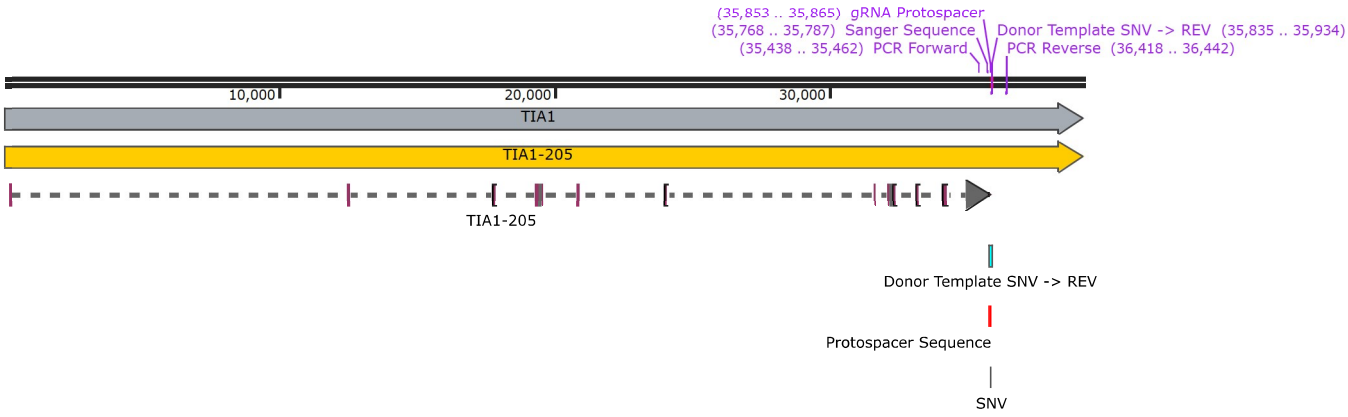

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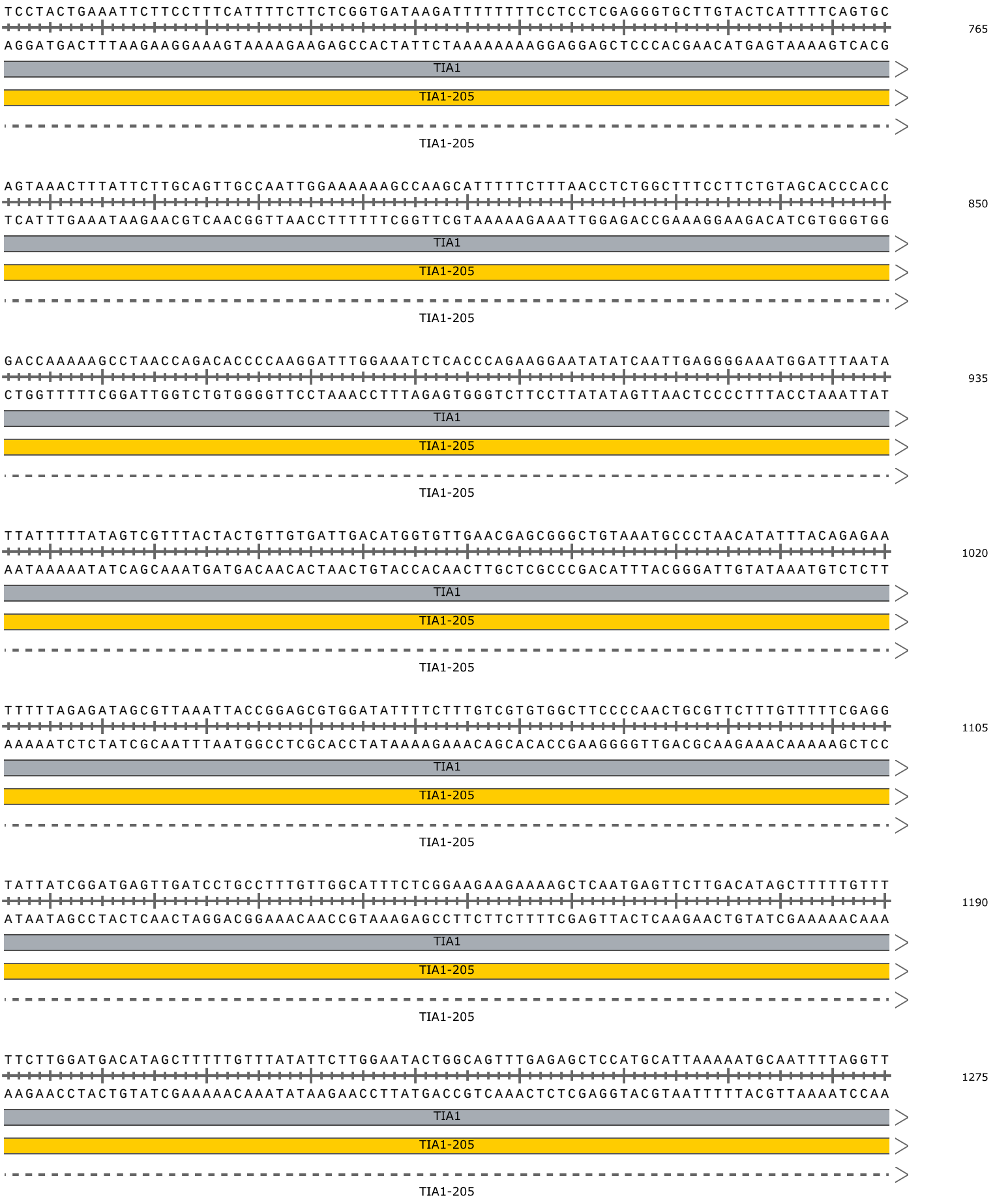
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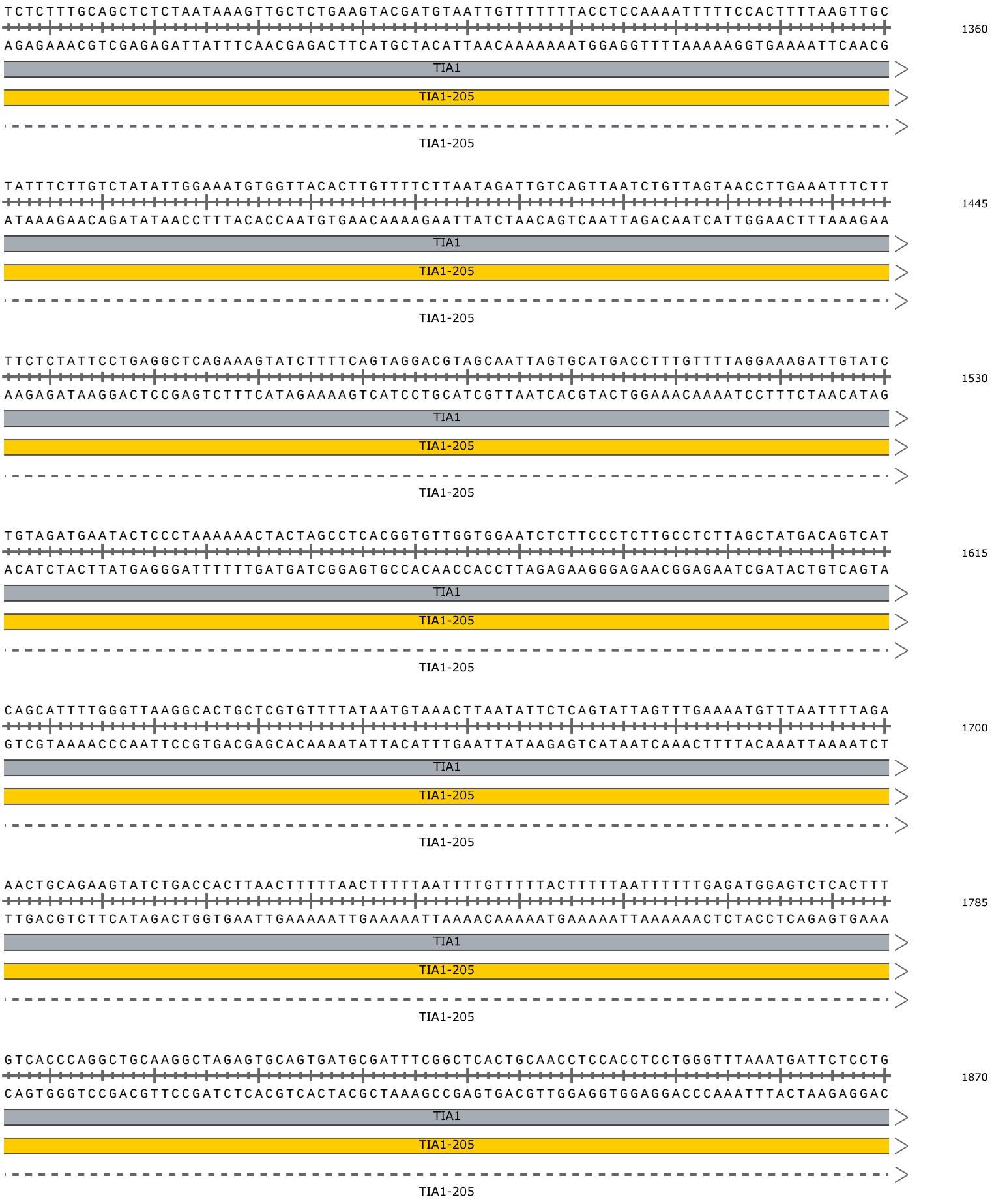
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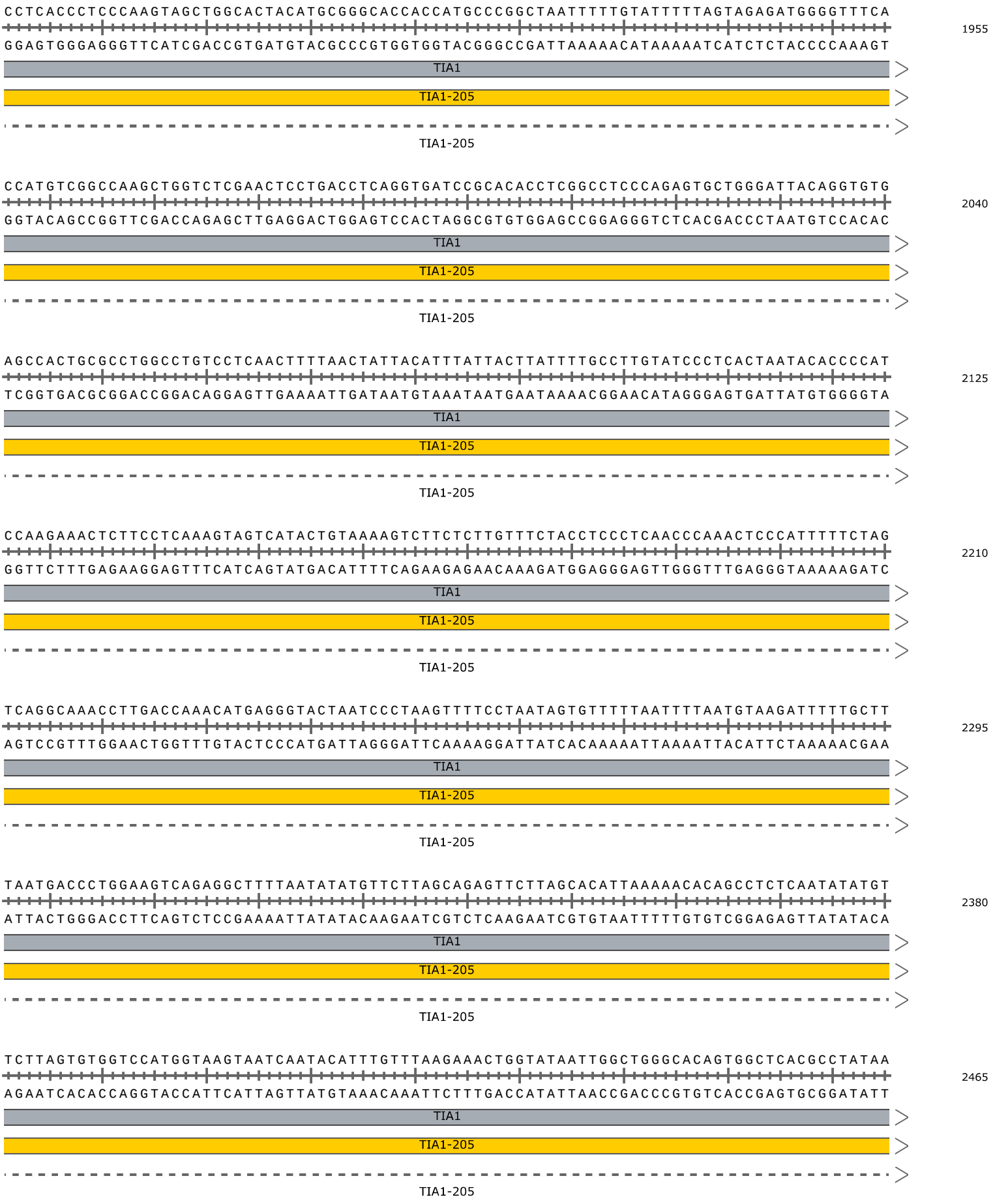
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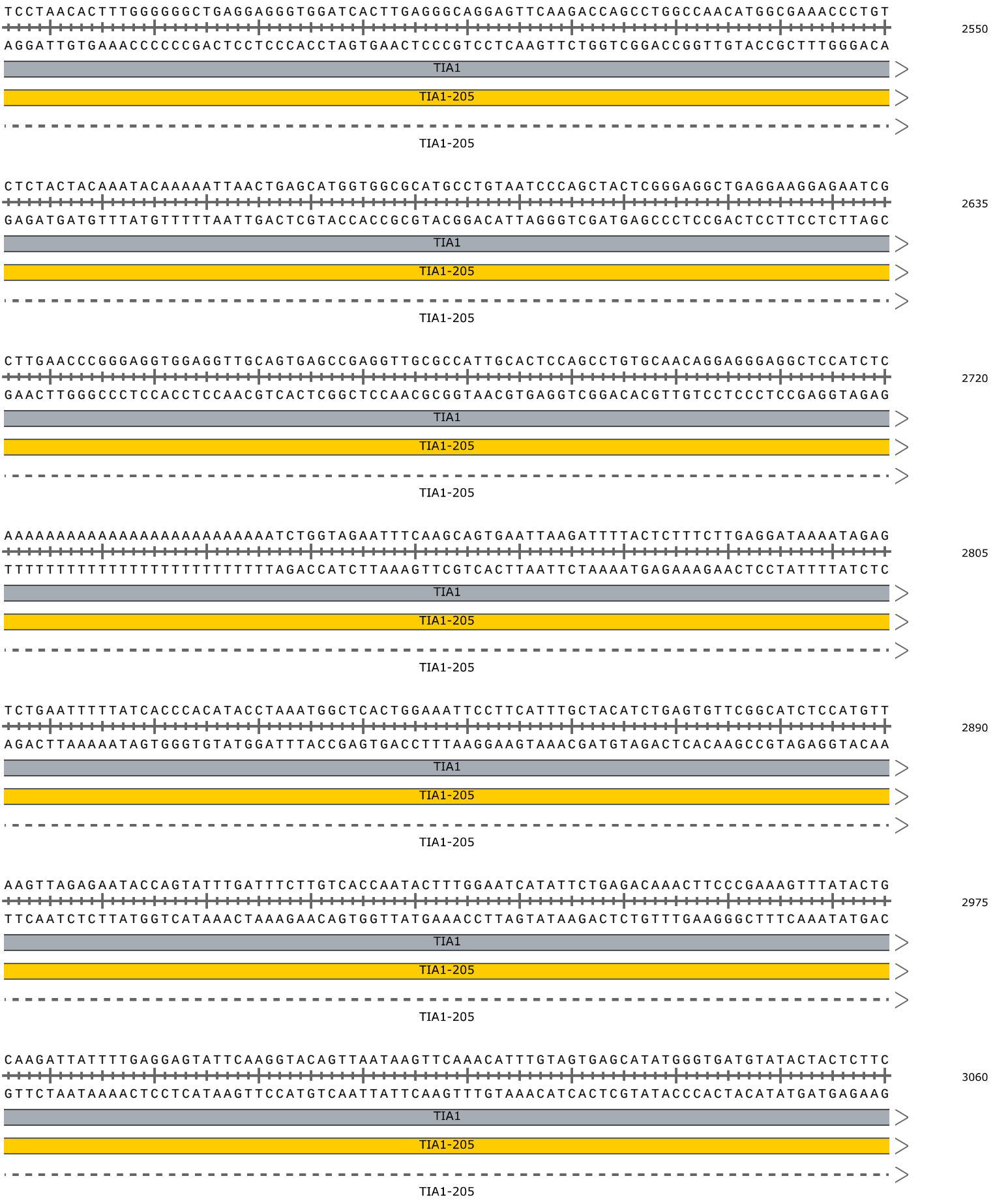
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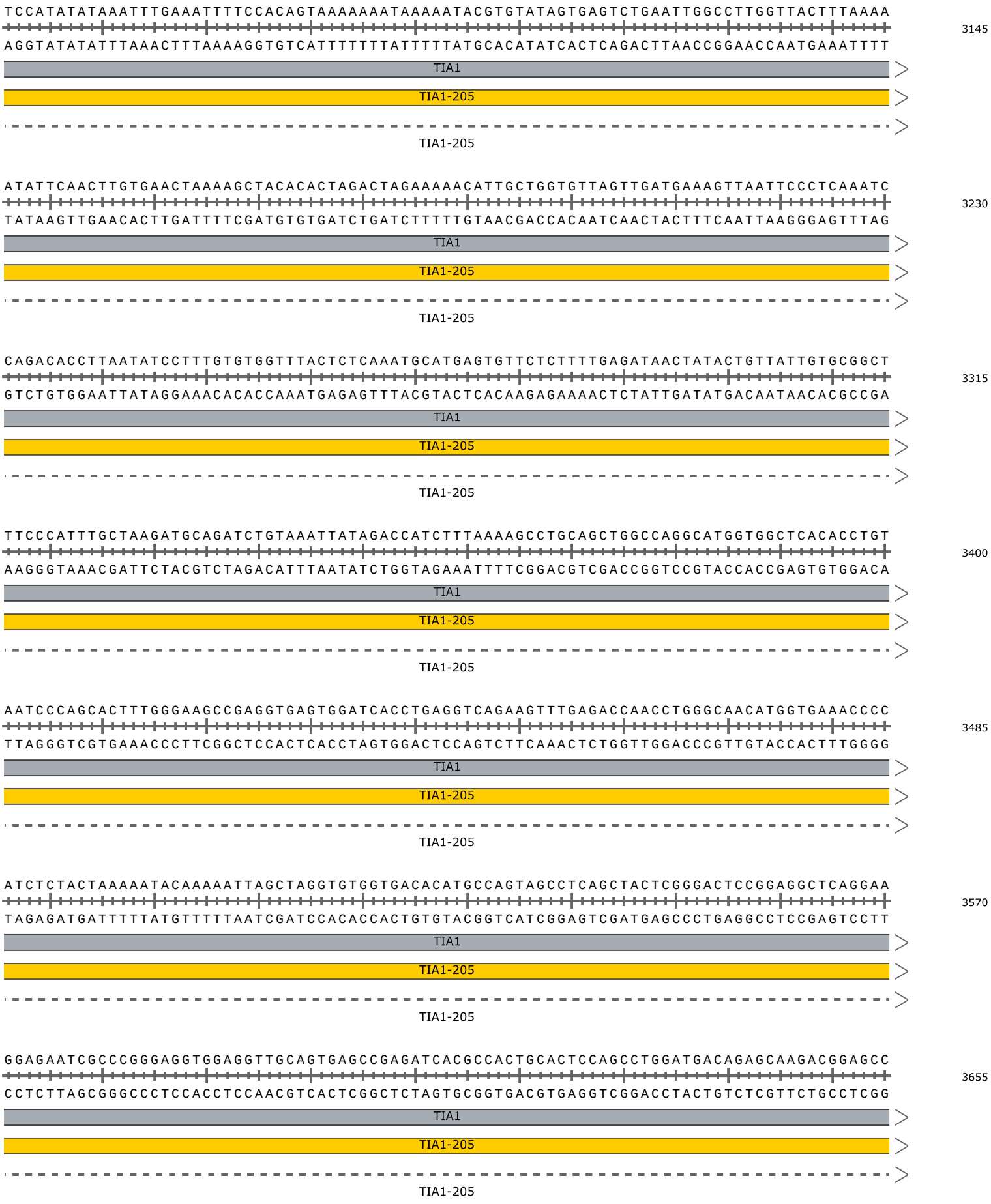
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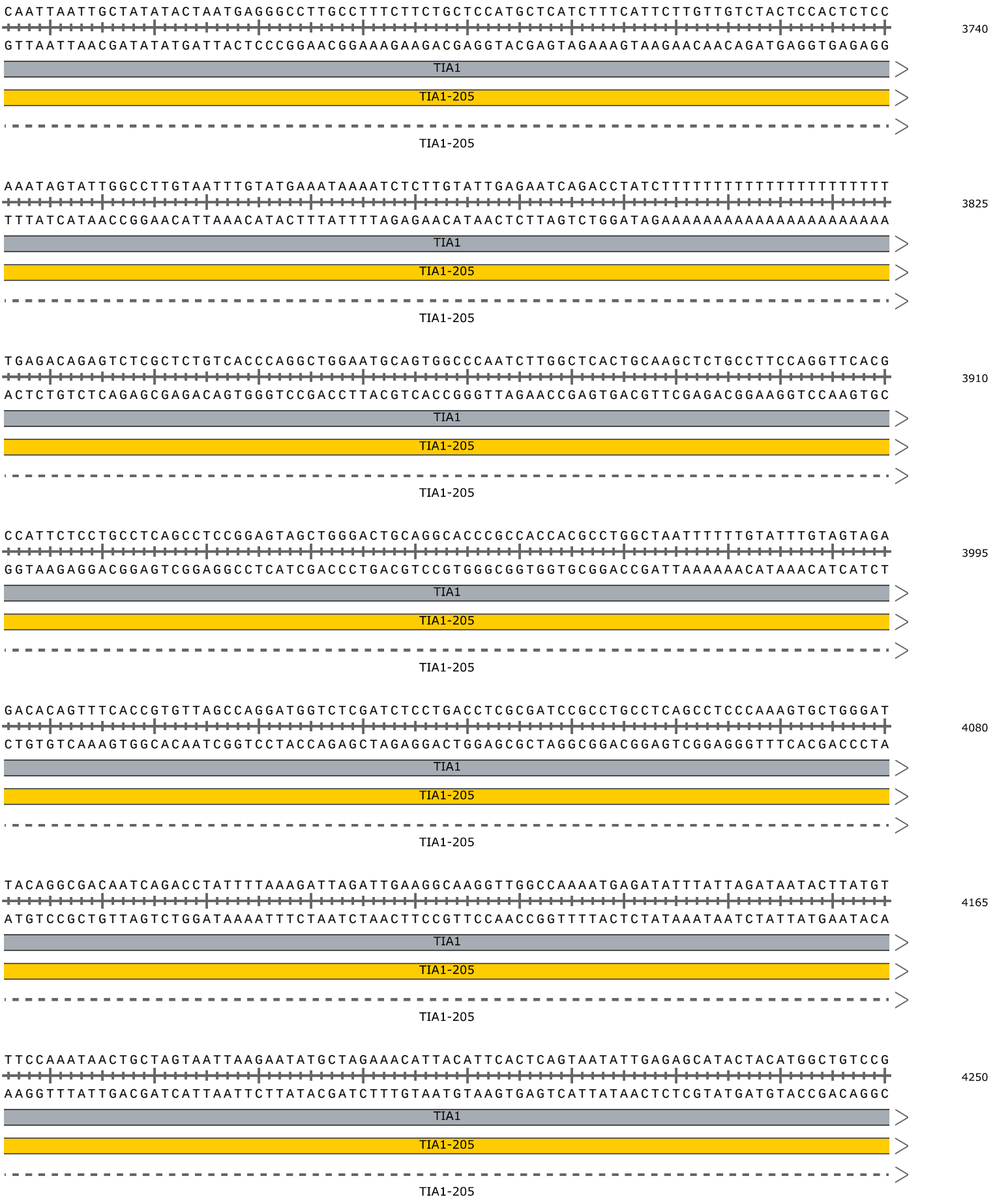
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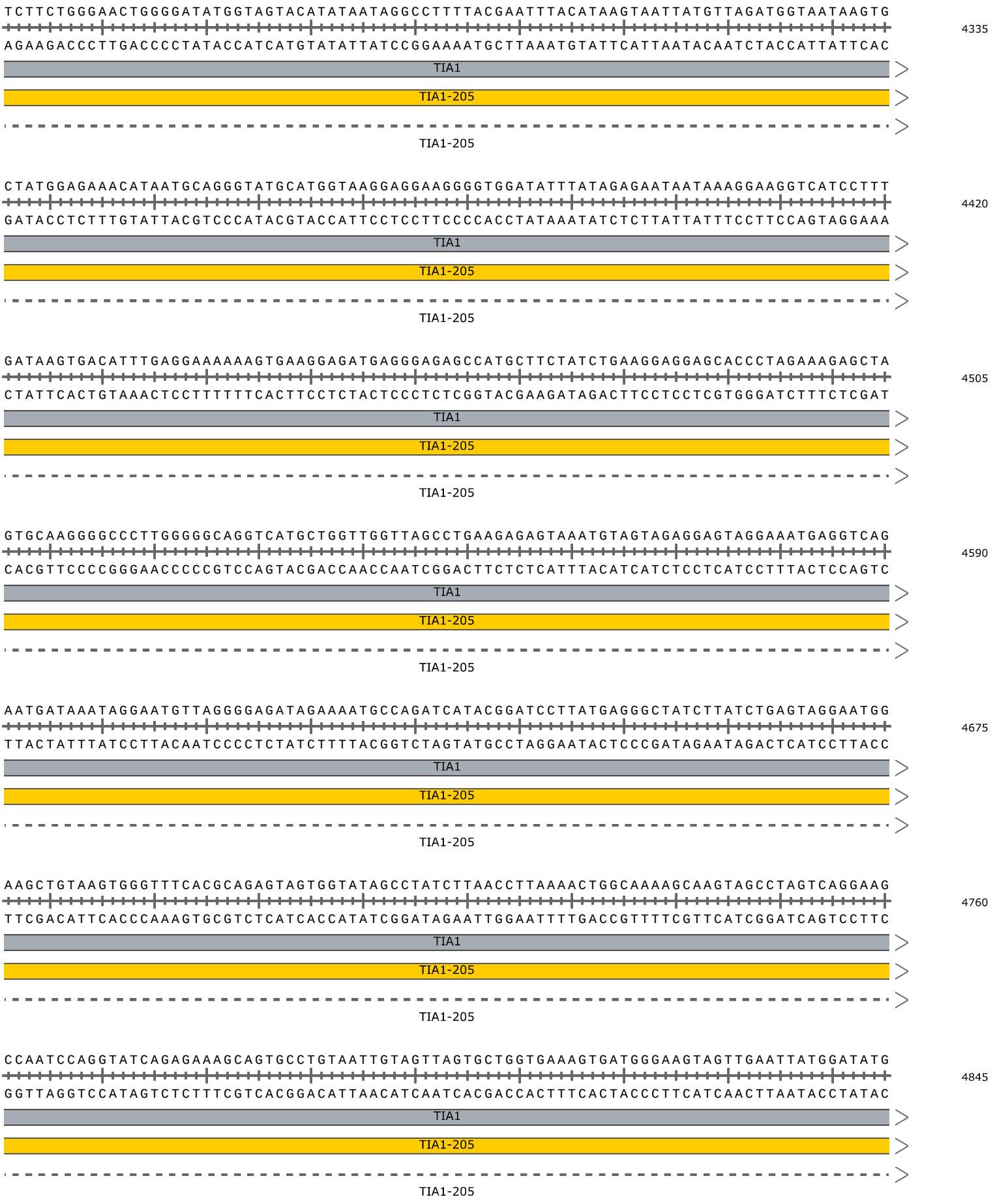
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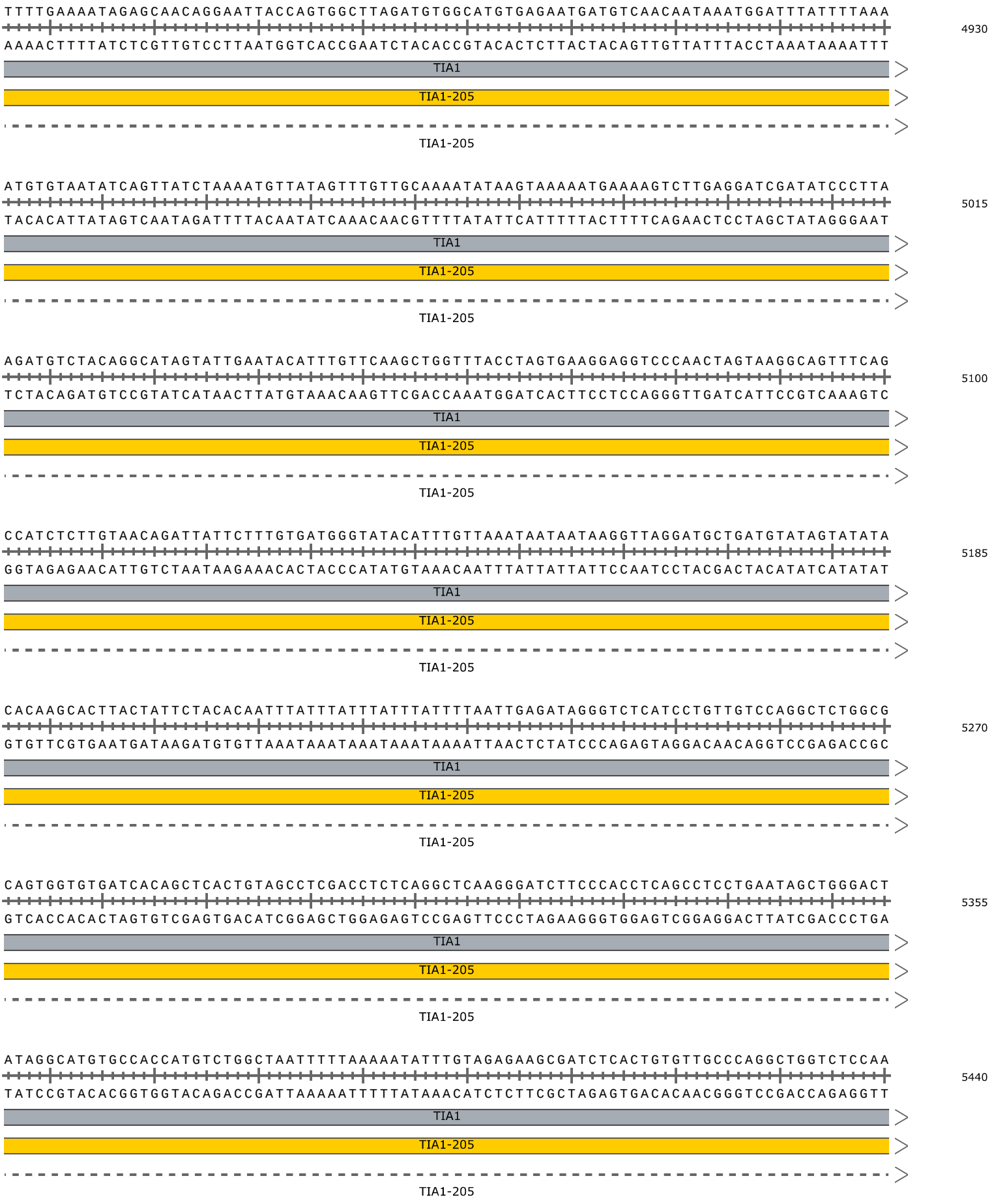
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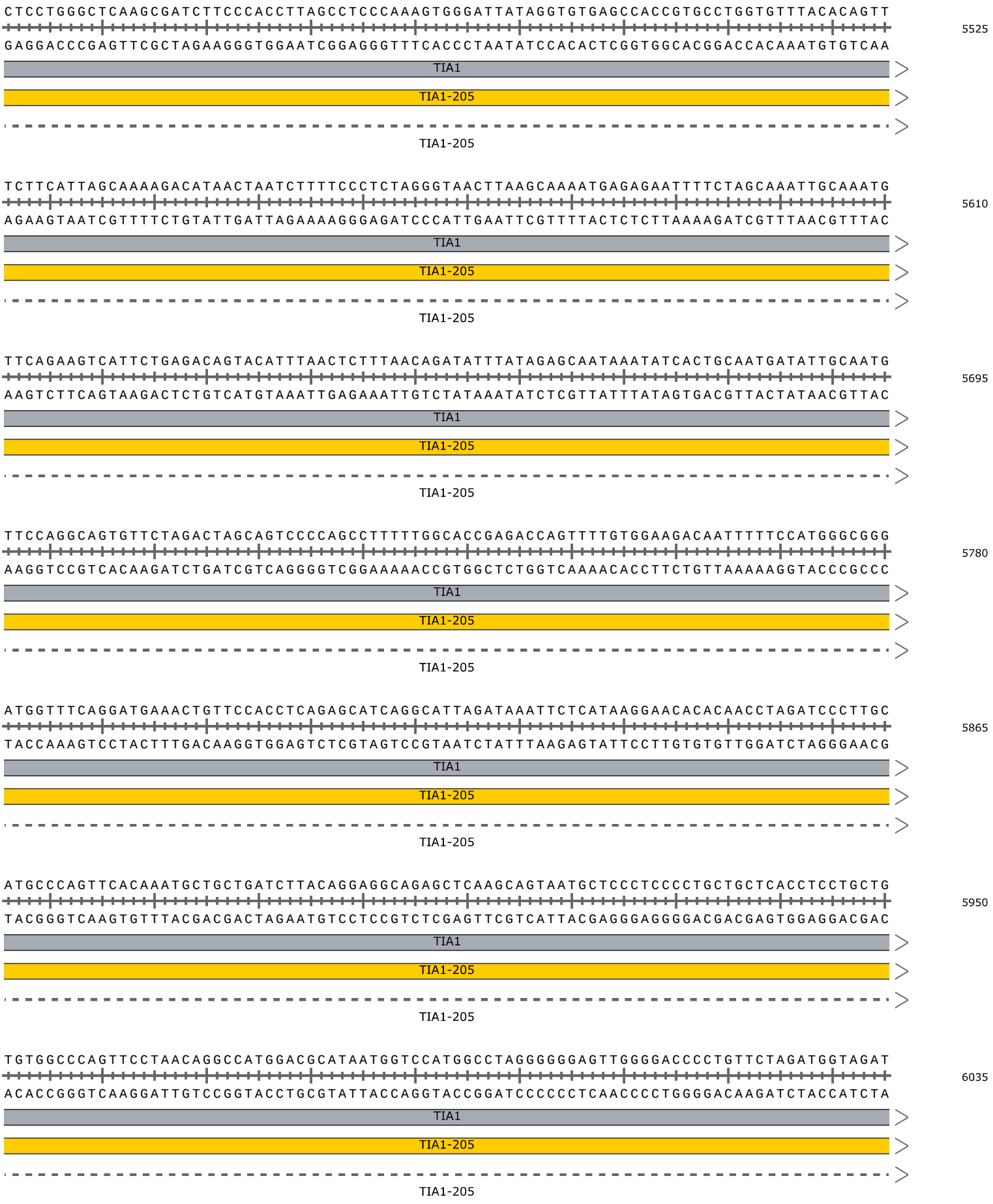
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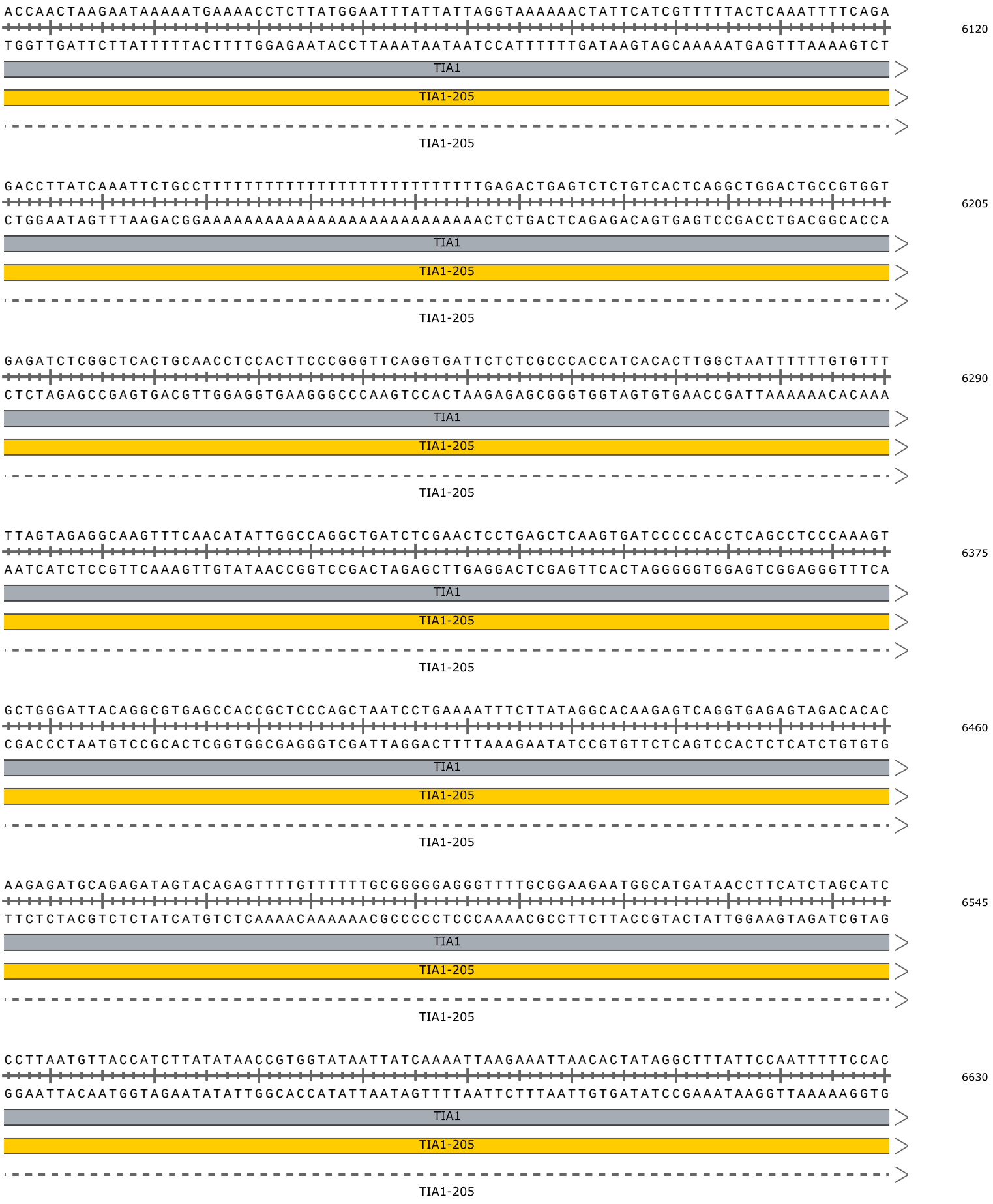
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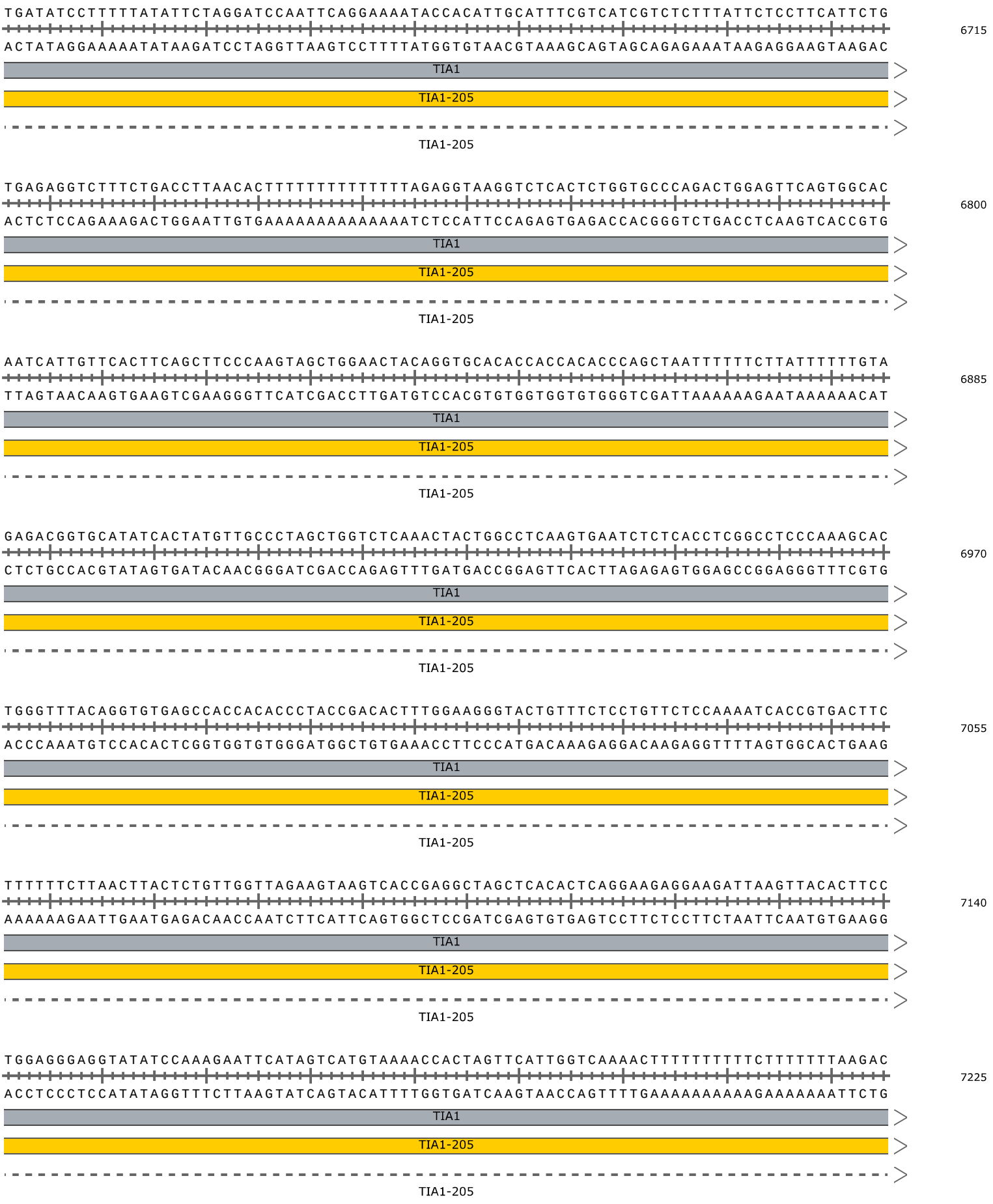
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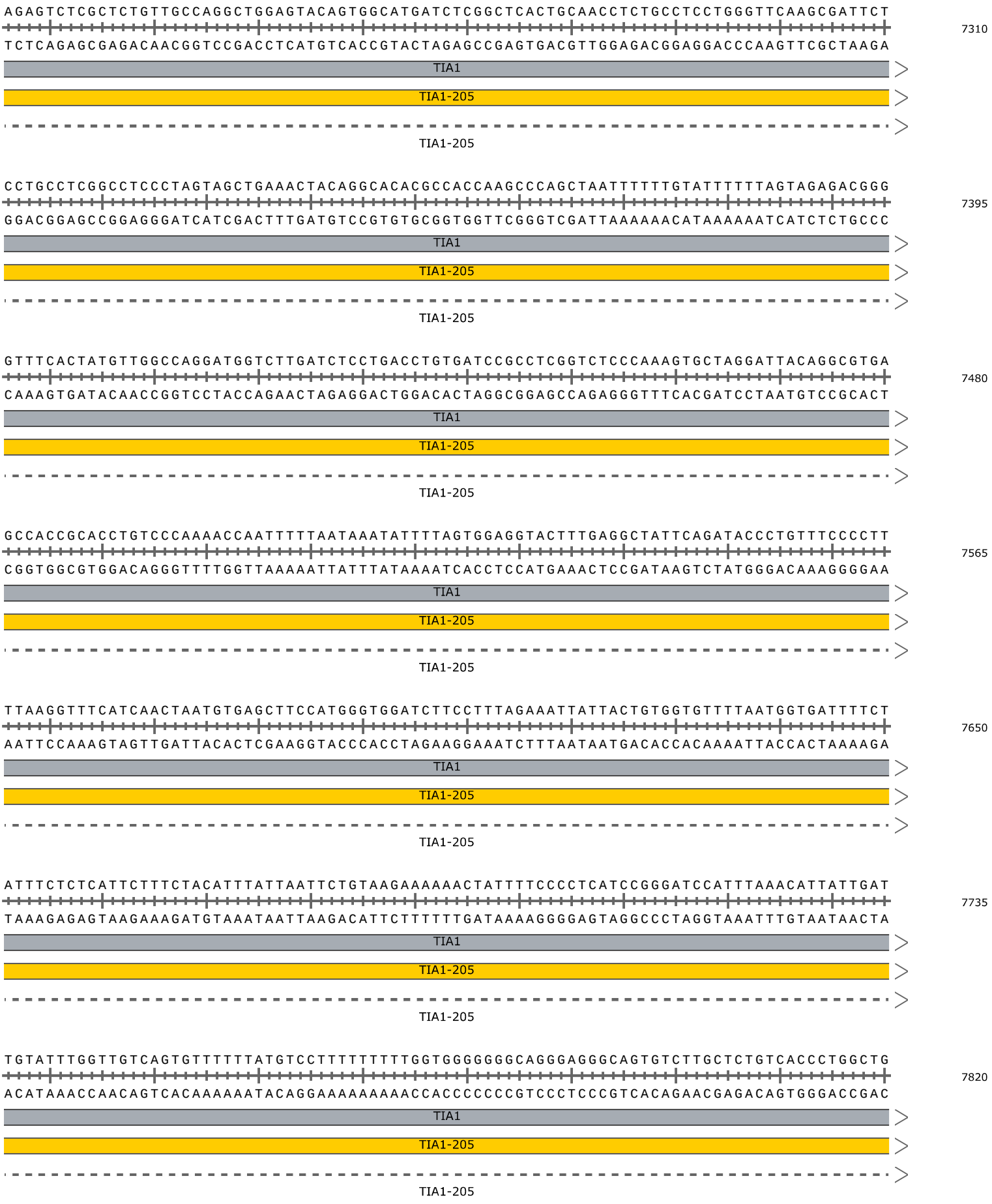
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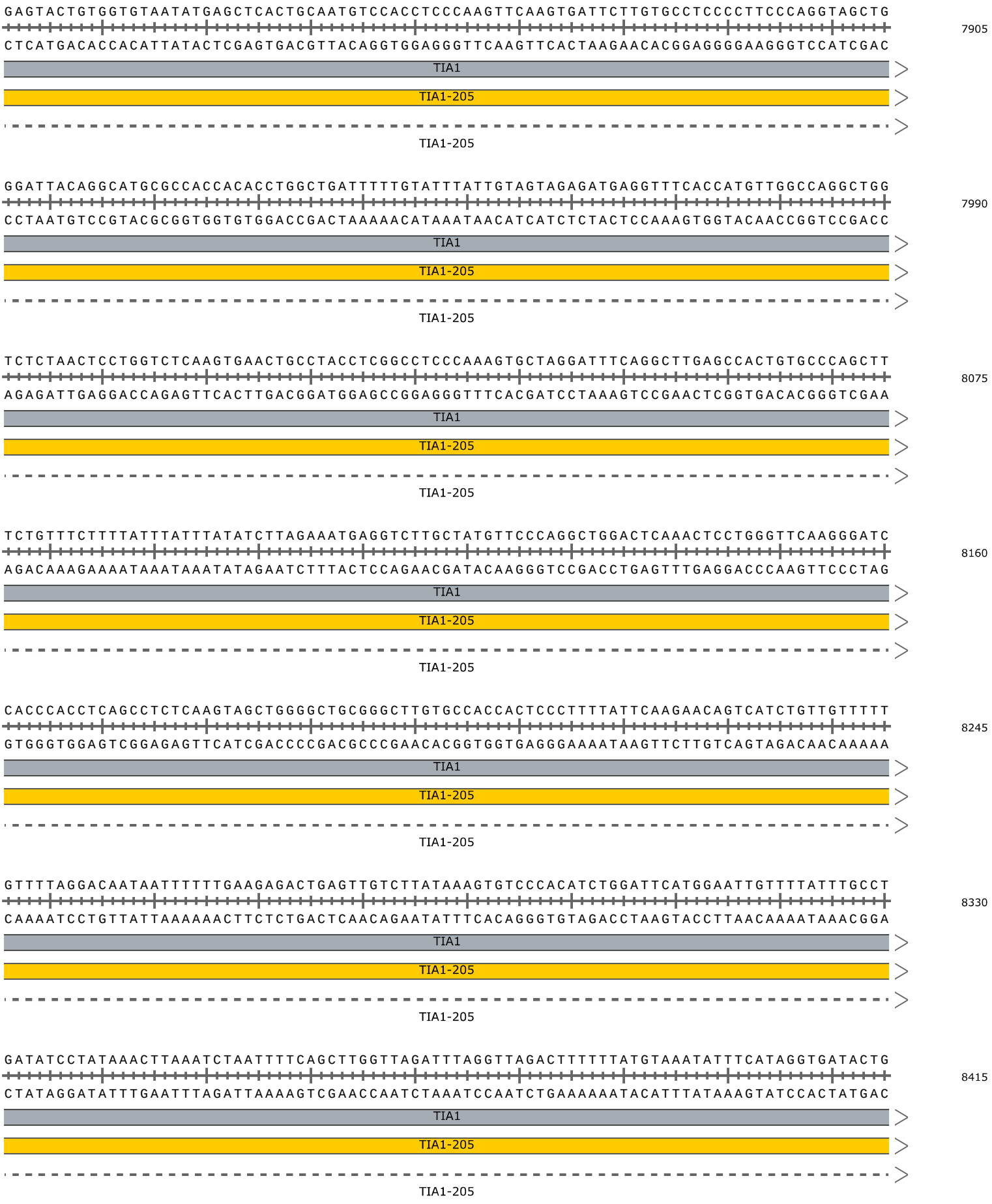
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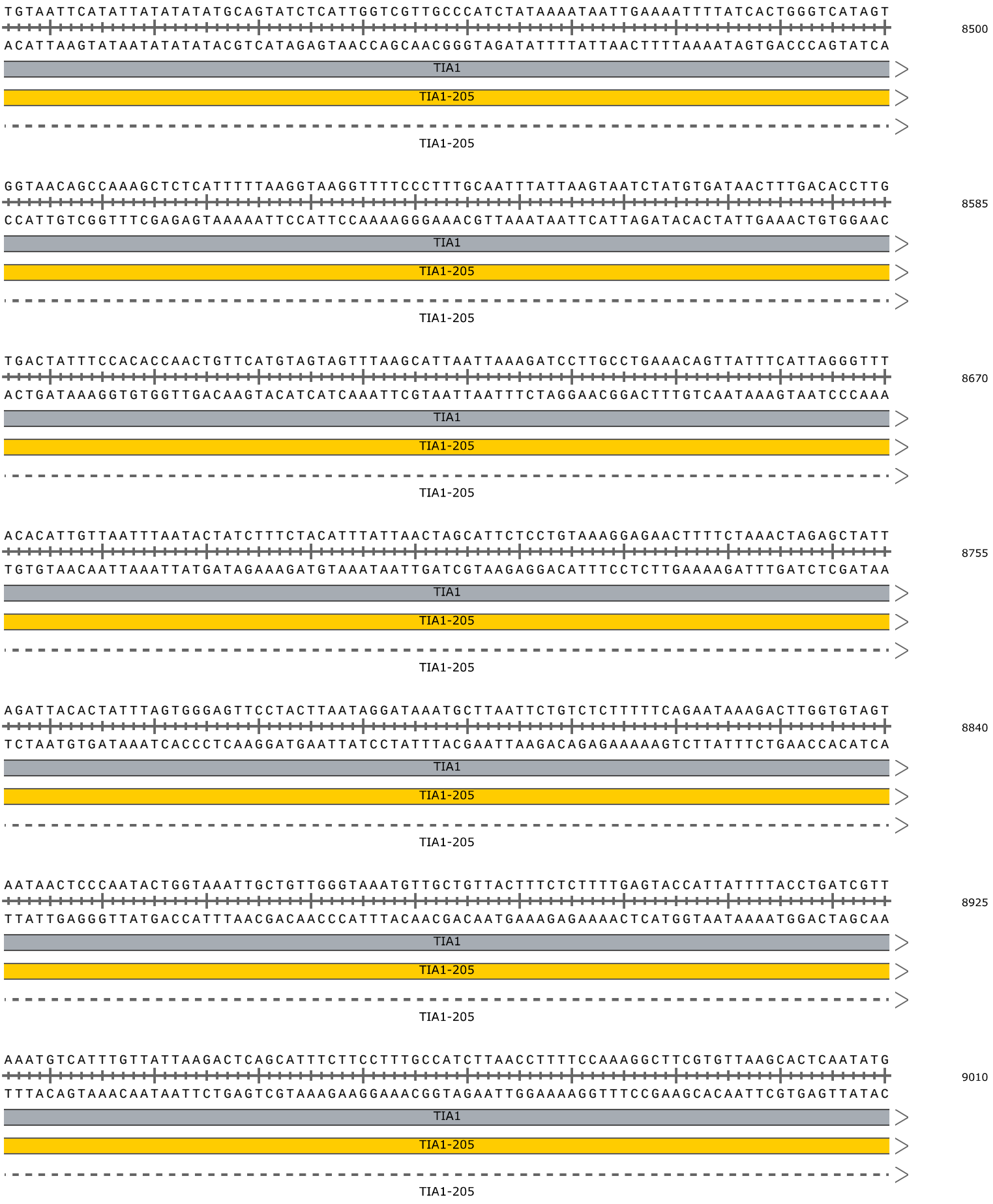
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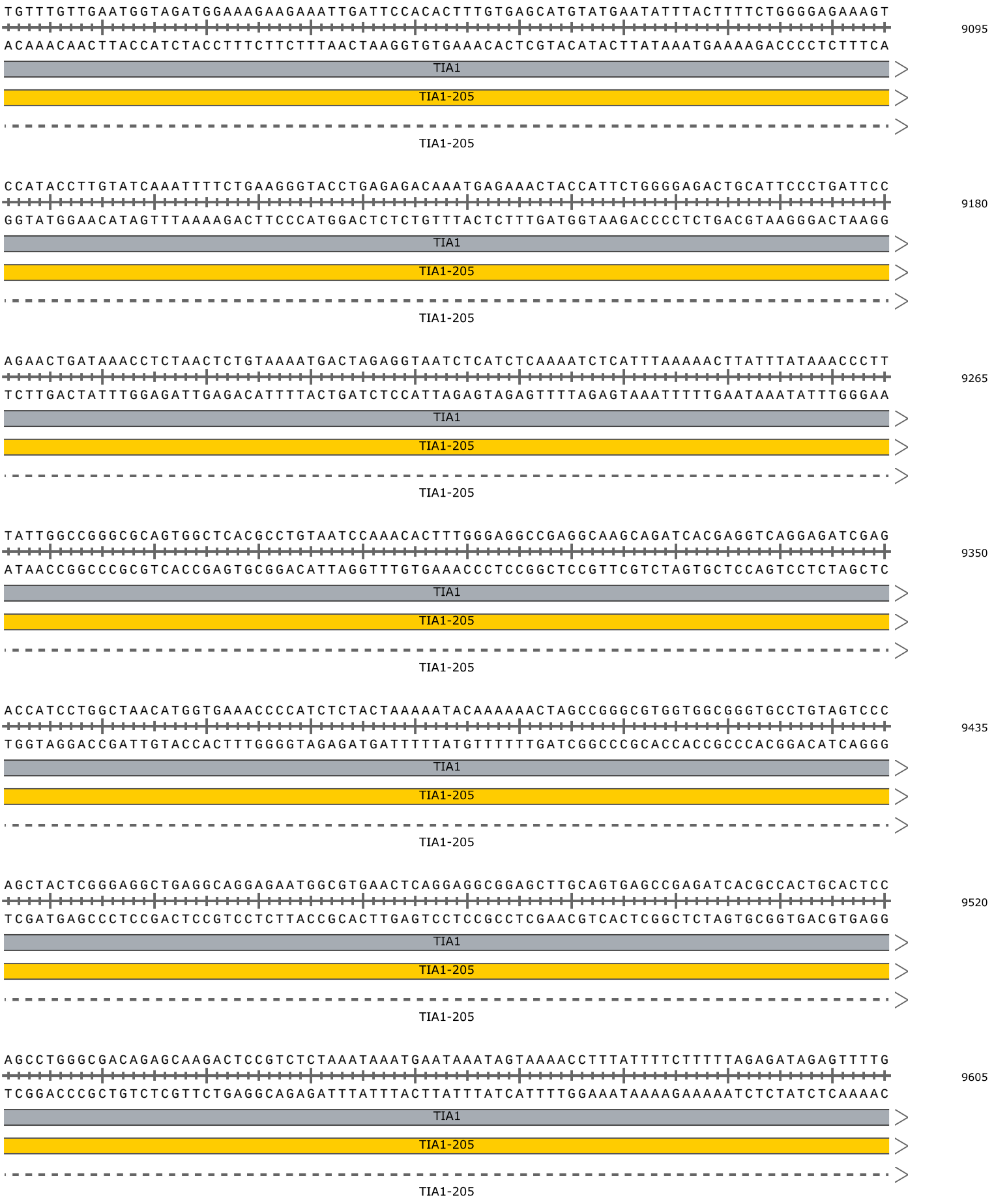
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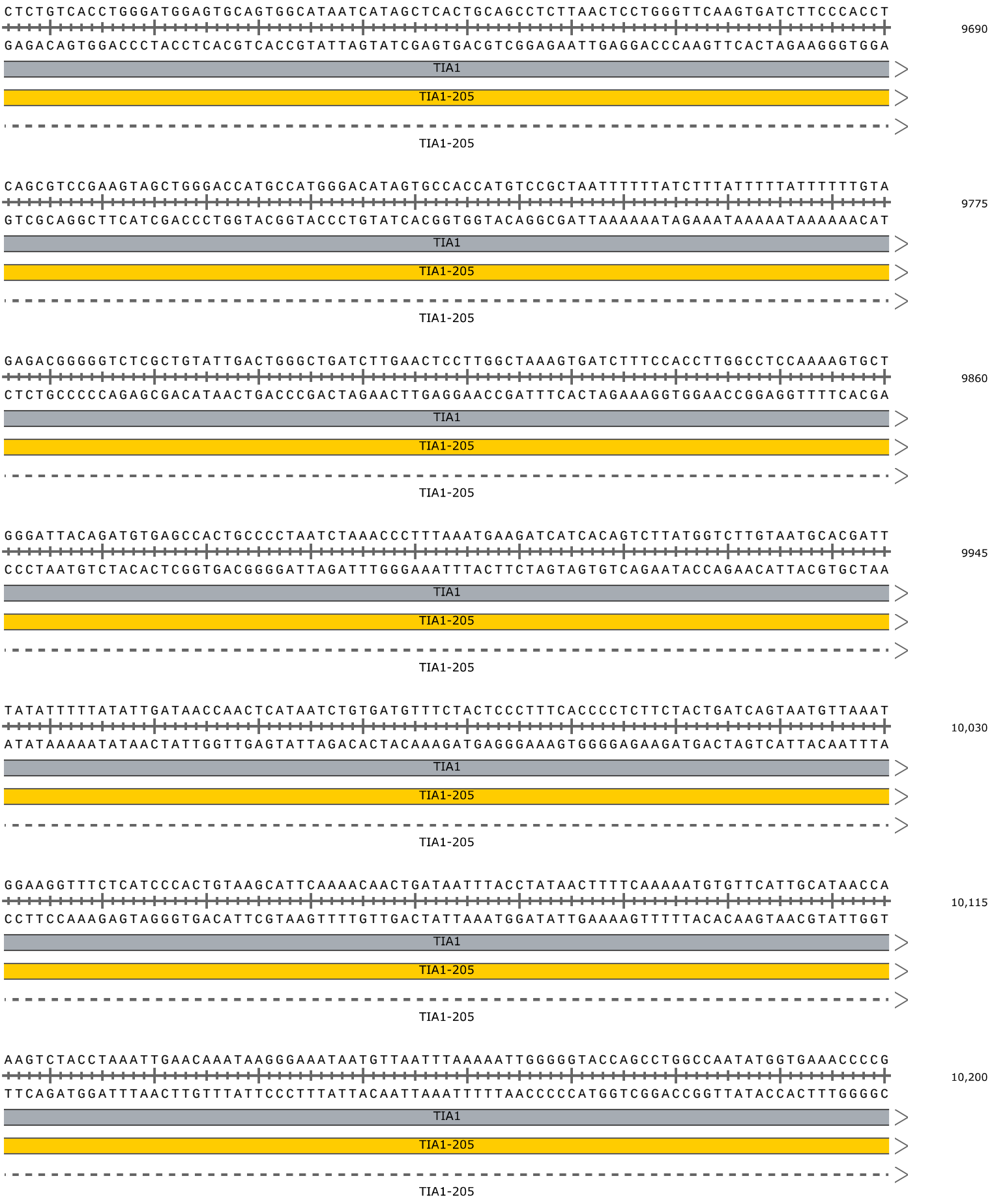
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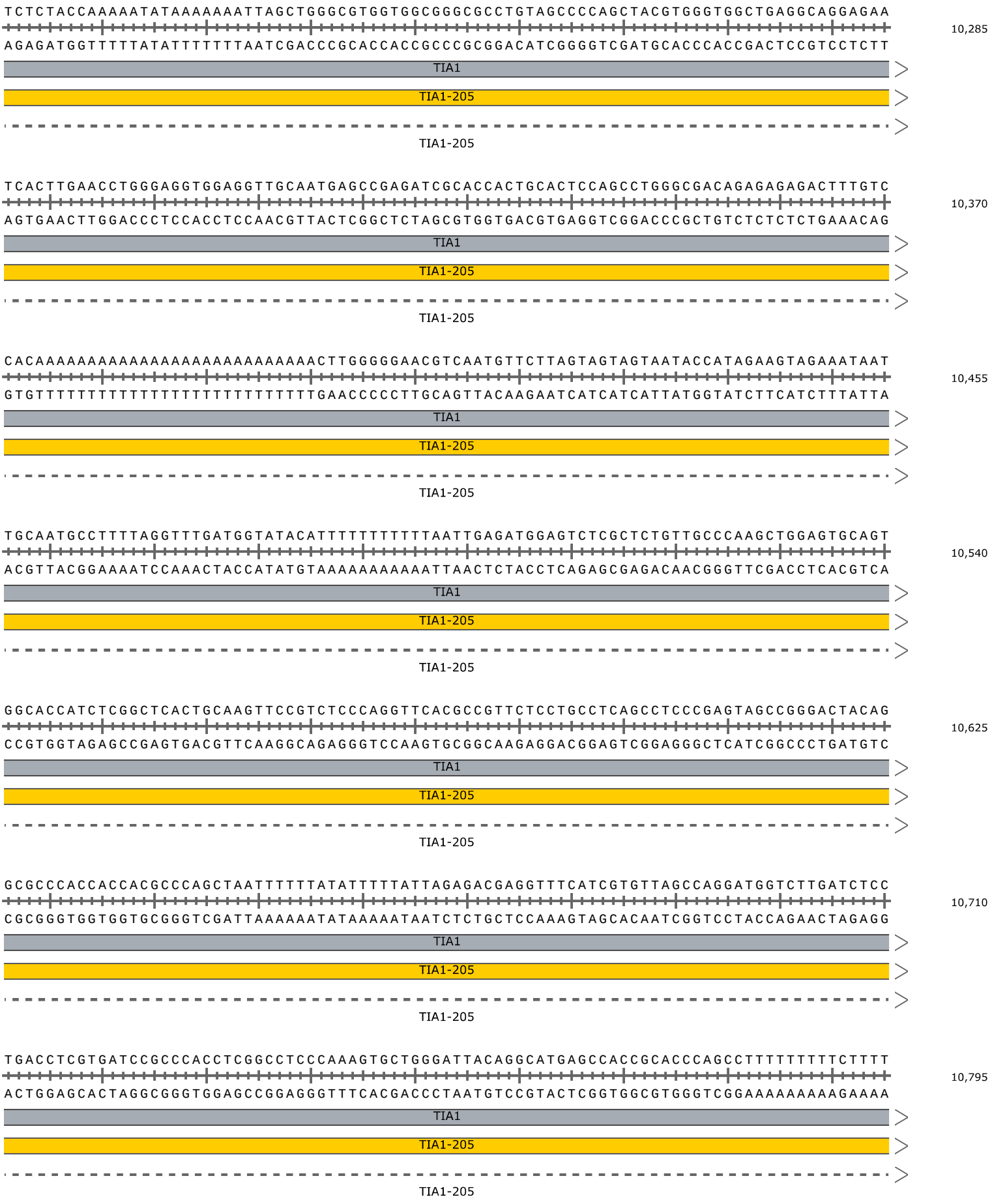
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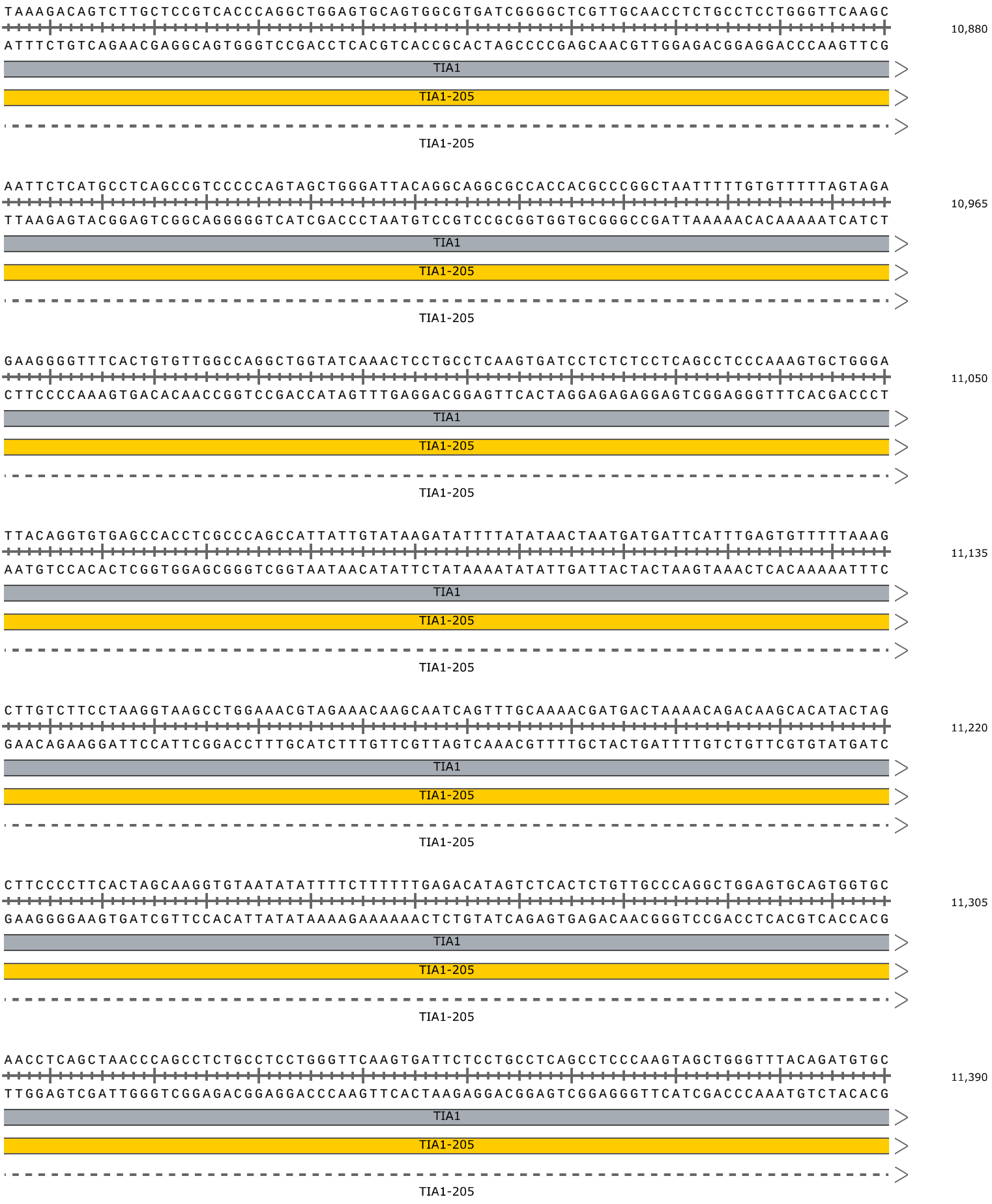
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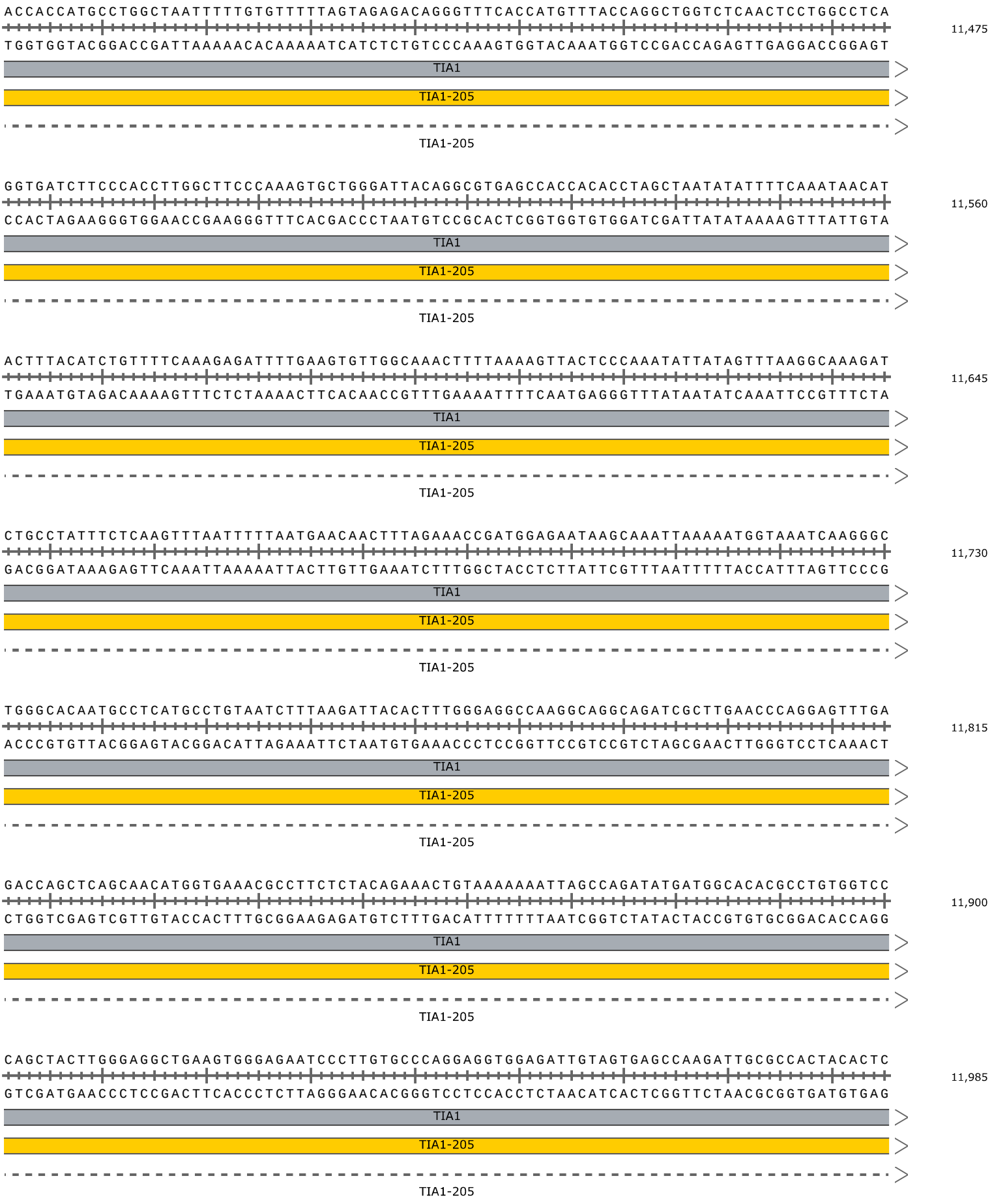
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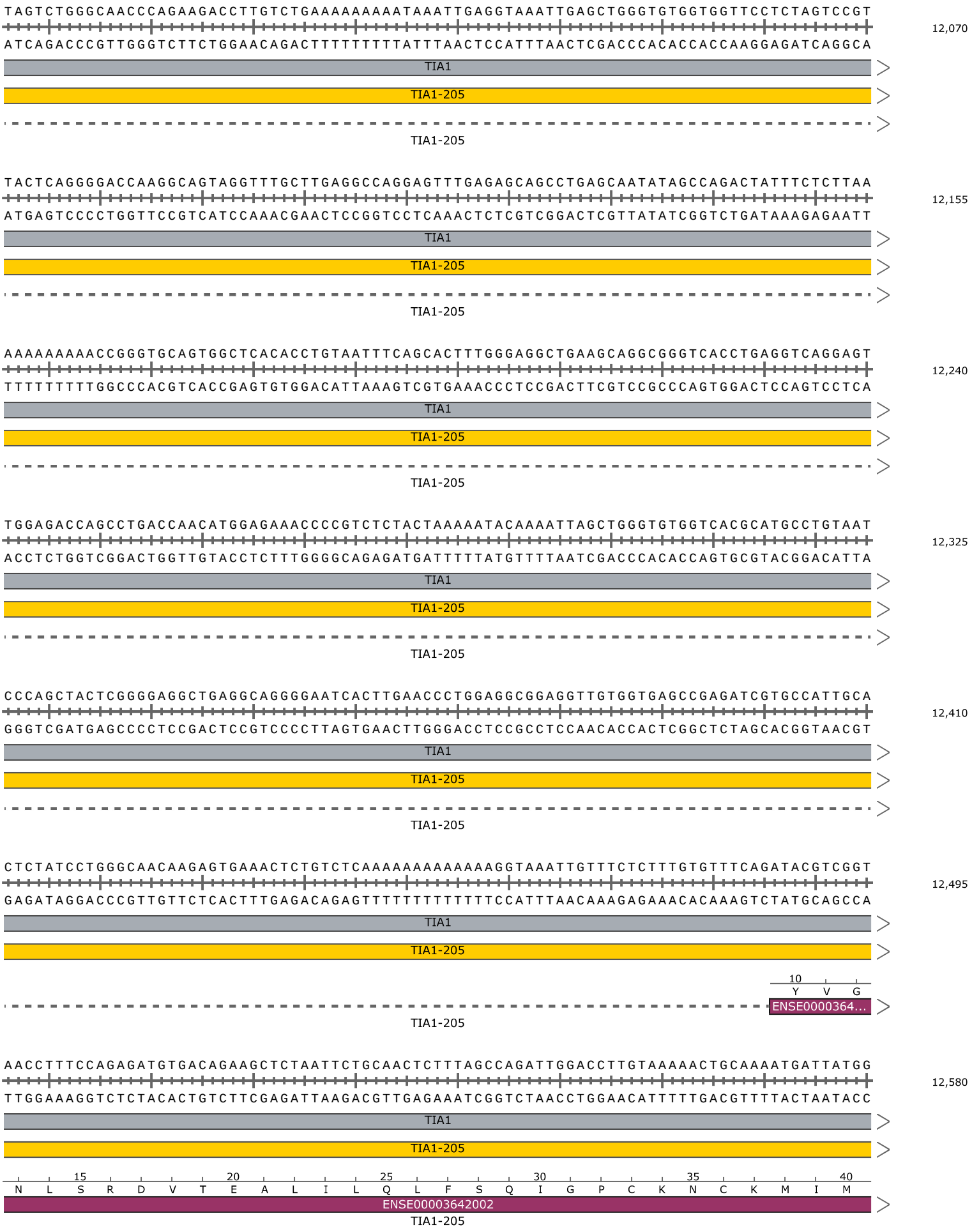
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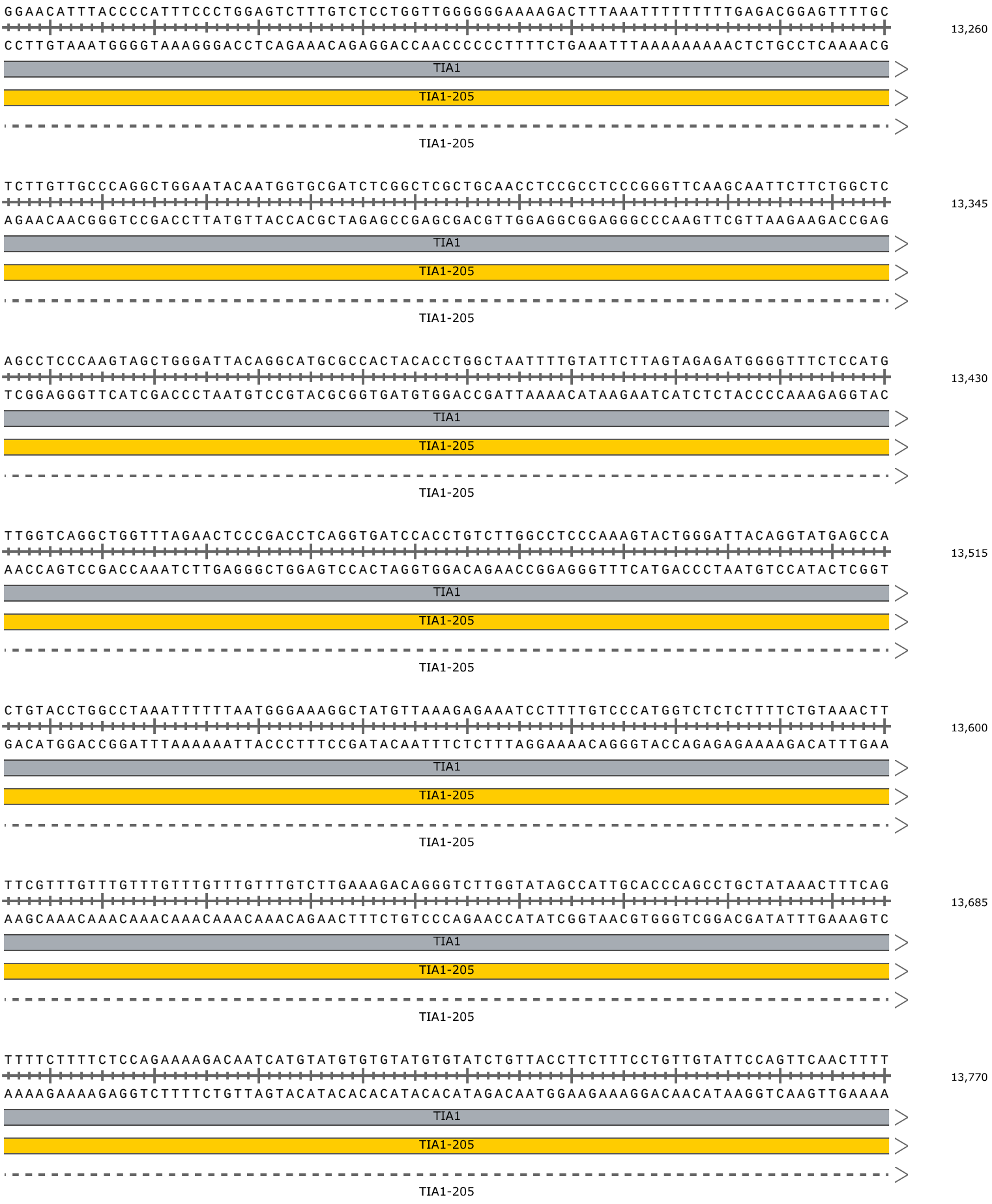
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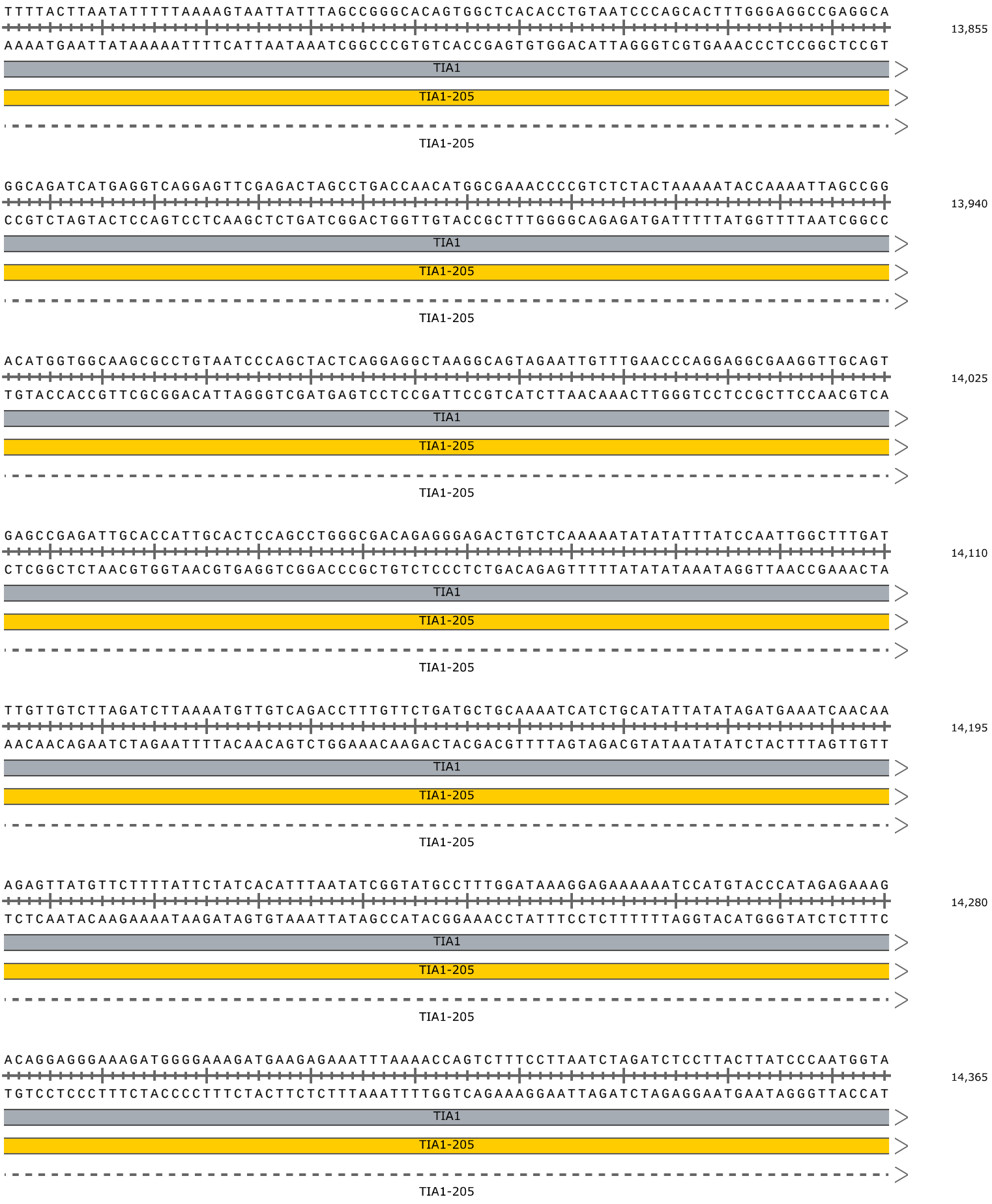
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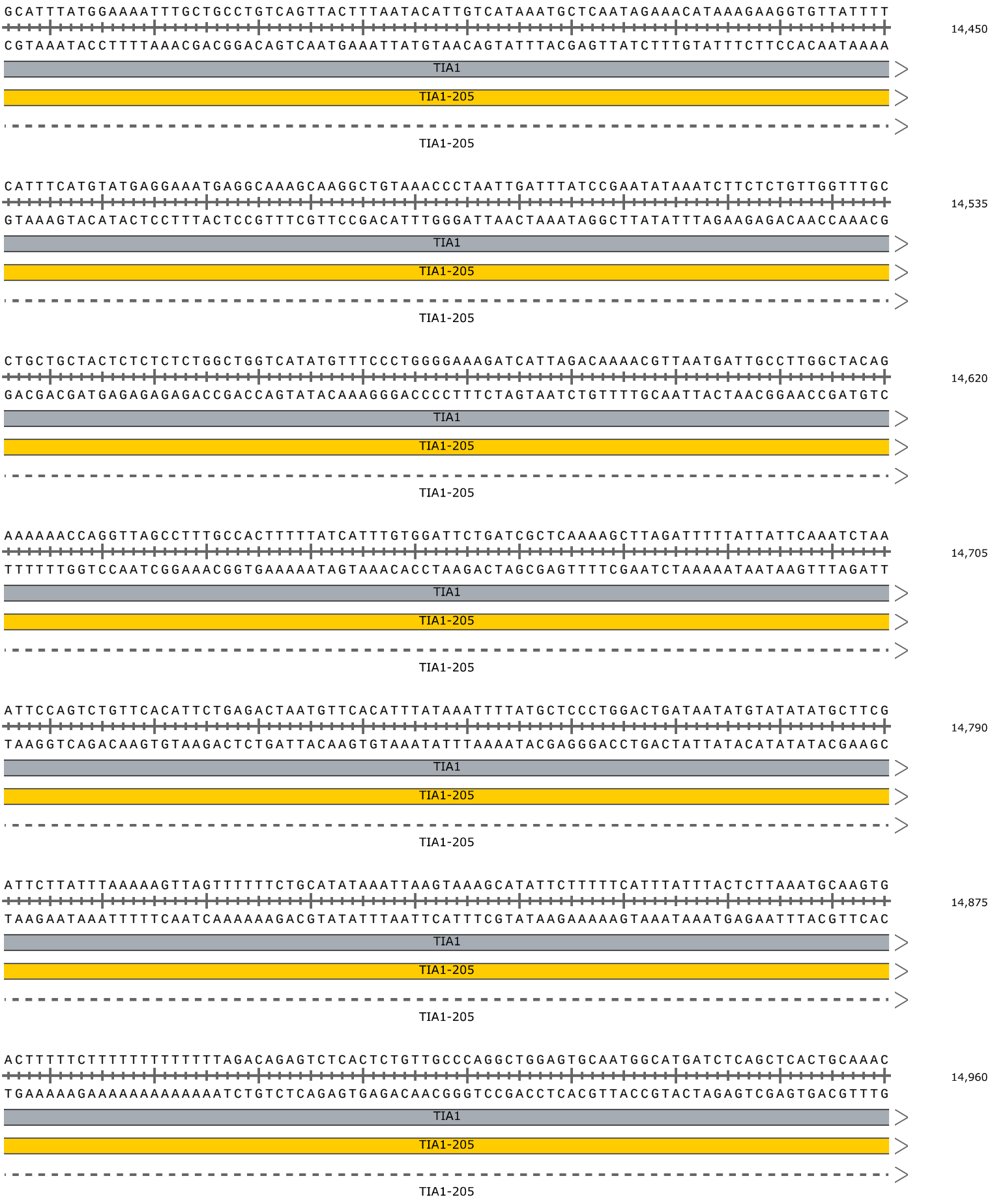
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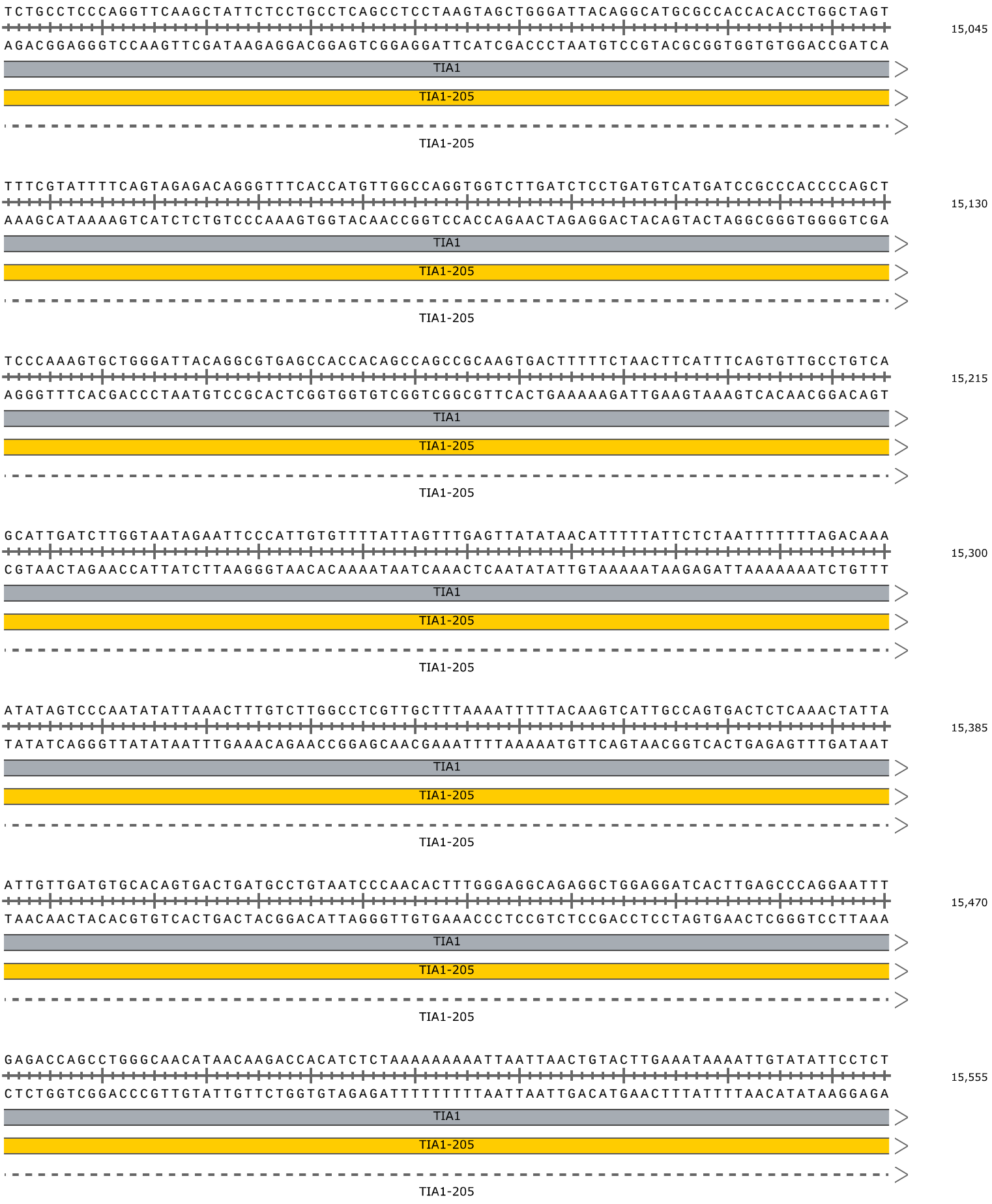
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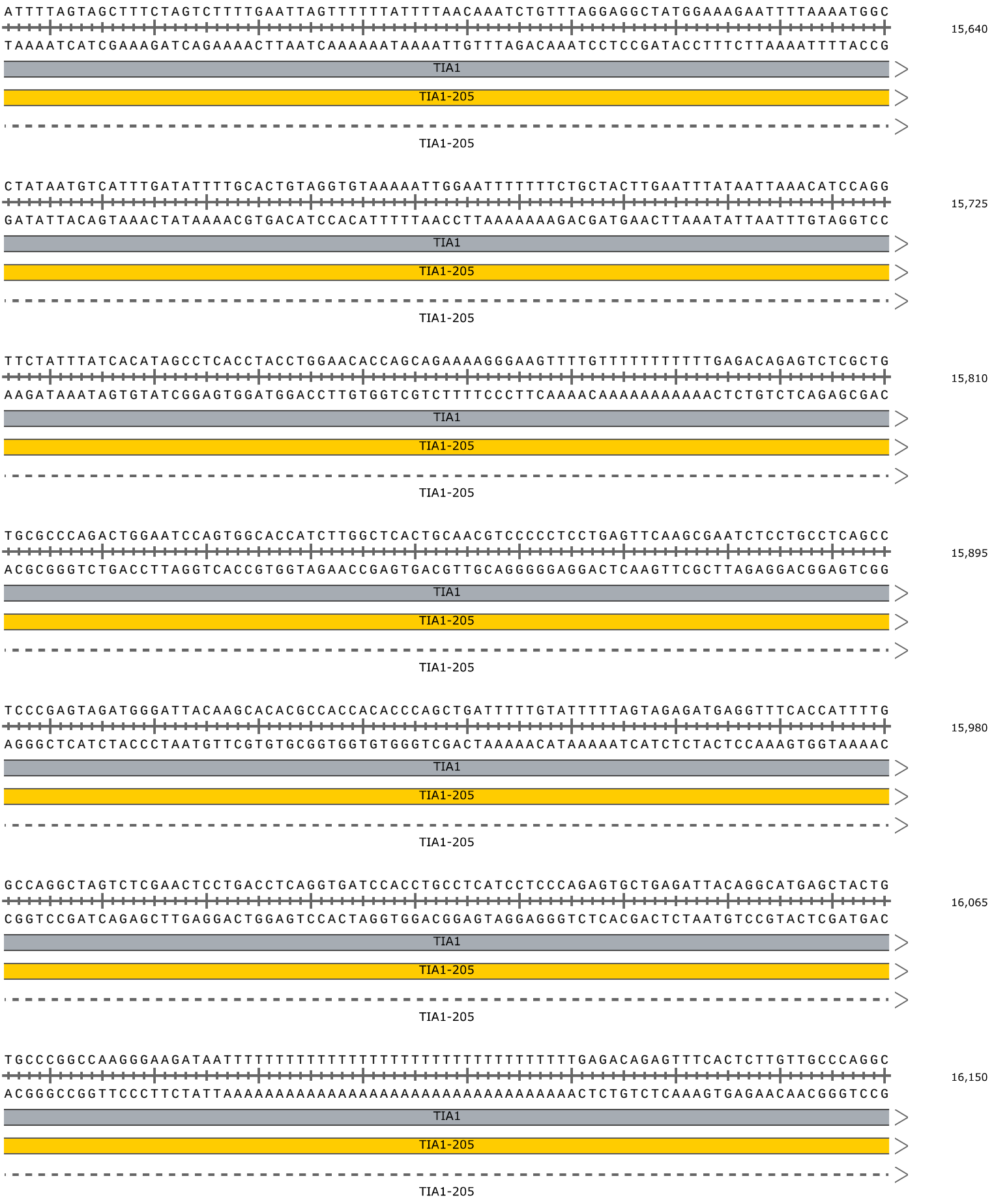
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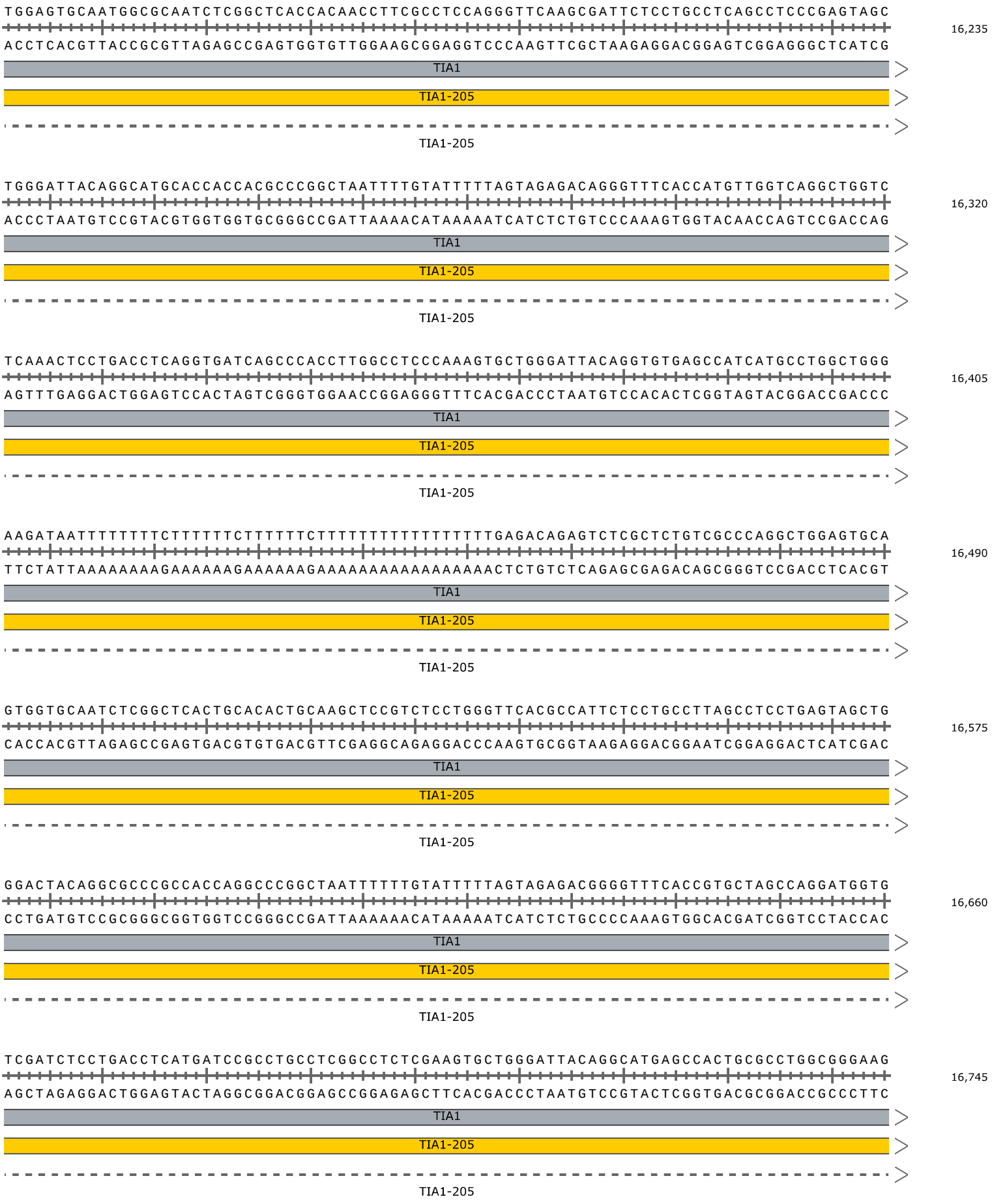
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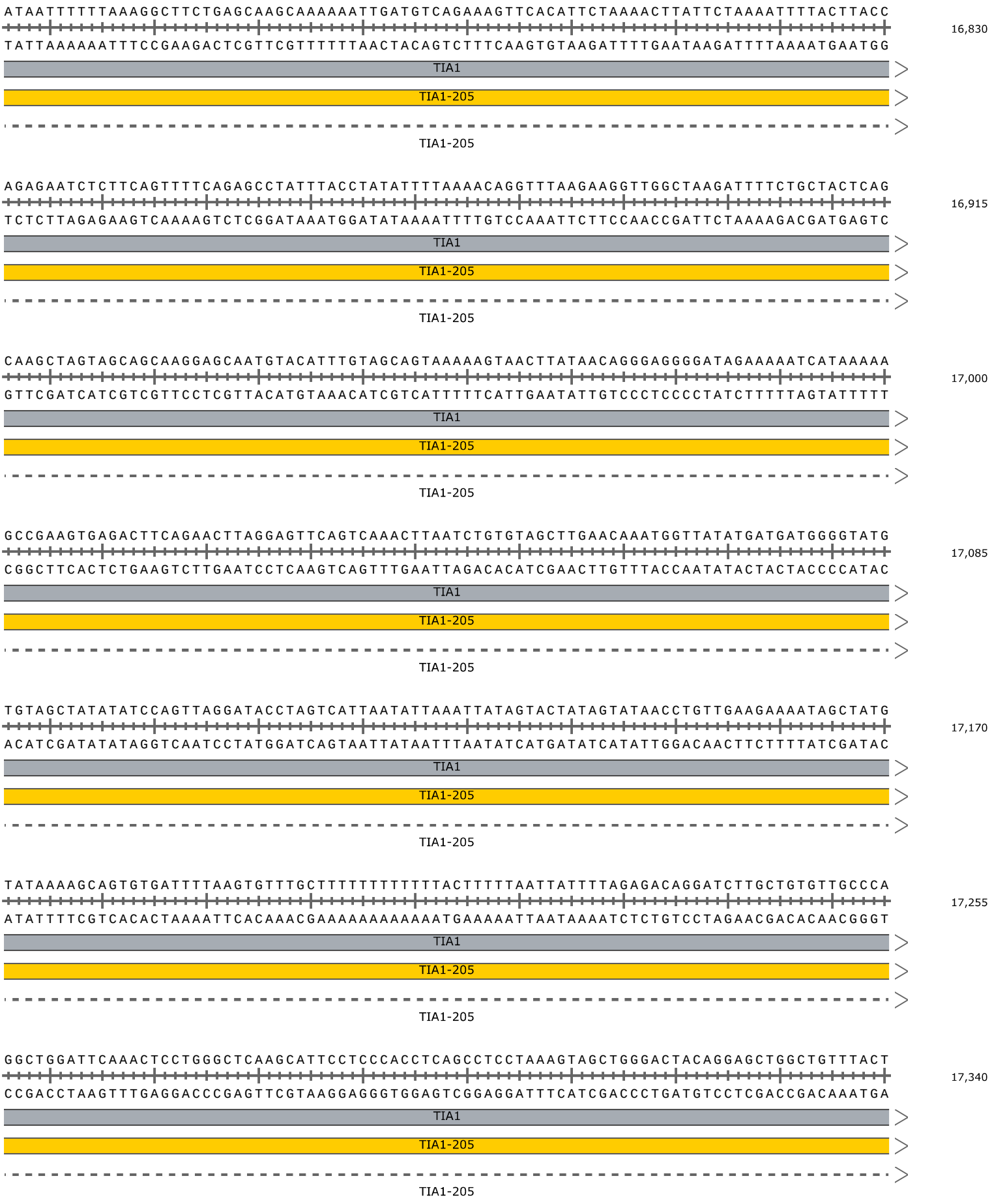
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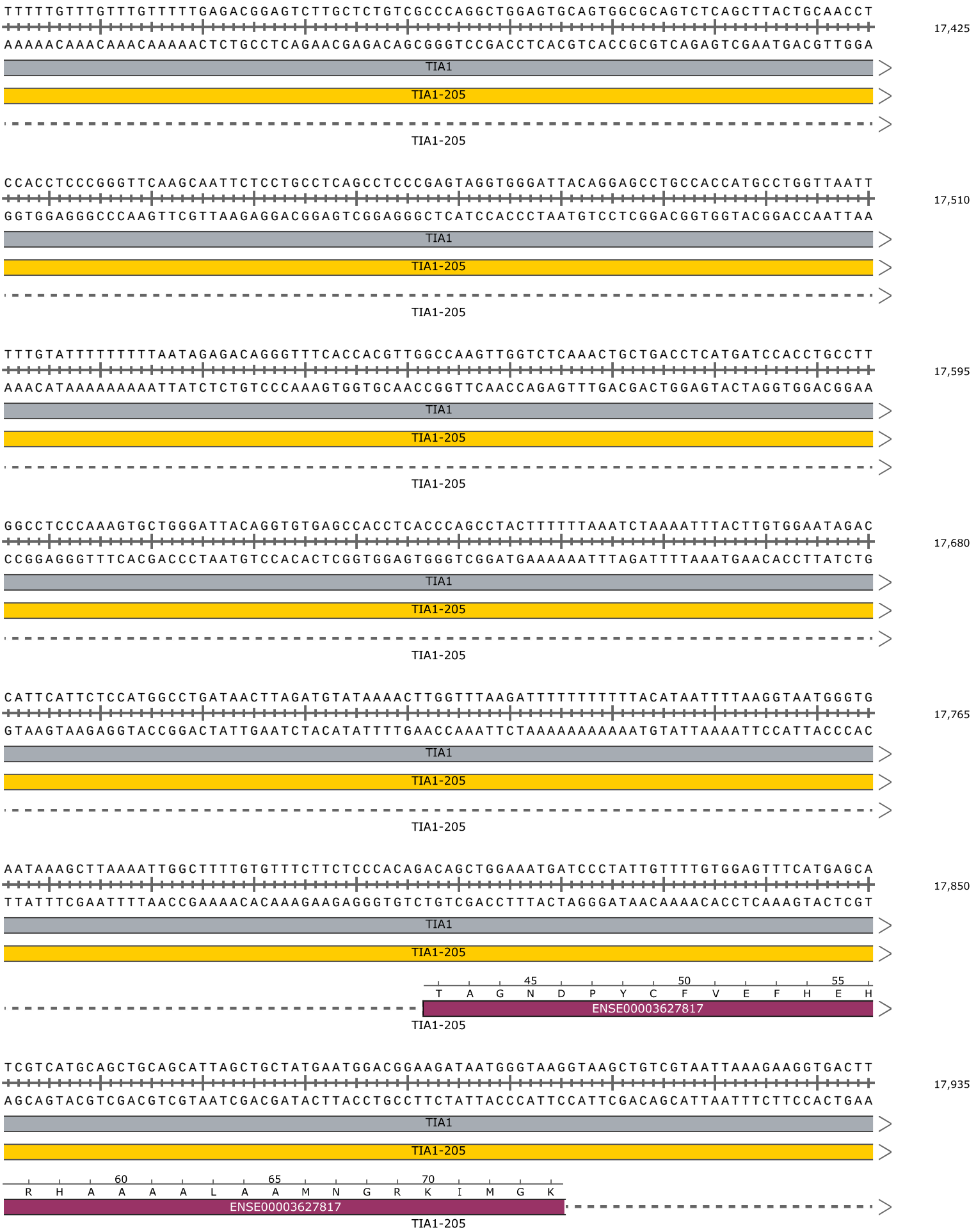
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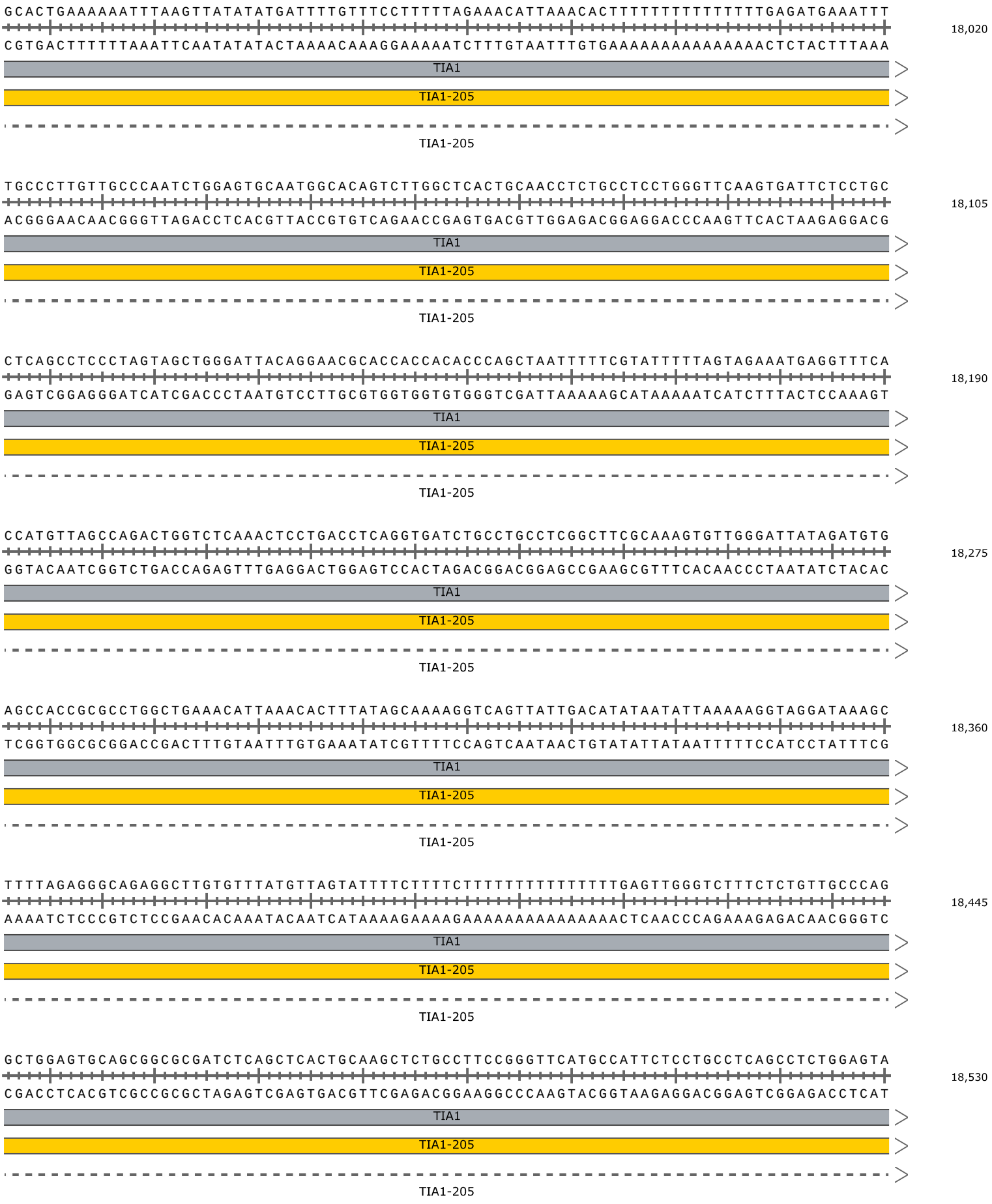
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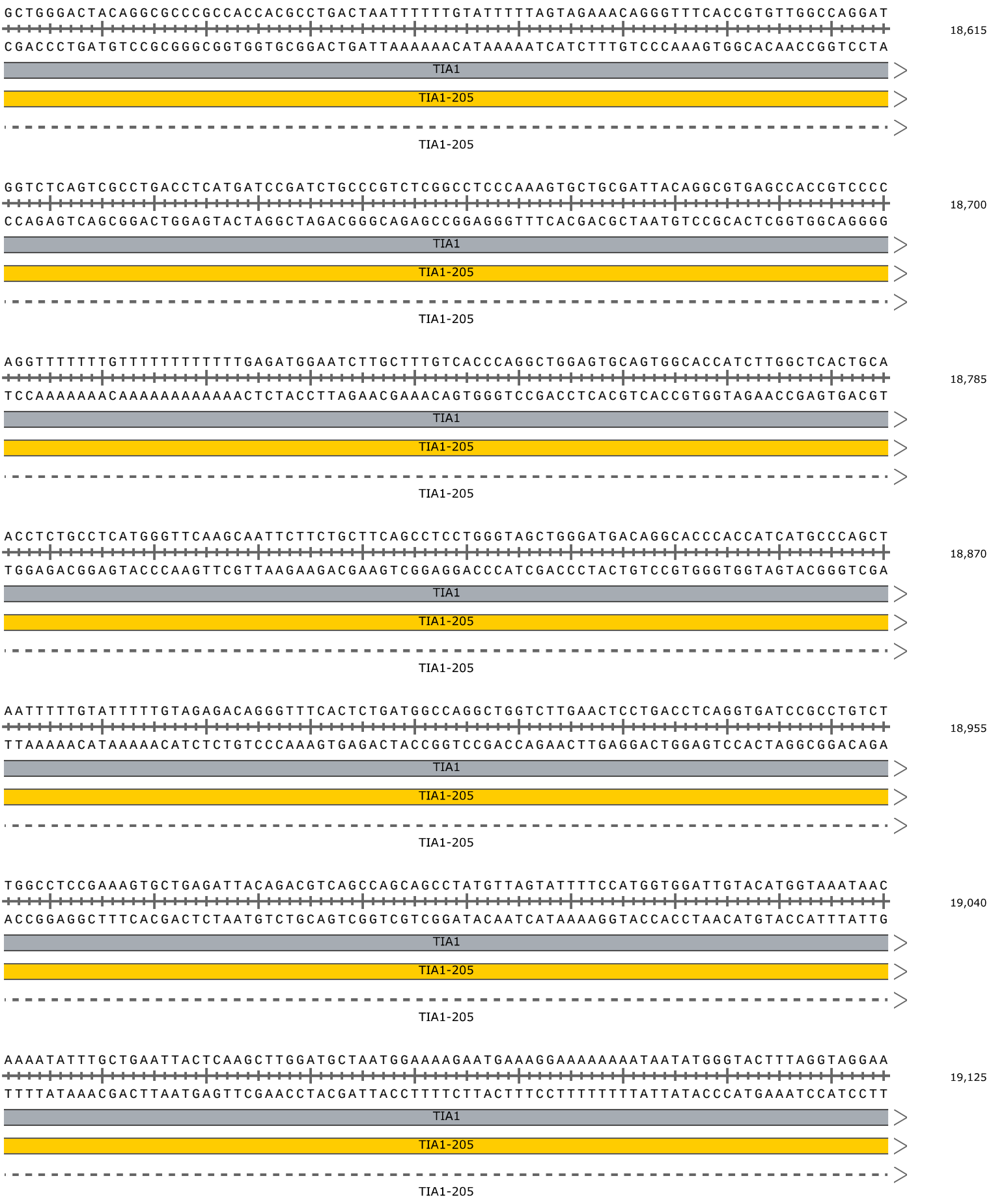
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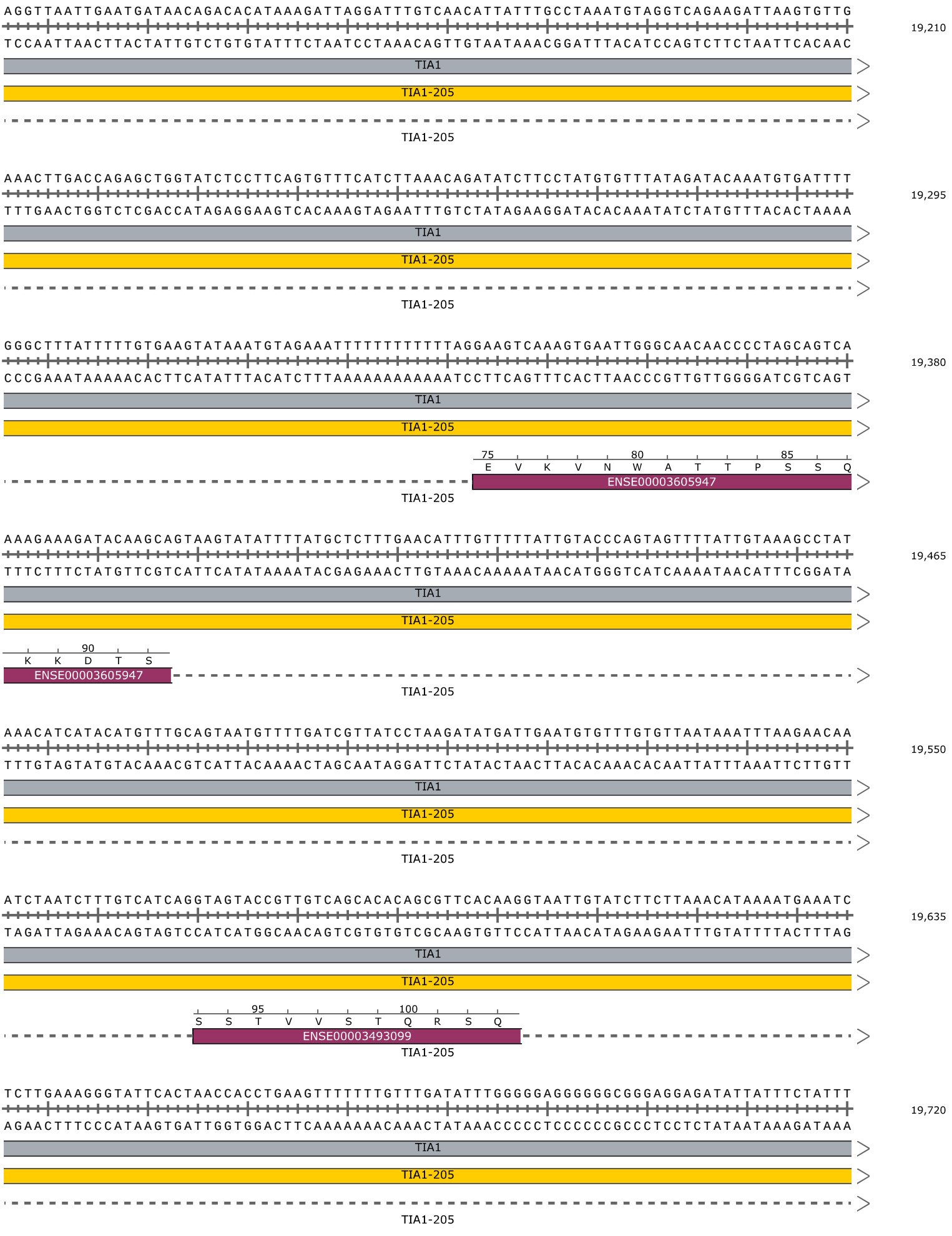
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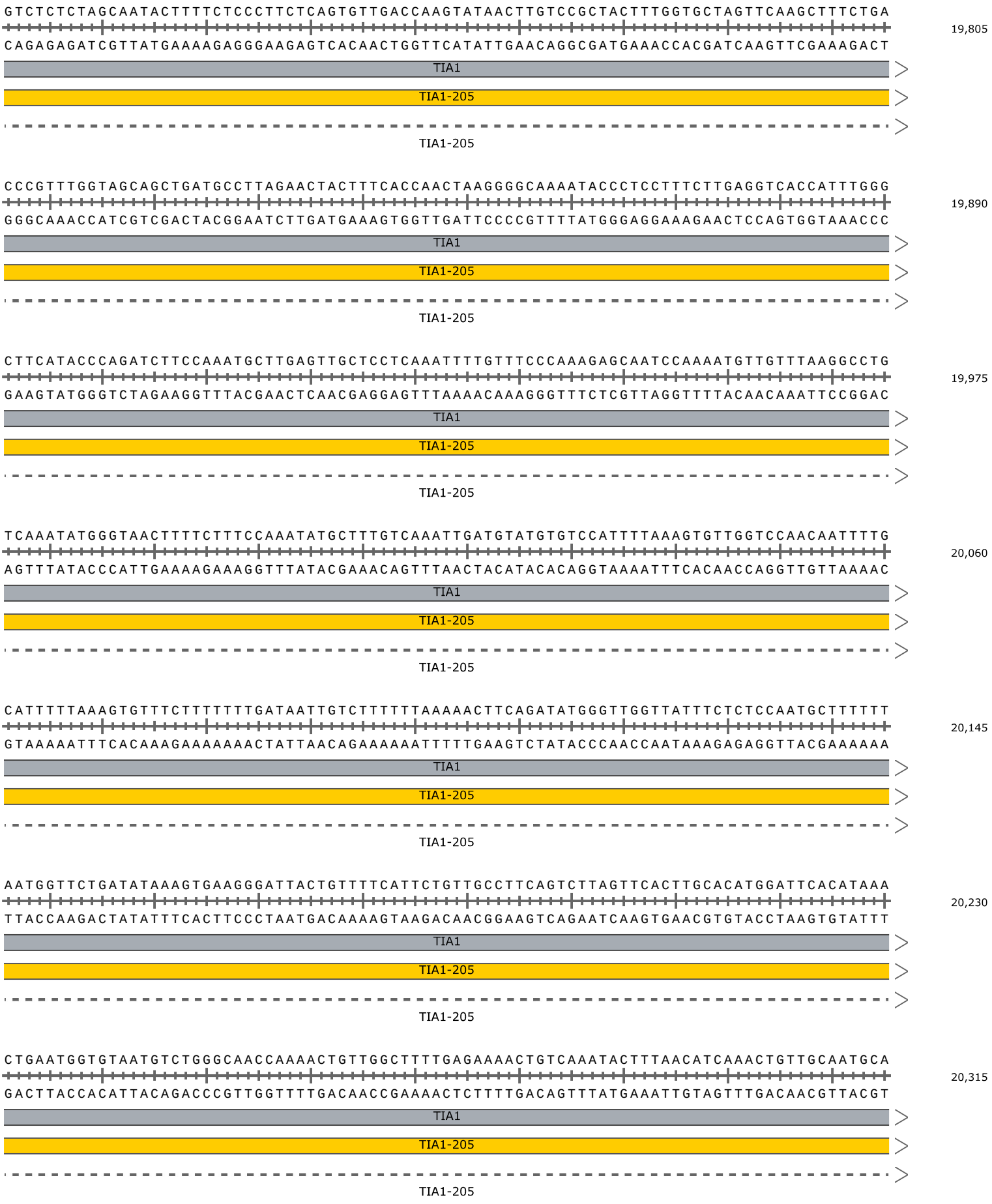
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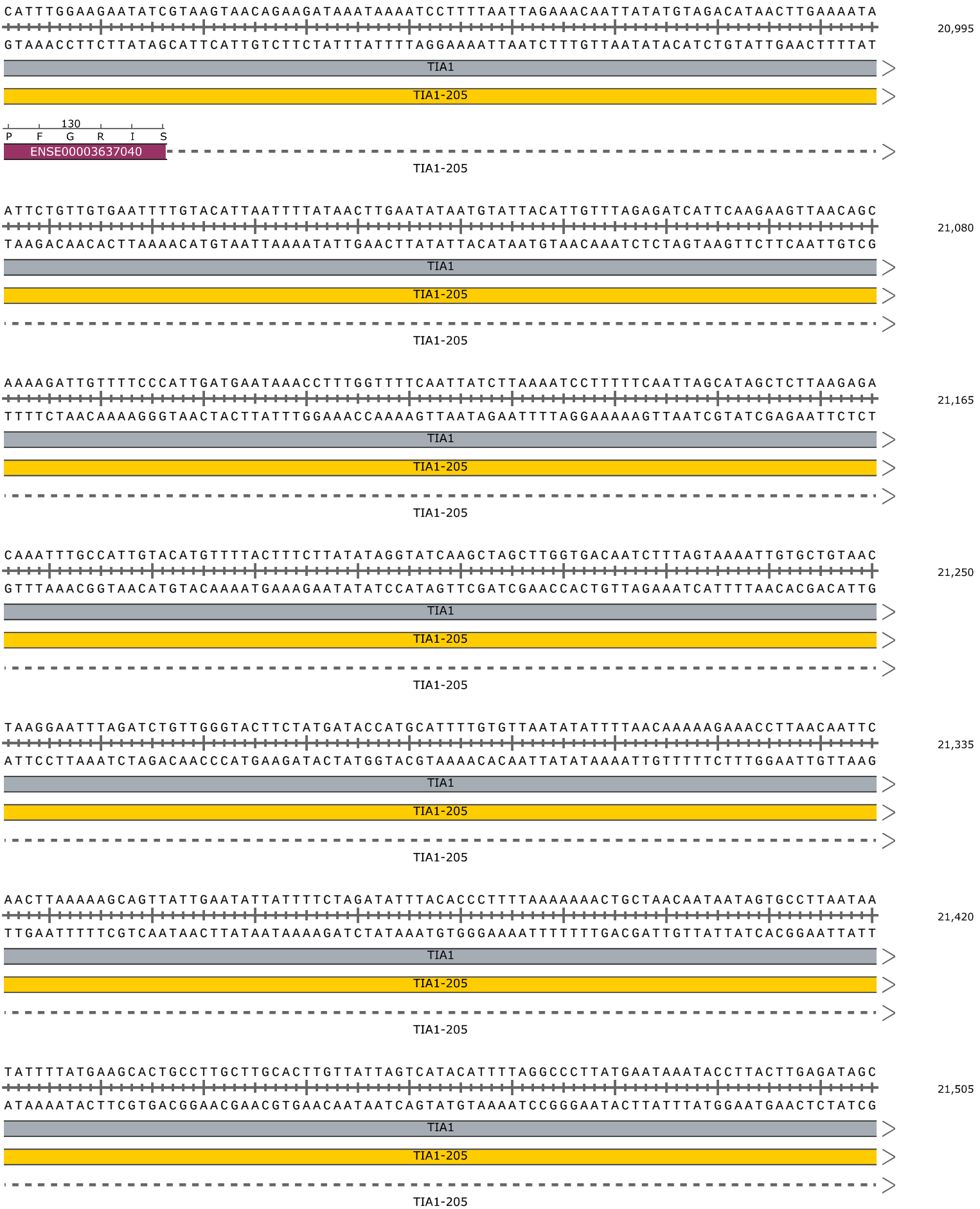
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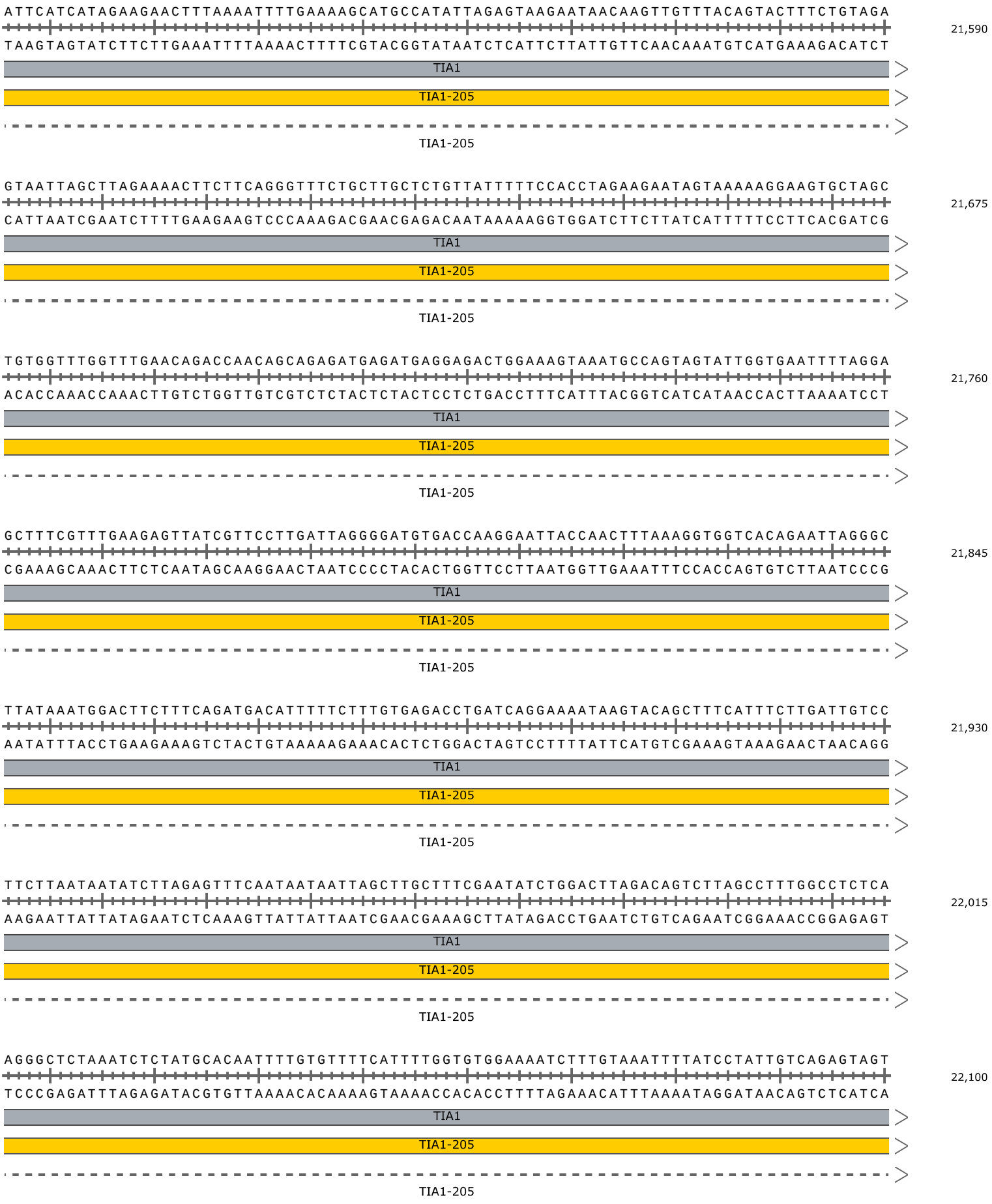
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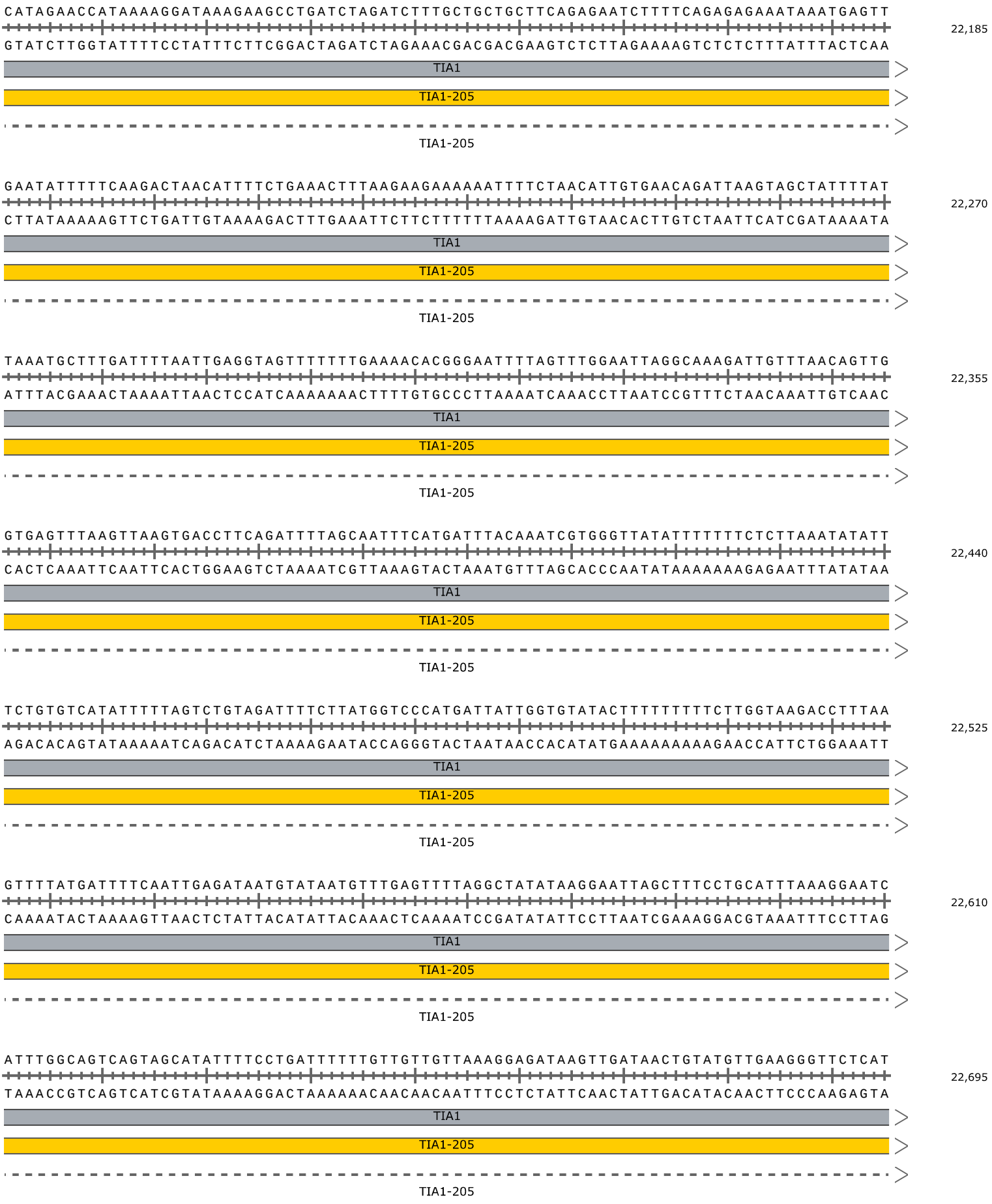
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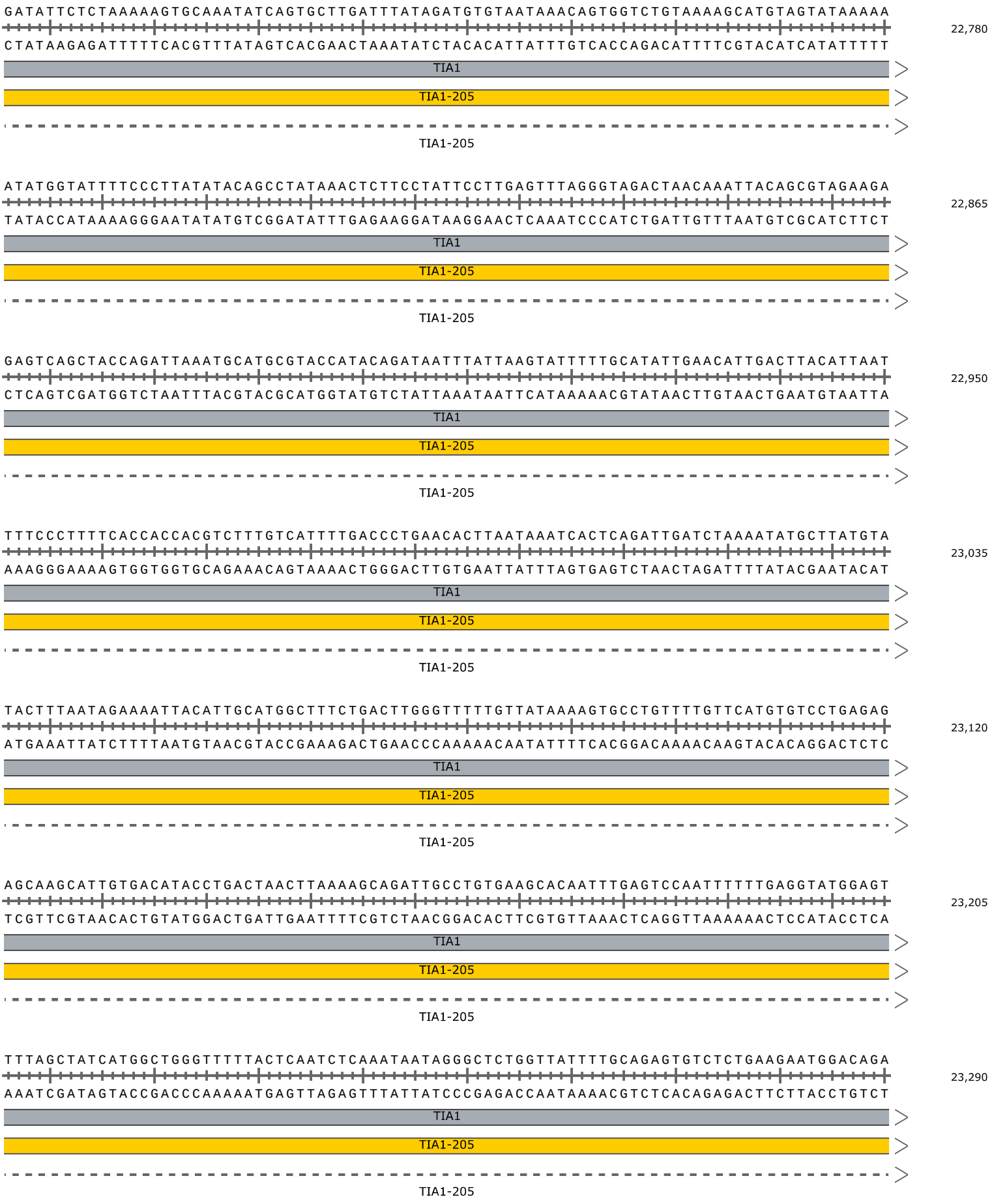
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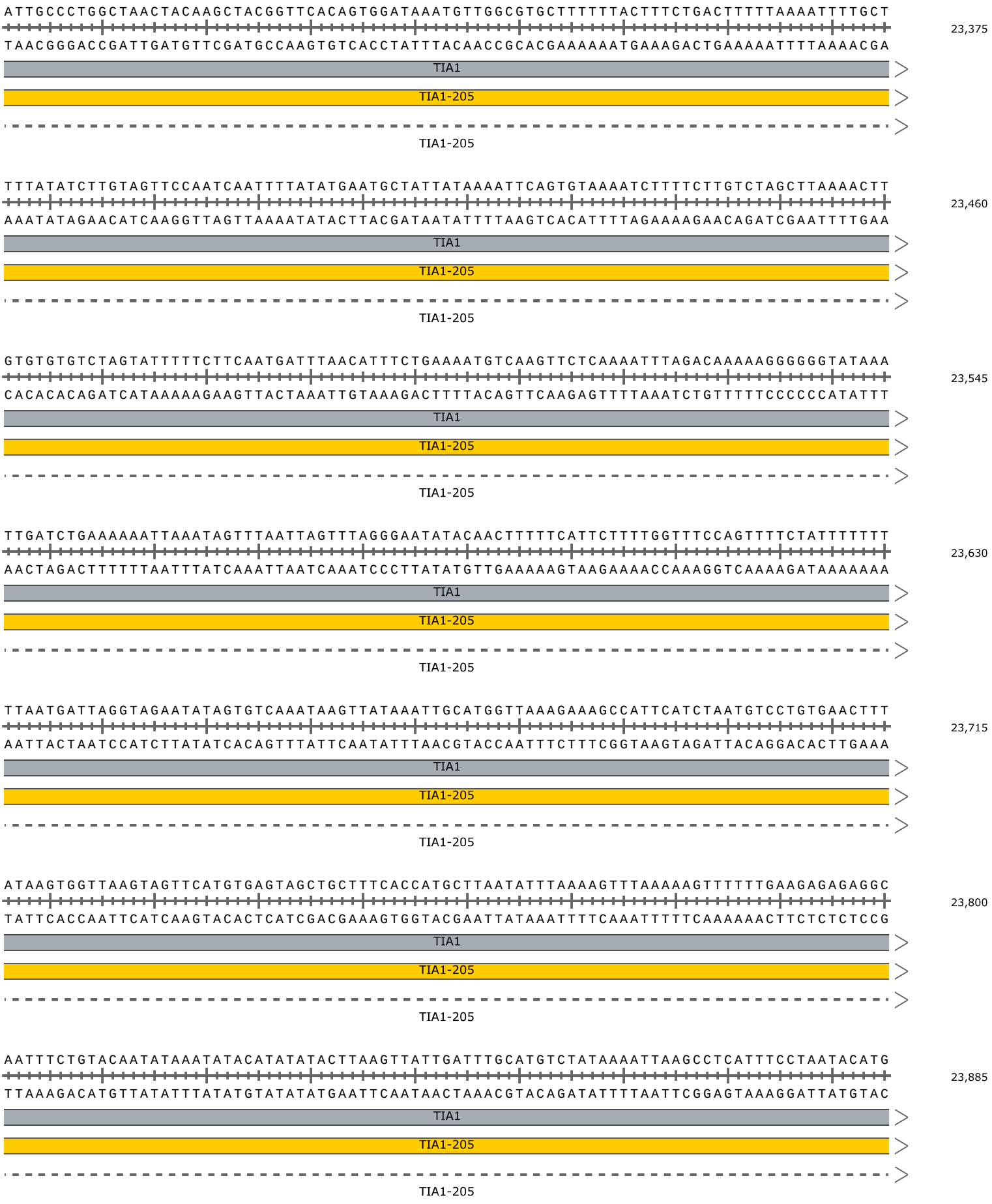
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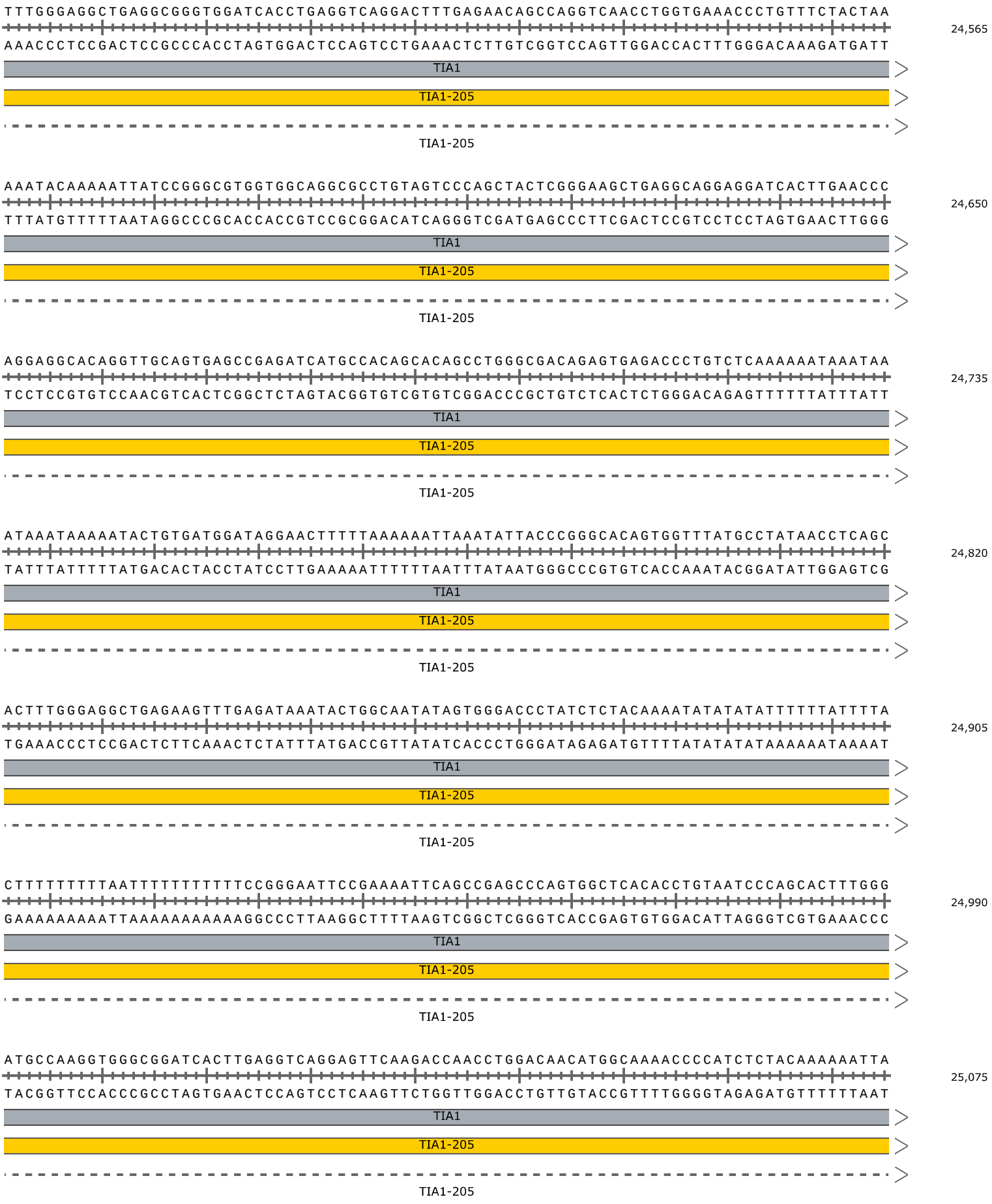
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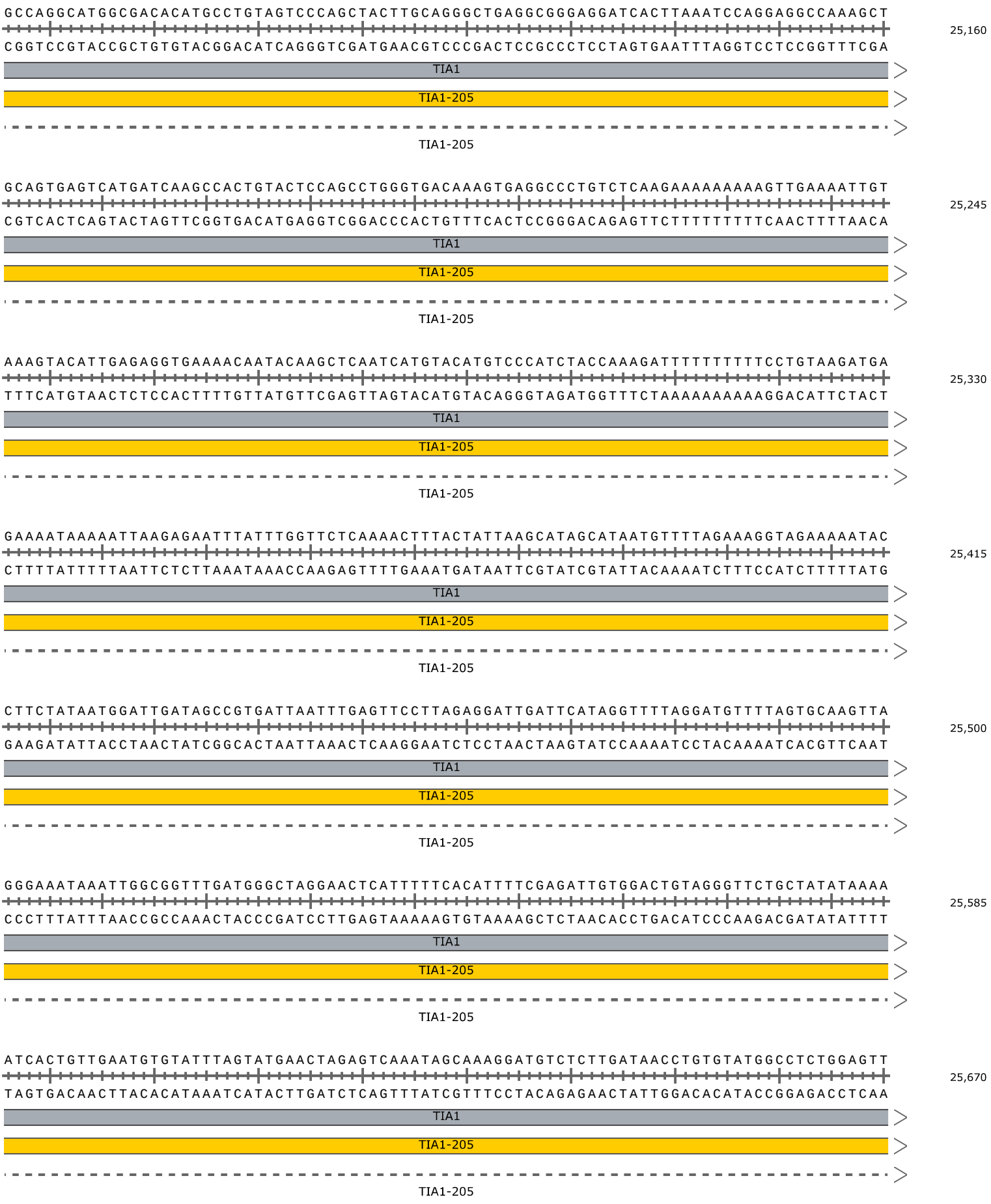
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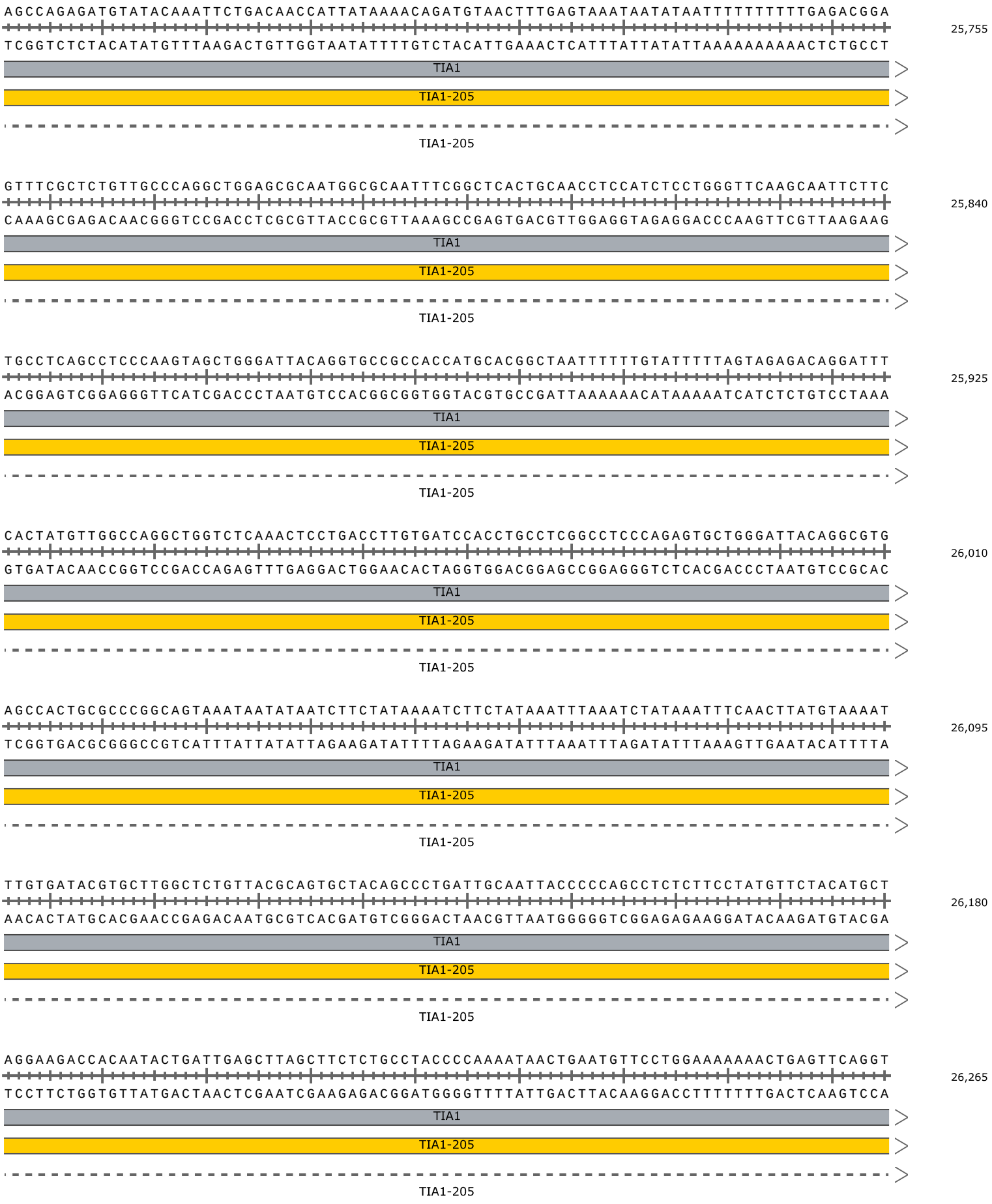
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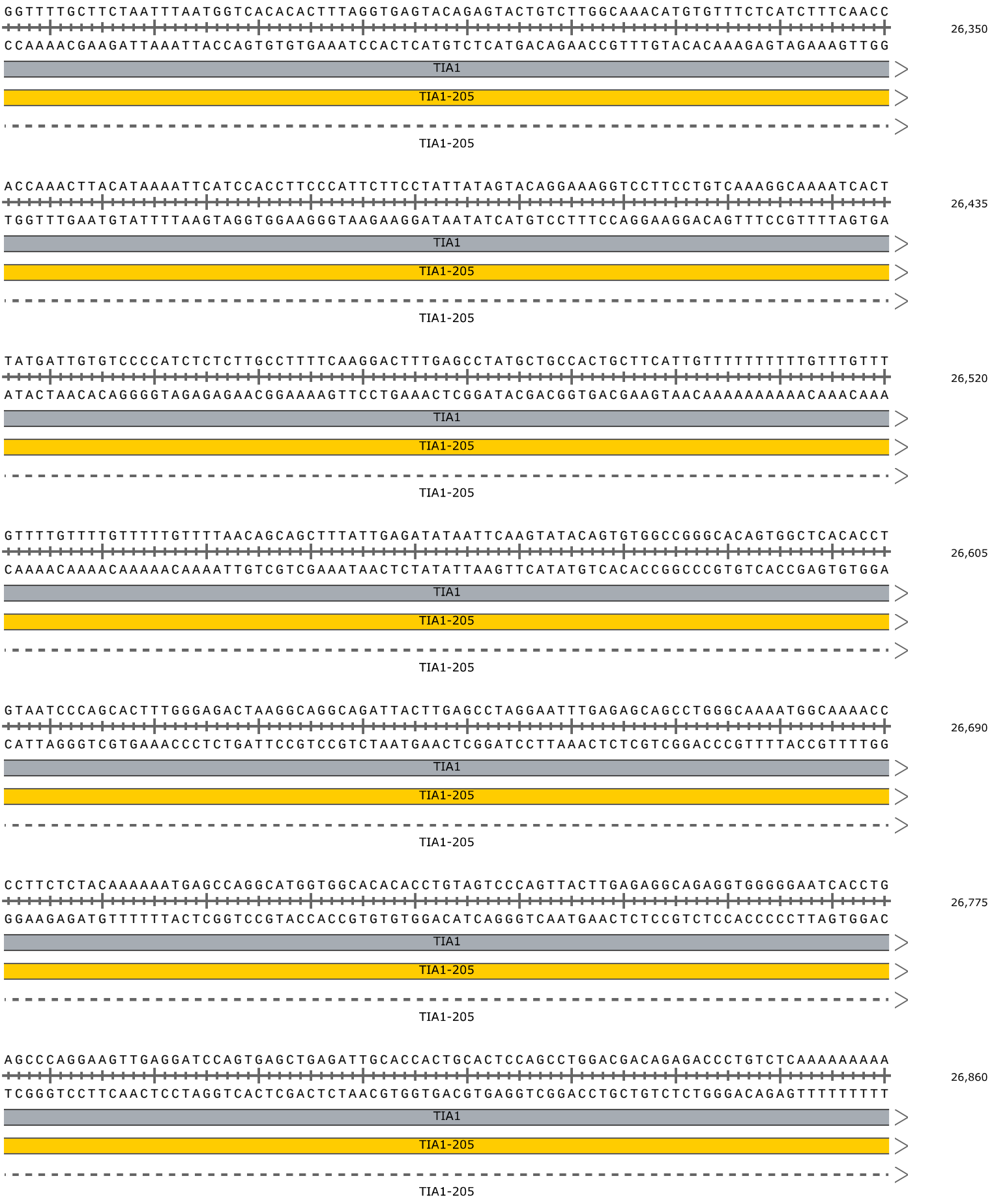
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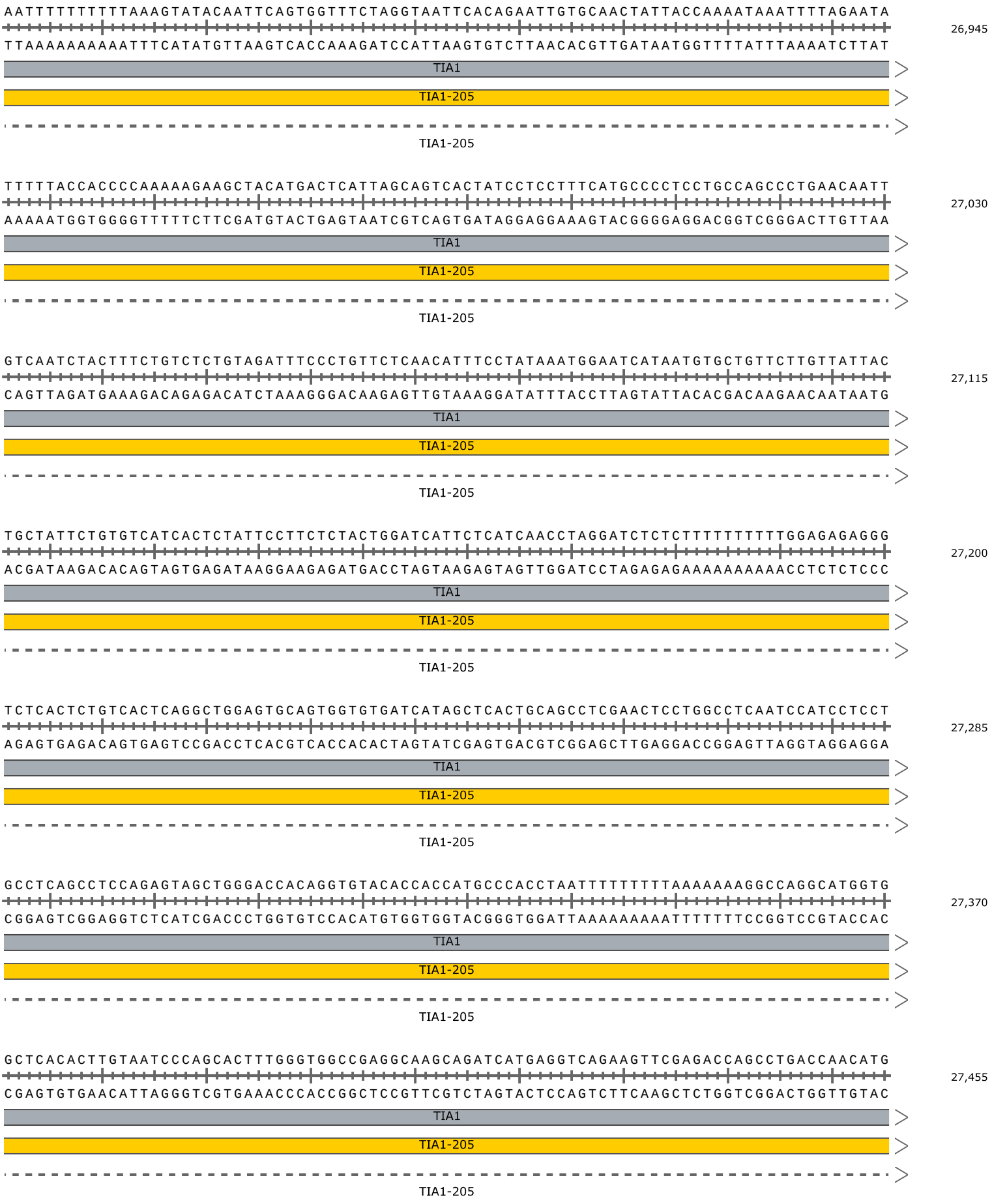
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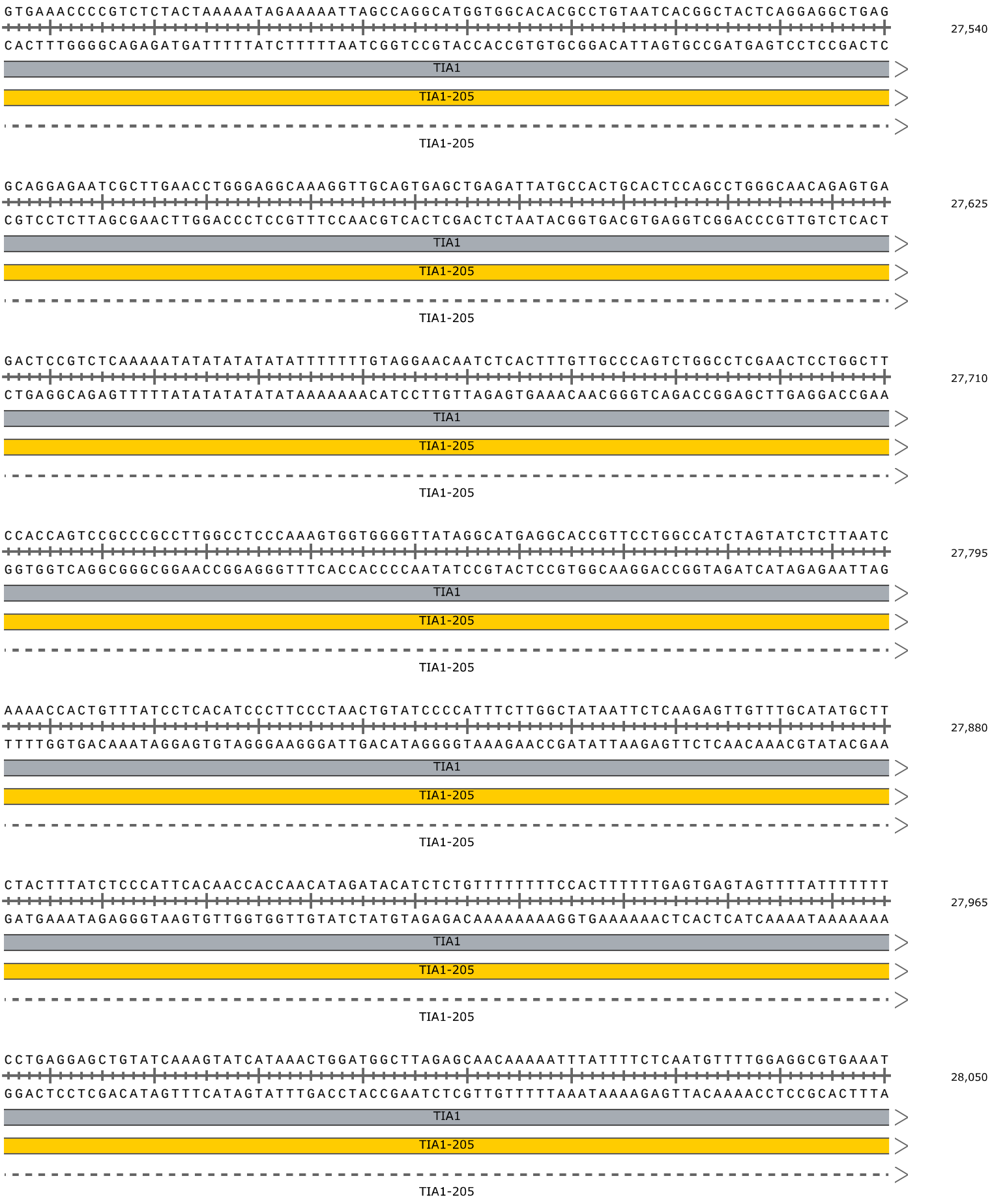
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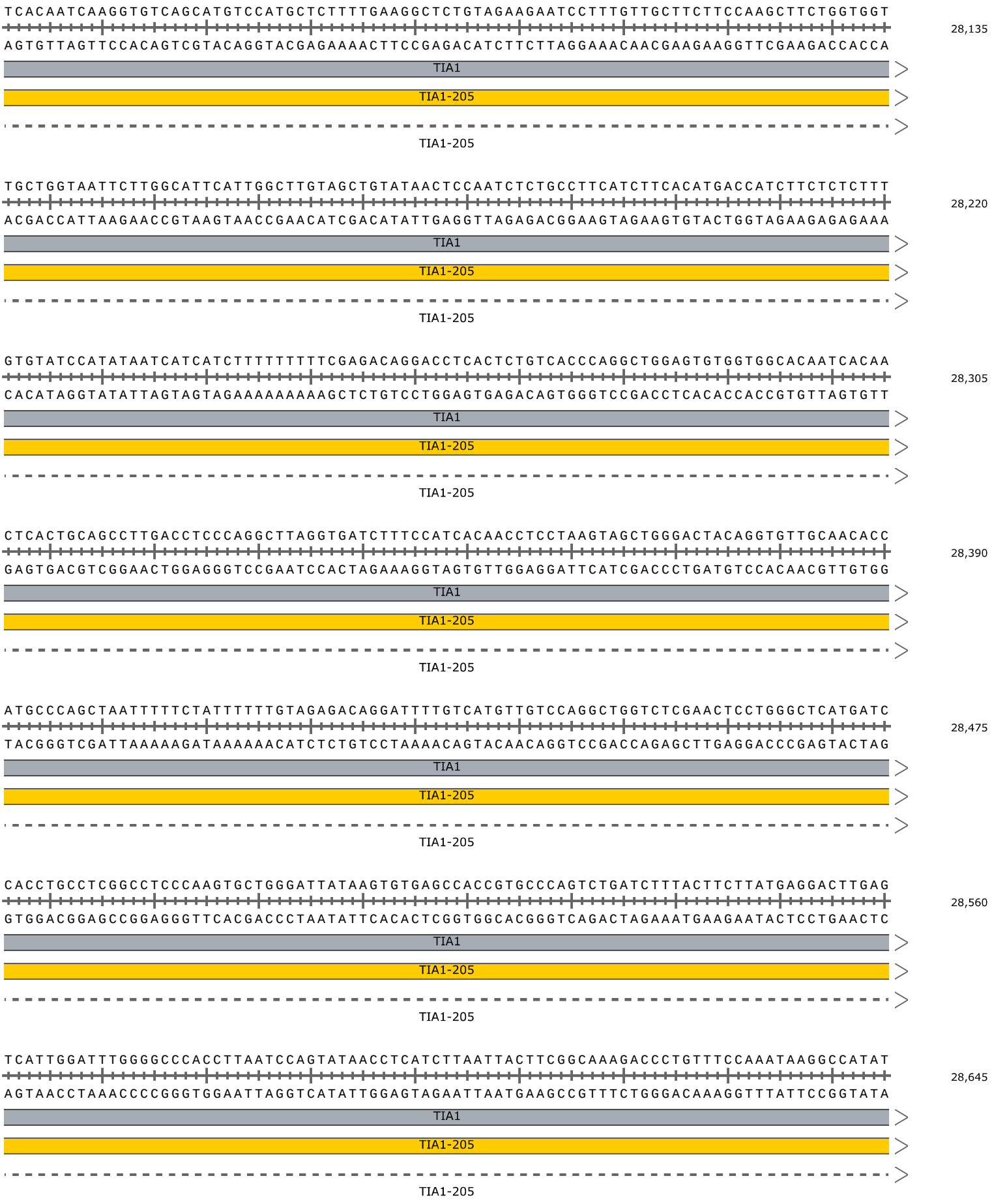
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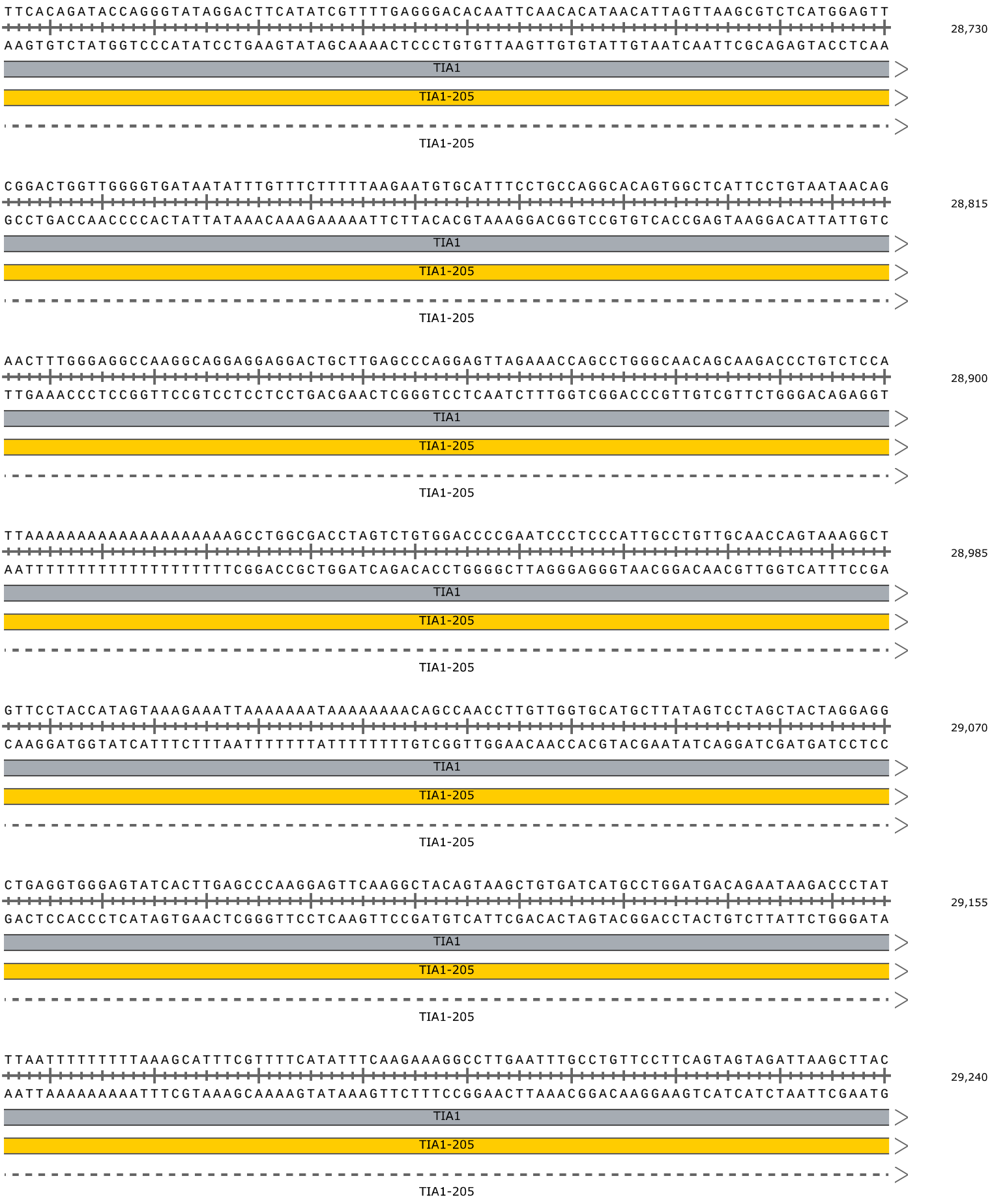
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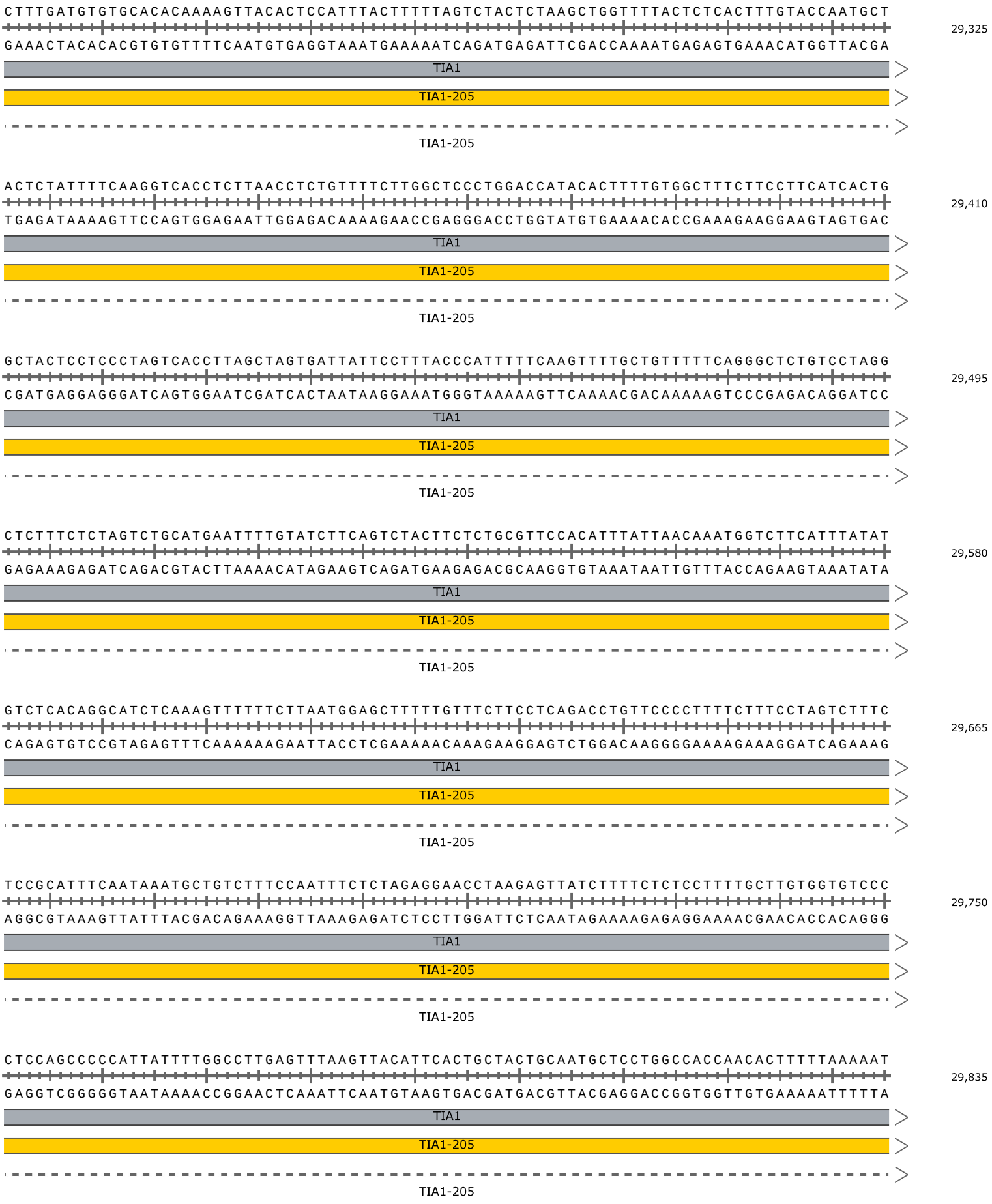
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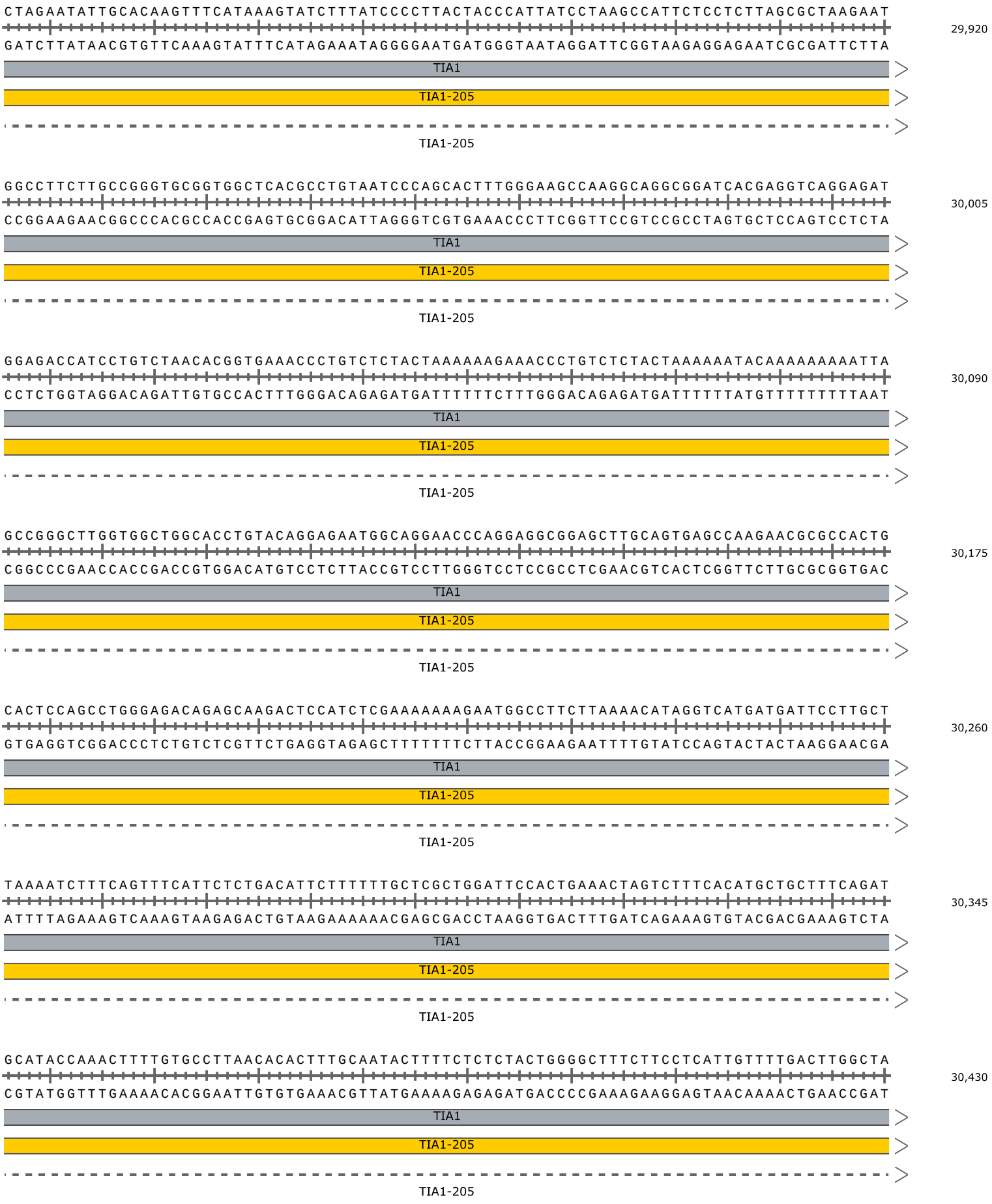
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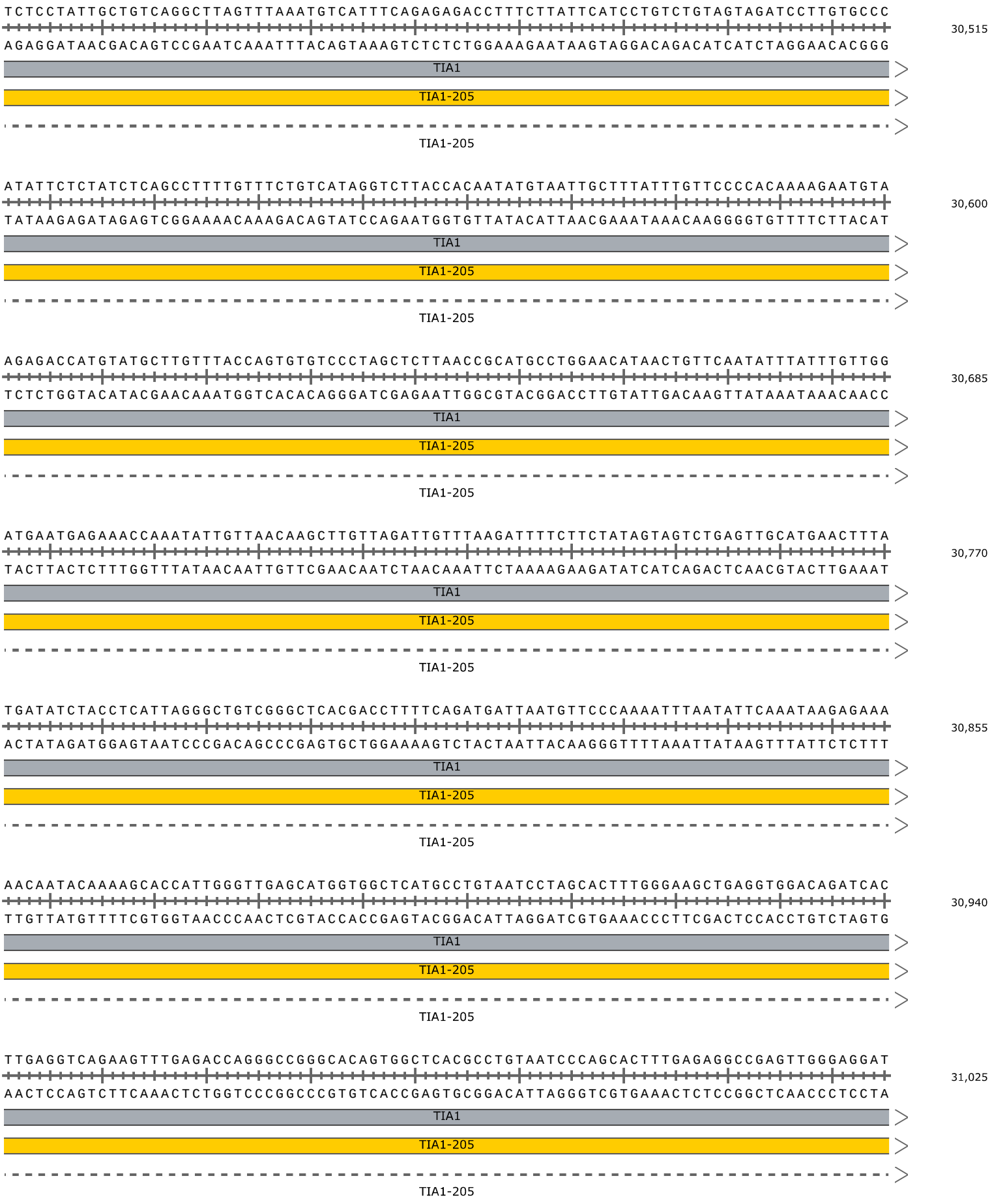
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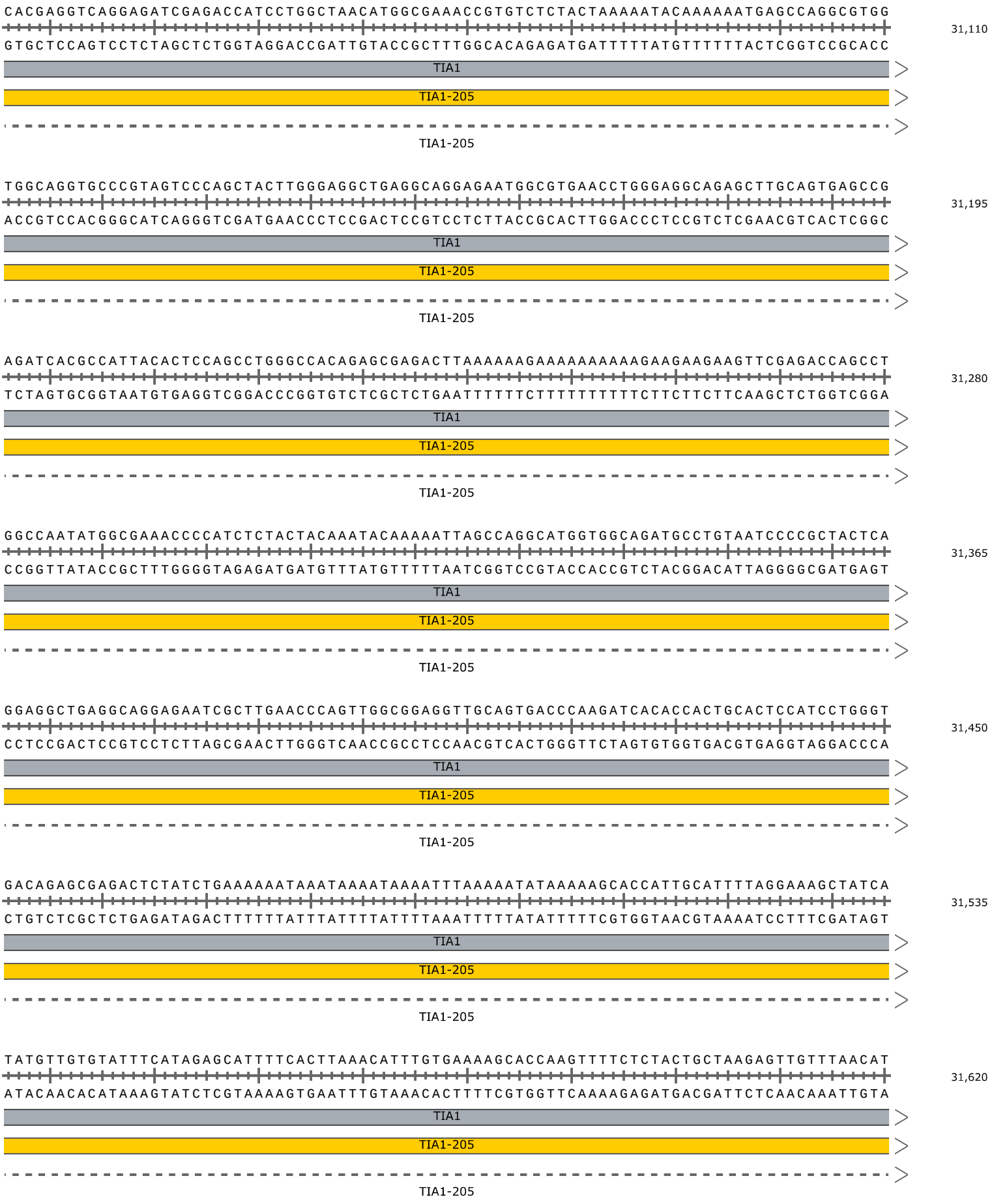
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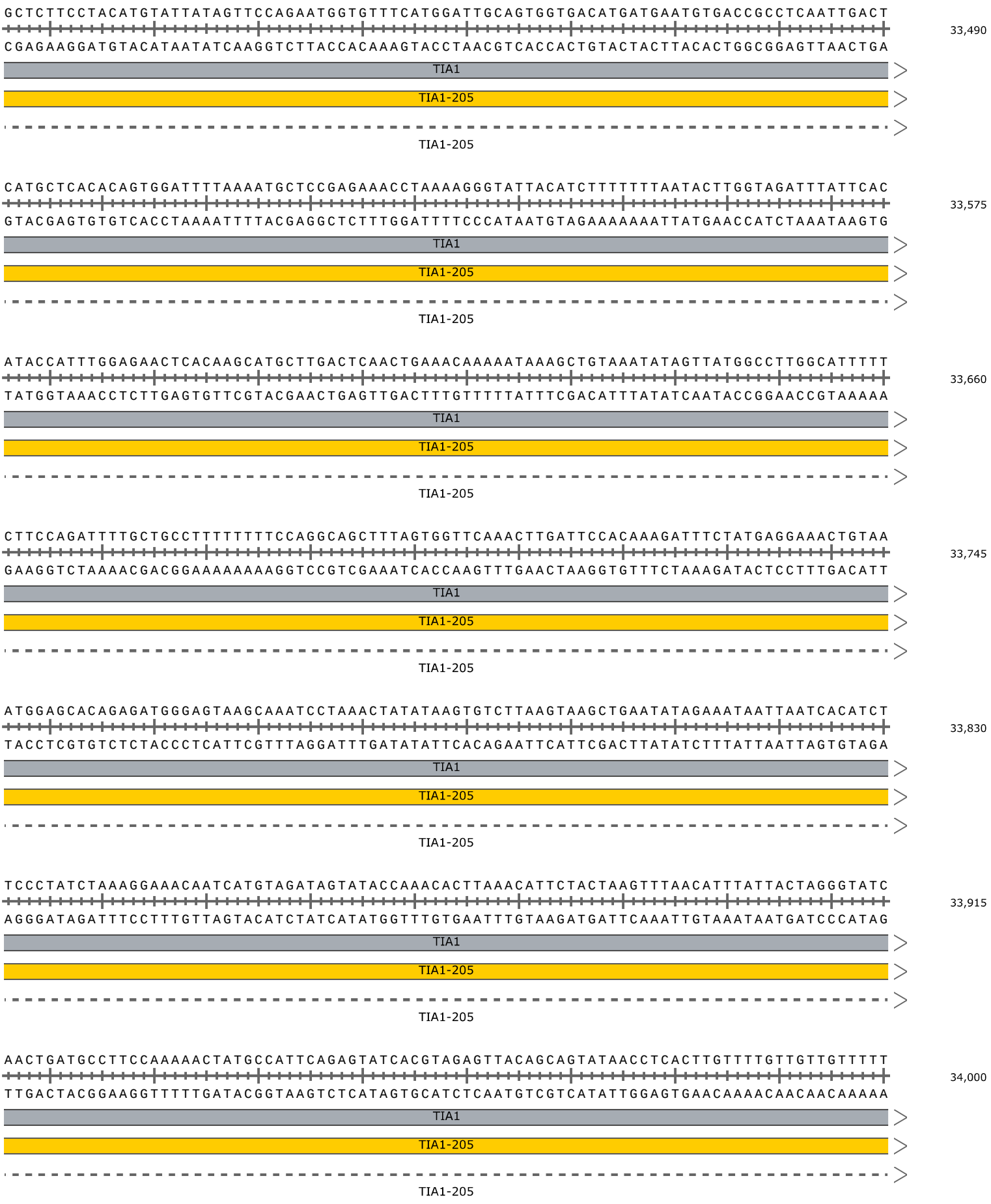
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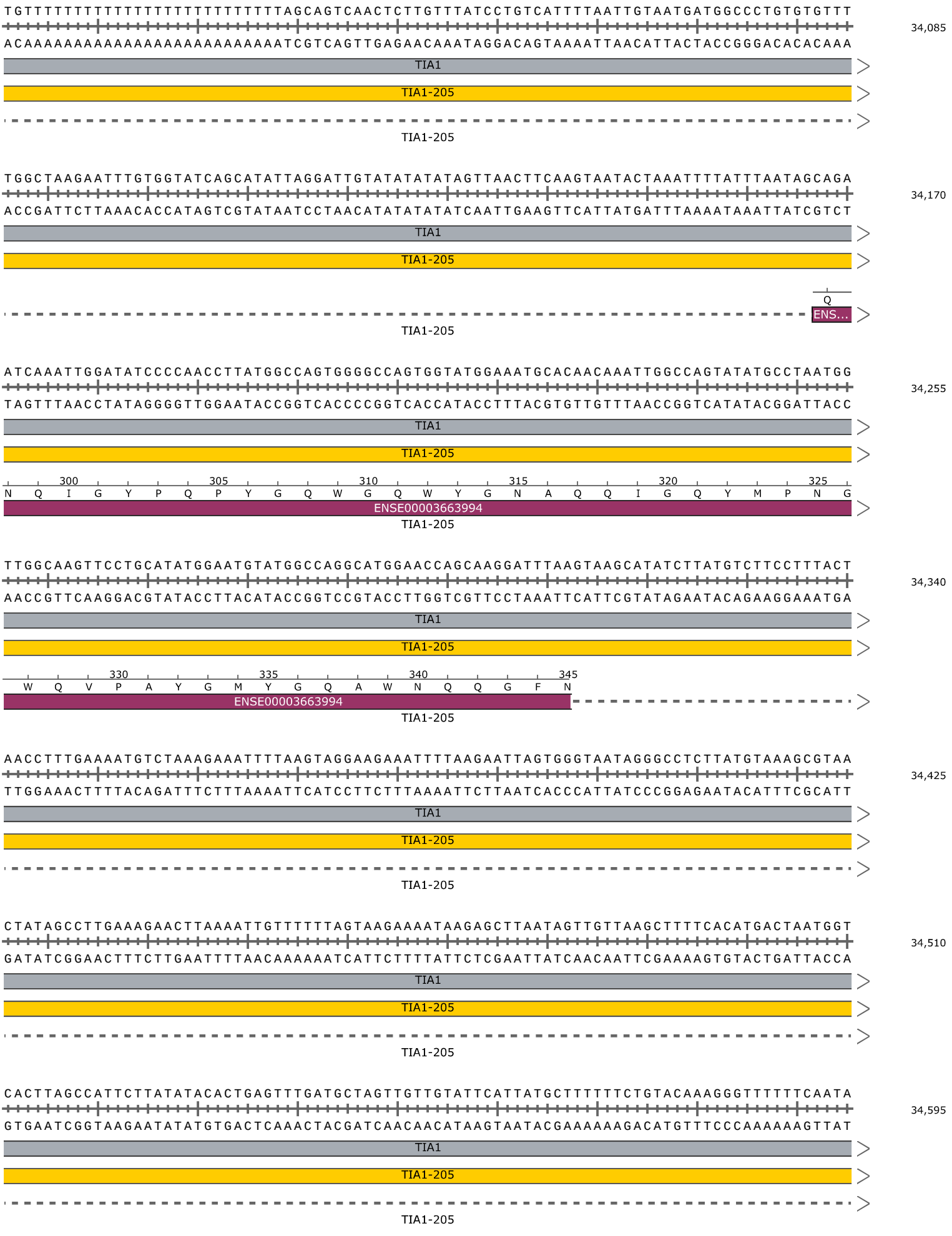
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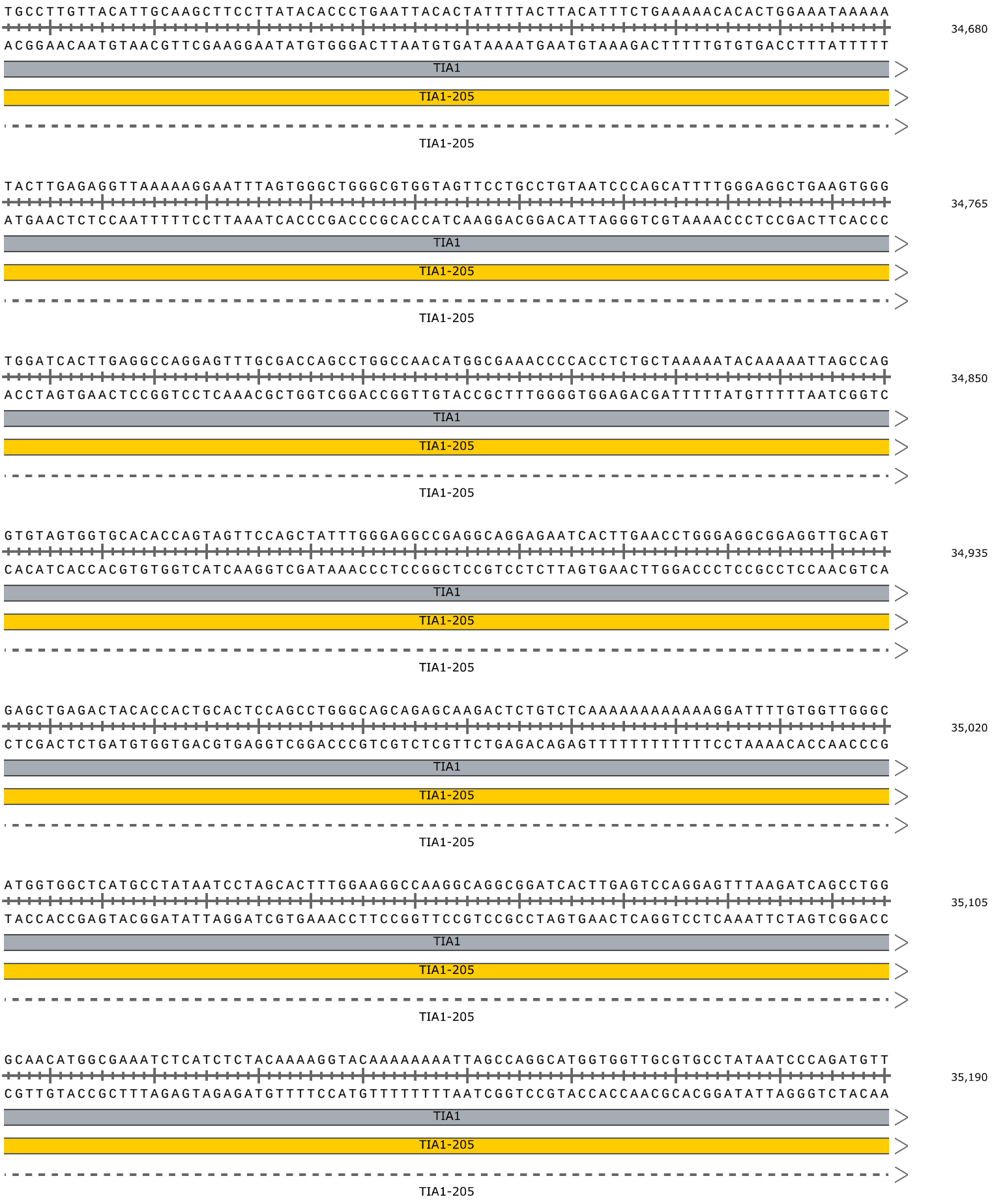
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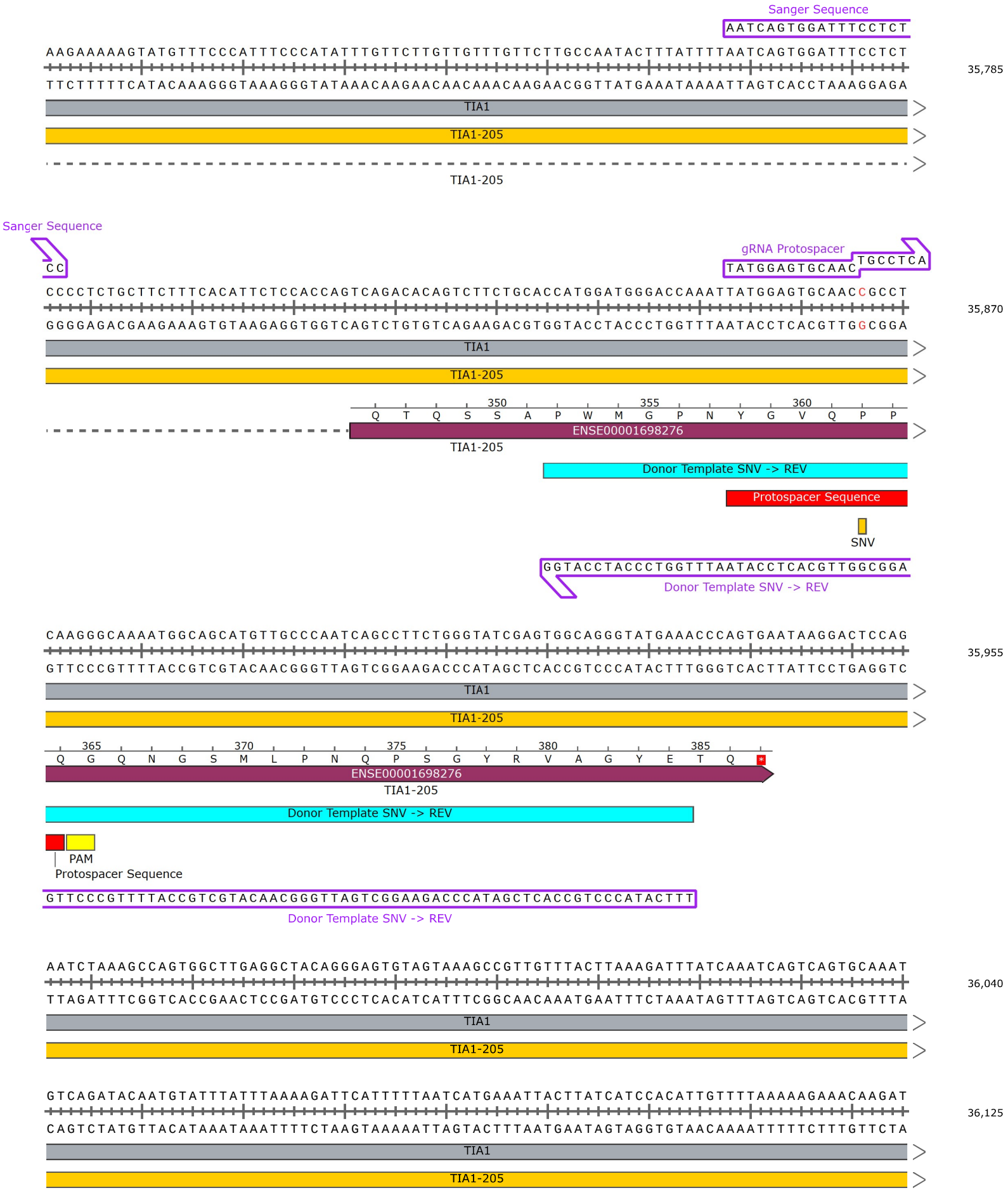
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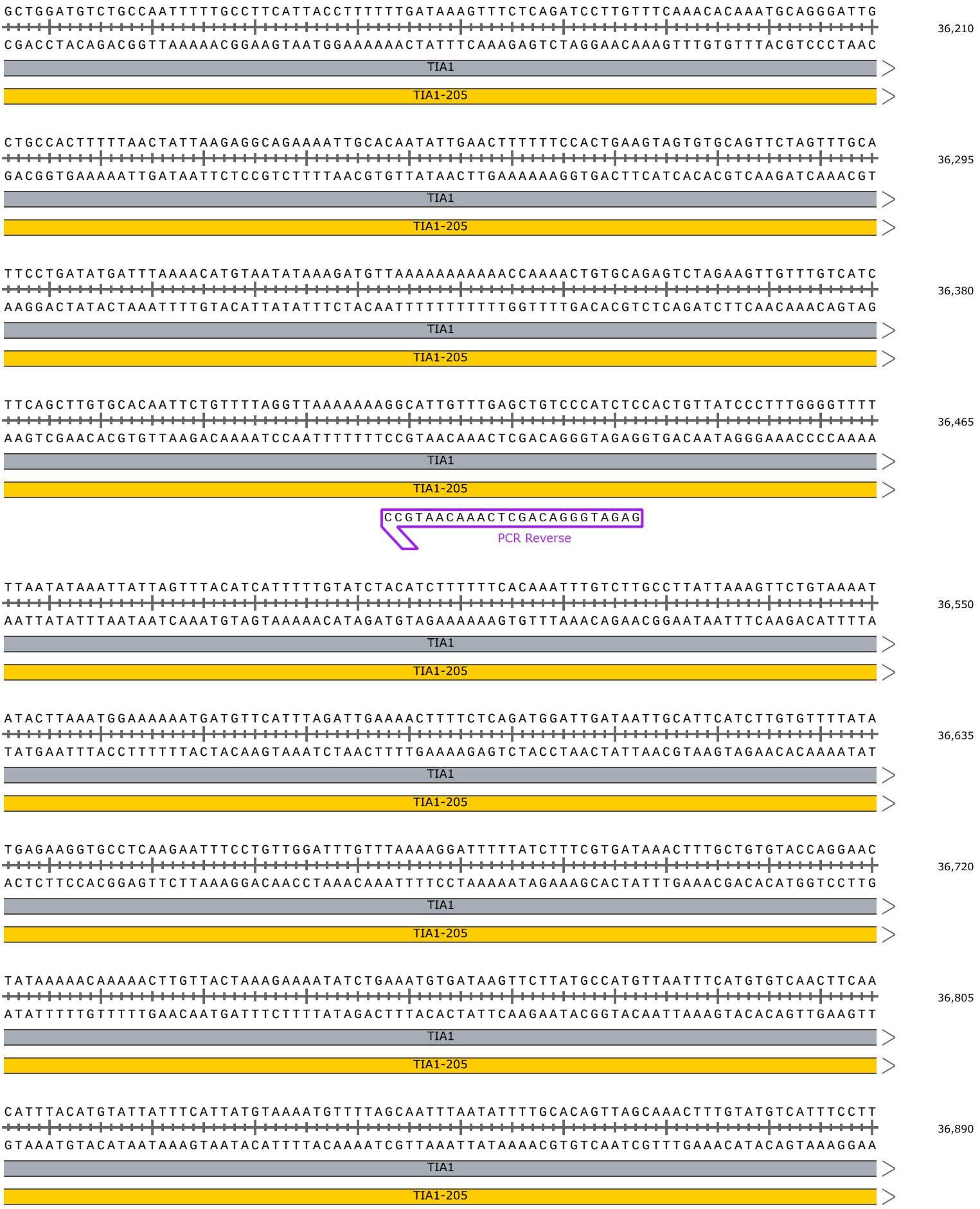
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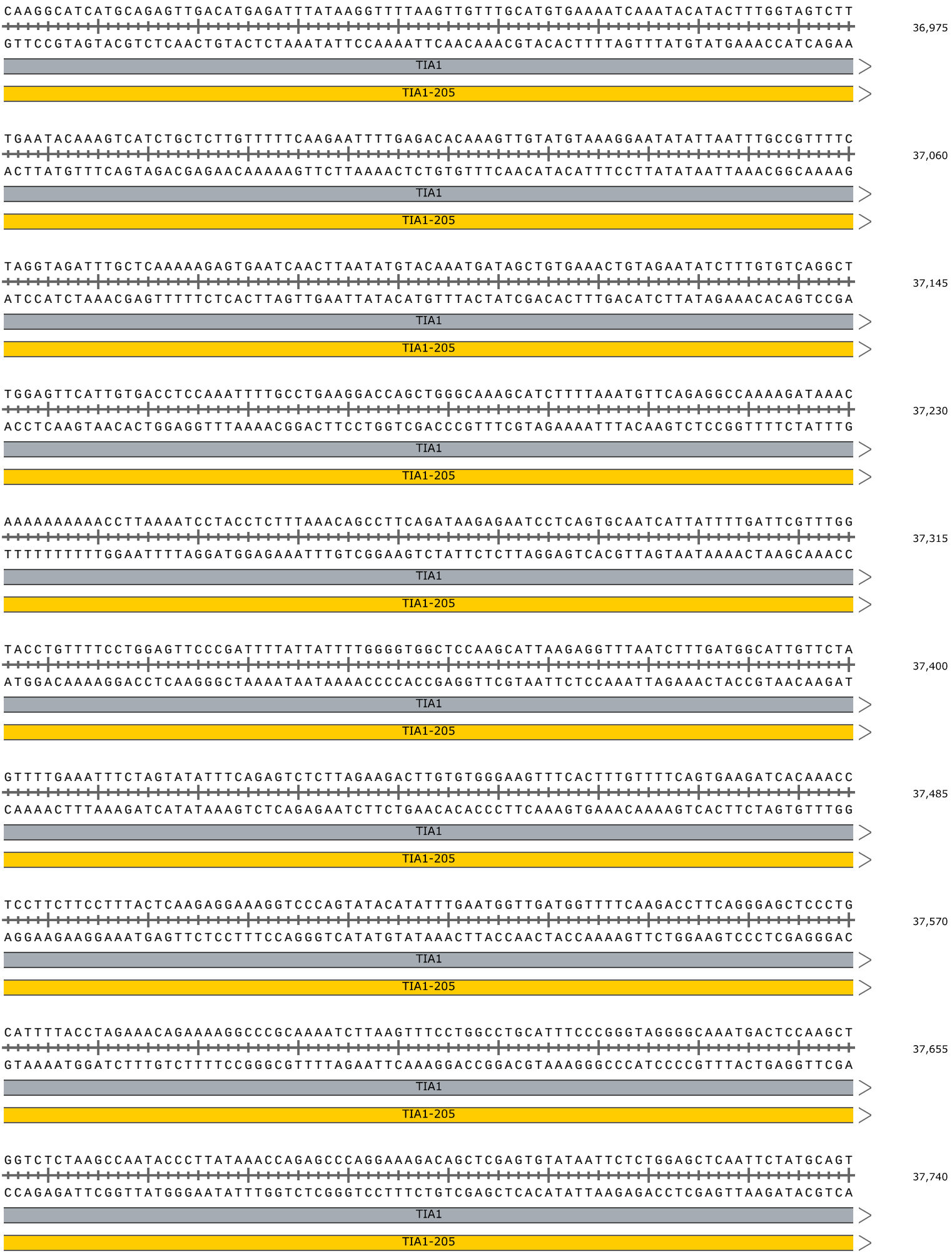
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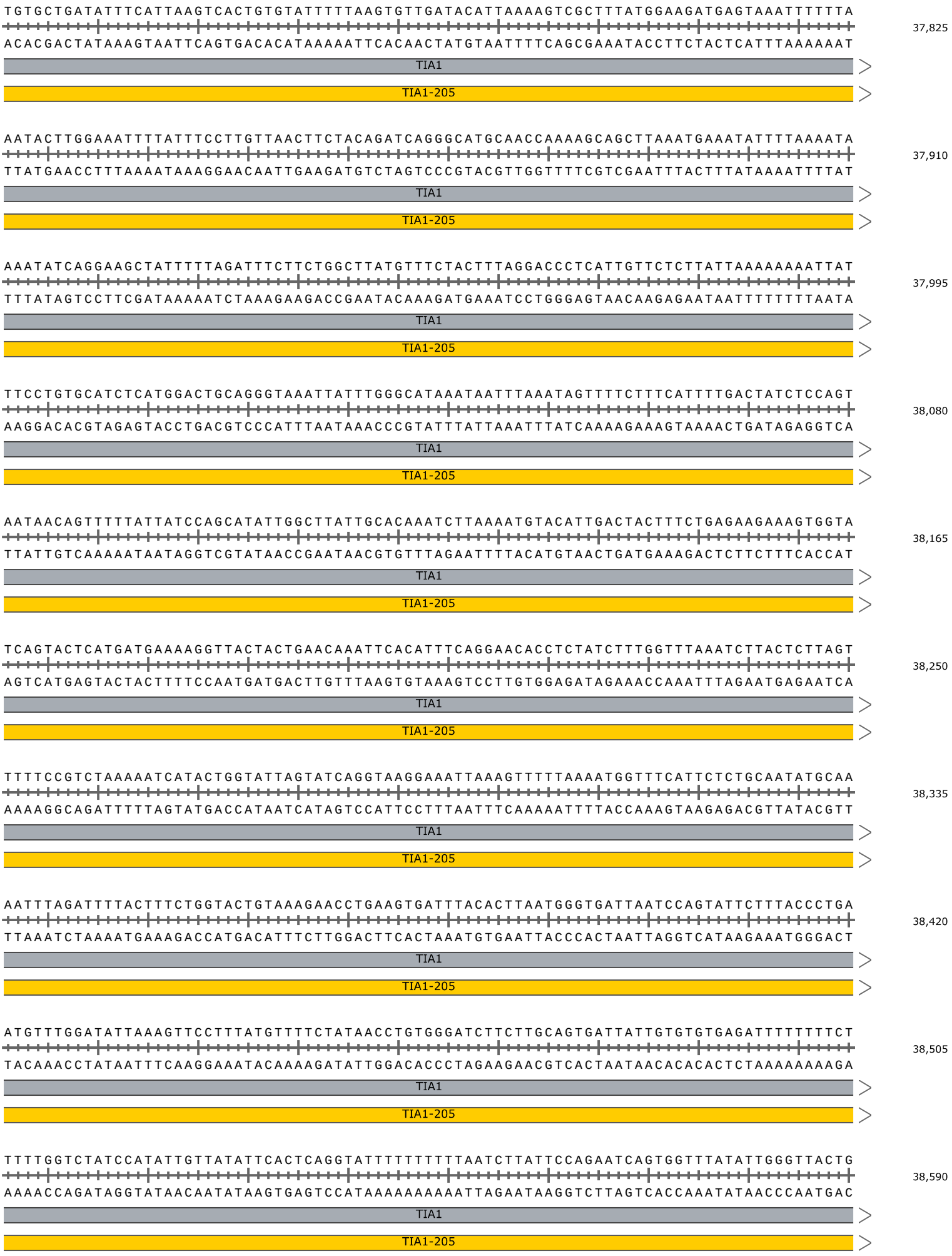
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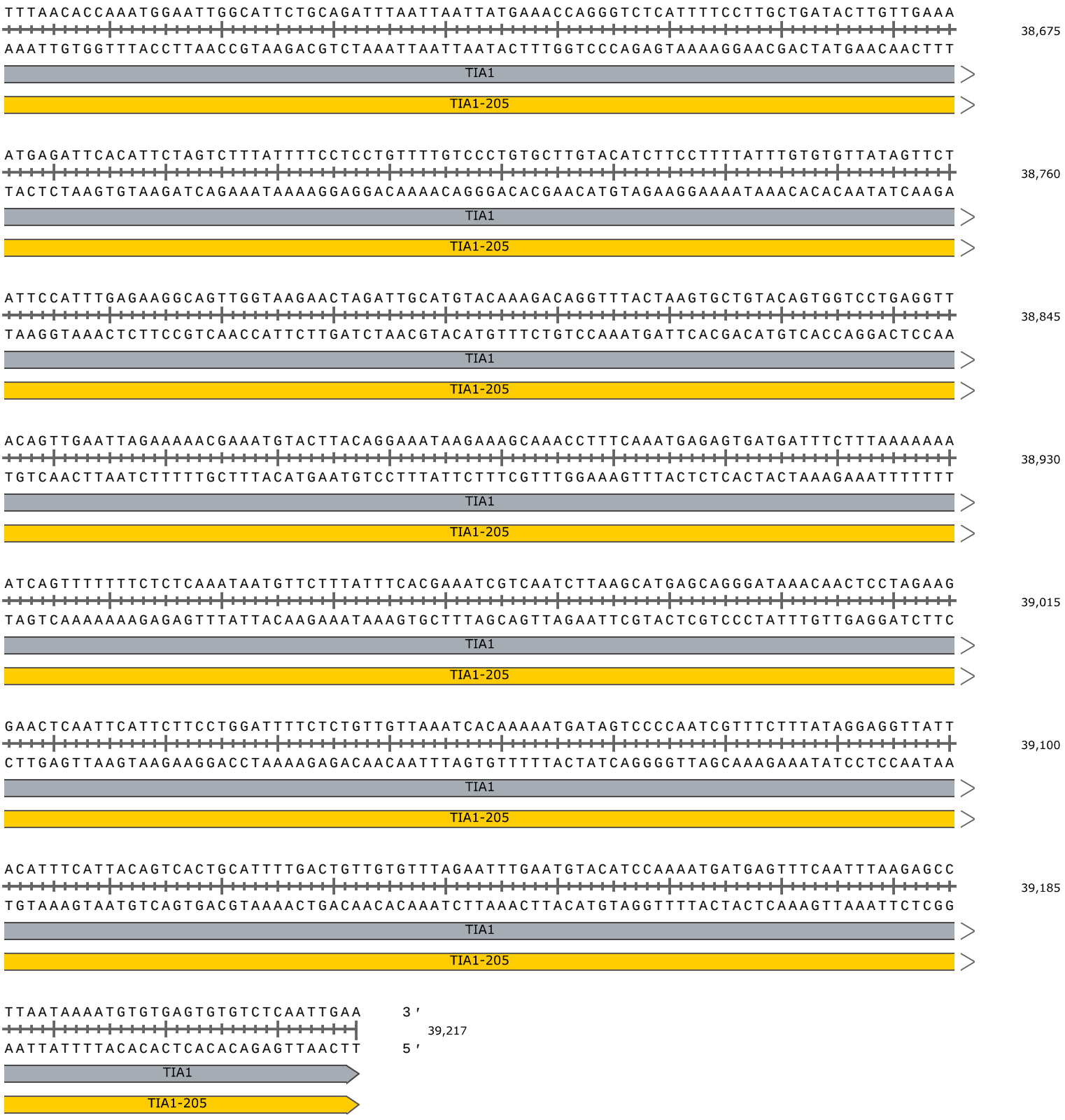
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	/note	= primary transcript ENST00000433529					
	TIA1-213		39 .. 19,471		19,433 bp	→	prim_transcript
	/note	= primary transcript ENST00000481650 Retained intron					
	C2orf42		46 .. 98,776		98,731 bp	→	gene
	/note	= gene ENSG00000115998 Protein coding					
	C2orf42-212		46 .. 67,031		66,986 bp	→	prim_transcript
	/note	= primary transcript ENST00000470096 protein_coding_CDS_not_defined					
	TIA1-211		50 .. 24,237		24,188 bp	→	prim_transcript
	/note	= primary transcript ENST00000477044 protein_coding_CDS_not_defined					
	TIA1-206		51 .. 36,344		36,294 bp	→	prim_transcript
	/note	= primary transcript ENST00000445587					
	TIA1-201		81 .. 38,457		38,377 bp	→	prim_transcript
	/note	= primary transcript ENST00000282574					
	TIA1-204		207 .. 31,989		31,783 bp	→	prim_transcript
	/note	= primary transcript ENST00000416149					
	TIA1-201		231 .. 35,942		35,712 bp	→	CDS
	▸ 13 segments = 1158 bp						
	/note	= coding sequence ENSP00000282574					
	/translation	= MEDEMPKTL,,YVGNLSRDVTEALILQLFSQIGPCKNCKMIMD,,TAGNDPYCFVEFHEHRHAAAALAAMNGRKIMGK,,EVKVNWATTPSSQKKDT S,,SSTVVSTQRSQ,,DHFHVFVGDLSPEITTEDIKAAFAPFGRIS,,DARVVKDMATGKSKGYGFVSFFNKW,,DAENAIQQMGGQWLGGRQIRTNW ATRKPPAPKSTYE,,SNTKQLSYDEVVNQSSPSNCTVYCGGVTSGLT,,EQLMRQTFSPFGQIMEIRVFPDKGYSFVR,,FNSHESAAHAIVSVNGTT IEGHVVKCYWGKETLDMINPVQQ,,NQIGYPQPYGQWGQWYGNAQQIGQYMPNGWQVPAYGMYGQAWNQQGFN,,QTQSSAPWMGPNYGV QPPQGQNGSML PNQPSGYRVAGYETQ* 385 amino acids = 42.8 kDa					
	TIA1-203		231 .. 35,942		35,712 bp	→	CDS
	▸ 12 segments = 1128 bp						
	/note	= coding sequence ENSP00000404023					
	/translation	= MEDEMPKTL,,YVGNLSRDVTEALILQLFSQIGPCKNCKMIMD,,TAGNDPYCFVEFHEHRHAAAALAAMNGRKIMGK,,EVKVNWATTPSSQKKDT S,,NHFHVFVGDLSPEITTEDIKAAFAPFGRIS,,DARVVKDMATGKSKGYGFVSFFNKW,,DAENAIQQMGGQWLGGRQIRTNWATRKPPAPKSTY E,,SNTKQLSYDEVVNQSSPSNCTVYCGGVTSGLT,,EQLMRQTFSPFGQIMEIRVFPDKGYSFVR,,FNSHESAAHAIVSVNGTTIEGHVVKCYWG KETLDMINPVQQ,,QNQIGYPQPYGQWGQWYGNAQQIGQYMPNGWQVPAYGMYGQAWNQQGFN,,QTQSSAPWMGPNYGVQPPQGQNGS ML PNQPSGYRVAGYETQ* 375 amino acids = 41.8 kDa					
✓	**TIA1-205**		231 .. 35,942		35,712 bp	→	CDS
	▸ 13 segments = 1161 bp						
	/note	= coding sequence ENSP00000401371					
	/translation	= MEDEMPKTL,,YVGNLSRDVTEALILQLFSQIGPCKNCKMIMD,,TAGNDPYCFVEFHEHRHAAAALAAMNGRKIMGK,,EVKVNWATTPSSQKKDT S,,SSTVVSTQRSQ,,DHFHVFVGDLSPEITTEDIKAAFAPFGRIS,,DARVVKDMATGKSKGYGFVSFFNKW,,DAENAIQQMGGQWLGGRQIRTNW ATRKPPAPKSTYE,,SNTKQLSYDEVVNQSSPSNCTVYCGGVTSGLT,,EQLMRQTFSPFGQIMEIRVFPDKGYSFVR,,FNSHESAAHAIVSVNGTT IEGHVVKCYWGKETLDMINPVQQ,,QNQIGYPQPYGQWGQWYGNAQQIGQYMPNGWQVPAYGMYGQAWNQQGFN,,QTQSSAPWMGPNYG VQPPQGQNGSML PNQPSGYRVAGYETQ* 388 amino acids = 42.0 kDa					

Feature	Location	Size		Type
TIA1-206	231 .. 35,942	35,712 bp	→	CDS

▸ 10 segments = 858 bp

/note = coding sequence ENSP00000399567

/translation = MEDEMPKTL,,YVGNLSRDVTEALILQLFSQIGPCKNCKMIMD,,TAGNDPYCFVEFHEHRHAAAALAAMNGRKIMGK,,EVKVNWATTPSSQKKDTS,,NHFHVFVGDLSPEITTEDIKAAFAPFGRIS,,DARVVKDMATGKSKGYGFVSFFNKW,,DAENAIQQMGGQWLGGRQIRTNWATRKPPAPKSTYE,,SNTKQLSYDEVVNQSSPSNCTVYCGGVTSGLT,,EQLMRQTFSPFGQIMEIRVFPDKGYSFVR,,QTQSSAPWMGPNYGVQPPQGQNGSMLPNQPSGYRVACYETQ*

285 amino acids = 31.6 kDa

TIA1-204	231 .. 31,837	31,607 bp	→	CDS

▸ 8 segments = 645 bp

/note = coding sequence ENSP00000413751

/translation = MEDEMPKTL,,YVGNLSRDVTEALILQLFSQIGPCKNCKMIMD,,TAGNDPYCFVEFHEHRHAAAALAAMNGRKIMGK,,EVKVNWATTPSSQKKDTS,,SSTVVSTQRSQ,,DHFHVFVGDLSPEITTEDIKAAFAPFGRIS,,DARVVKDMATGKSKGYGFVSFFNKW,,DAENAIQQMGGQWLGGRQIRTNWATRKPPAPKSTYECRQICEEKEMWNFGEKYARF*

214 amino acids = 24.1 kDa

TIA1-202	12,486 .. 24,235	11,750 bp	→	prim_transcript

/note = primary transcript ENST00000361692

TIA1-202	12,486 .. 24,149	11,664 bp	→	CDS

▸ 5 segments = 457 bp

/note = coding sequence ENSP00000354838

/translation = IRR*PFQRCDRSSNSATL*PDWTL*KLQNDYG,,YSWK*SLLFCGVS*ASSCSCSISCYEWTEDNG*,,GSQSELGNNP*QSKERYKQ,,SFPCLCW*SQPRNYN*RYKSCFCTIWKNI,,RCPSGKRHGNRKV*GIWLCLLFQQMGELSEKCMDNA*RV

152 codons (11 internal stop codons)

TIA1-207	19,343 .. 34,309	14,967 bp	→	prim_transcript

/note = primary transcript ENST00000454815

TIA1-218	20,822 .. 32,427	11,606 bp	→	prim_transcript

/note = primary transcript ENST00000496096
Retained intron

TIA1-212	20,838 .. 32,508	11,671 bp	→	prim_transcript

/note = primary transcript ENST00000477415
Retained intron

TIA1-209	23,595 .. 31,839	8245 bp	→	prim_transcript

/note = primary transcript ENST00000474699
Retained intron

TIA1-214	24,069 .. 33,536	9468 bp	→	prim_transcript

/note = primary transcript ENST00000482876
protein_coding_CDS_not_defined

TIA1-215	31,501 .. 32,236	736 bp	→	prim_transcript

/note = primary transcript ENST00000484065
Retained intron

TIA1-208	31,817 .. 34,297	2481 bp	→	prim_transcript

/note = primary transcript ENST00000468787
protein_coding_CDS_not_defined

TIA1-220	31,833 .. 32,542	710 bp	→	prim_transcript

/note = primary transcript ENST00000497672
Retained intron

TIA1-207	32,377 .. 34,309	1933 bp	→	CDS

▸ 3 segments = 344 bp

/note = coding sequence ENSP00000402263

/translation = MRQTFSPFGQIMEIRVFPDKGYSFVR,,FNSHESAAHAIVSVNGTTIEGHVVKCYWGKETLDMINPVQQ,,QNQIGYPQPYGQWGQWYGNAQQIGQYMPNGWQVPAYGMYGQAWNQQG

114 amino acids = 13.1 kDa

TIA1-217	33,001 .. 35,912	2912 bp	→	prim_transcript

/note = primary transcript ENST00000495774
Retained intron

TIA1-216	33,339 .. 35,985	2647 bp	→	prim_transcript

/note = primary transcript ENST00000486392
Retained intron

✓ **Donor Template SNV -> REV**	35,835 .. 35,934	100 bp	⊢	misc_feature
✓ **Protospacer Sequence**	35,853 .. 35,872	20 bp	⊢	misc_feature

	Feature		Location			Size			Type
✓	**SNV**		35,866	..	35,866	1 bp			misc_feature
	/note	=	REV = C SNV = T						
✓	**PAM**		35,873	..	35,875	3 bp			misc_feature

	Primer	Length	Binding Sites		Tm	Date Added
✓	**PCR Forward**	25-mer	35,438 .. 35,462	→	60°C	Jan 18, 2023
	/sequence = TCTTTCAGGTAGTGGTTTCCTCAGC 48% GC / 7630.0 Da					
✓	**Sanger Sequence**	20-mer	35,768 .. 35,787	→	54°C	Jan 18, 2023
	/sequence = AATCAGTGGATTTCCTCTCC 45% GC / 6043.0 Da					
✓	**Donor Template SNV -> REV**	100-mer	35,835 .. 35,934	←	79°C	Jan 18, 2023
	/sequence = TTTCATACCCTGCCACTCGATACCCAGAAGGCTGATTGGGCAACATGCTGCCATTTTGCCCTTGAGGCGGTTGCACTCCATAATTTGGTC 62% GC / 13,637.9 Da					
✓	**gRNA Protospacer**	20-mer	35,853 .. 35,865	→	42°C	Jan 18, 2023
	/sequence = TATGGAGTGCAACTGCCTCA 50% GC / 6117.0 Da					
✓	**PCR Reverse**	25-mer	36,418 .. 36,442	←	62°C	Jan 18, 2023
	/sequence = GAGATGGGACAGCTCAAACAATGCC 52% GC / 7709.1 Da					