYQ*Q*VQQSPLPLGSLGGTRRND*ISLVPHLEVPGAFGEGGGSETHSFHHCVVQEIQSFPCLSAEYLPSSNPICGFSLFQ**G LDENNVGI*RLGFSPTFGSLV
114 codons (6 internal stop codons)

KIF5A-219	36,577 .. 38,623	2047 bp	→	prim_transcript

/note = primary transcript ENST00000675866

KIF5A-219	36,577 .. 38,199	1623 bp	→	CDS

▸ 2 segments = 35 bp

/note = coding sequence ENSP00000502341
/translation = EMPQISMTI,,VS
11 amino acids = 1.2 kDa

KIF5A-210	36,577 .. 37,190	614 bp	→	prim_transcript

/note = primary transcript ENST00000675201
protein_coding_CDS_not_defined

KIF5A-228	36,577 .. 37,190	614 bp	→	prim_transcript

/note = primary transcript ENST00000676265
protein_coding_CDS_not_defined

KIF5A-208	37,076 .. 40,608	3533 bp	→	prim_transcript

/note = primary transcript ENST00000674980

KIF5A-214	37,076 .. 40,608	3533 bp	→	prim_transcript

/note = primary transcript ENST00000675433

KIF5A-207	37,076 .. 37,481	406 bp	→	prim_transcript

/note = primary transcript ENST00000674858

KIF5A-207	37,076 .. 37,154	79 bp	→	CDS

/note = coding sequence ENSP00000502170
/translation = E*PAVWL*G*GPGQAFPSPPRDSSQL
26 codons (3 internal stop codons)

KIF5A-208	37,076 .. 37,154	79 bp	→	CDS

/note = coding sequence ENSP00000501935
/translation = E*PAVWL*G*GPGQAFPSPPRDSSQL
26 codons (3 internal stop codons)

KIF5A-214	37,076 .. 37,154	79 bp	→	CDS

/note = coding sequence ENSP00000502122
/translation = E*PAVWL*G*GPGQAFPSPPRDSSQL
26 codons (3 internal stop codons)

	Primer	Length	Binding Sites		Tm	Date Added
✓	**PCR Forward**	25-mer	22,721 .. 22,745	→	62°C	Jan 18, 2023
	/sequence = TGTAATATGTGGCAGGGGTTAGGGG 52% GC / 7873.2 Da					
✓	**Sanger Sequencing**	20-mer	22,867 .. 22,886	→	61°C	Jan 18, 2023
	/sequence = TGGAACGAGGTGGTGACAGC 60% GC / 6247.1 Da					
✓	**Donor Template WT -> SNV**	100-mer	22,970 .. 23,069	←	78°C	Jan 18, 2023
	/sequence = GGGTGAGGGGACCTAAGGATCACTCACAGTGCCCTCAGCCAGTGCGGAGATCACATTGCCCAGAGCTGACAGTGACTTGCTGATATTCT 56% GC / 10827.0 Da					
✓	**gRNA Protospacer**	20-mer	22,988 .. 23,007	→	56°C	Jan 18, 2023
	/sequence = CAACAAGTCACTGTCAGCTC 50% GC / 6046.0 Da					
✓	**PCR Reverse**	25-mer	23,503 .. 23,527	←	61°C	Jan 18, 2023
	/sequence = TTCTTAATGGTCTTTGCCCTGGGTG 48% GC / 7661.0 Da					