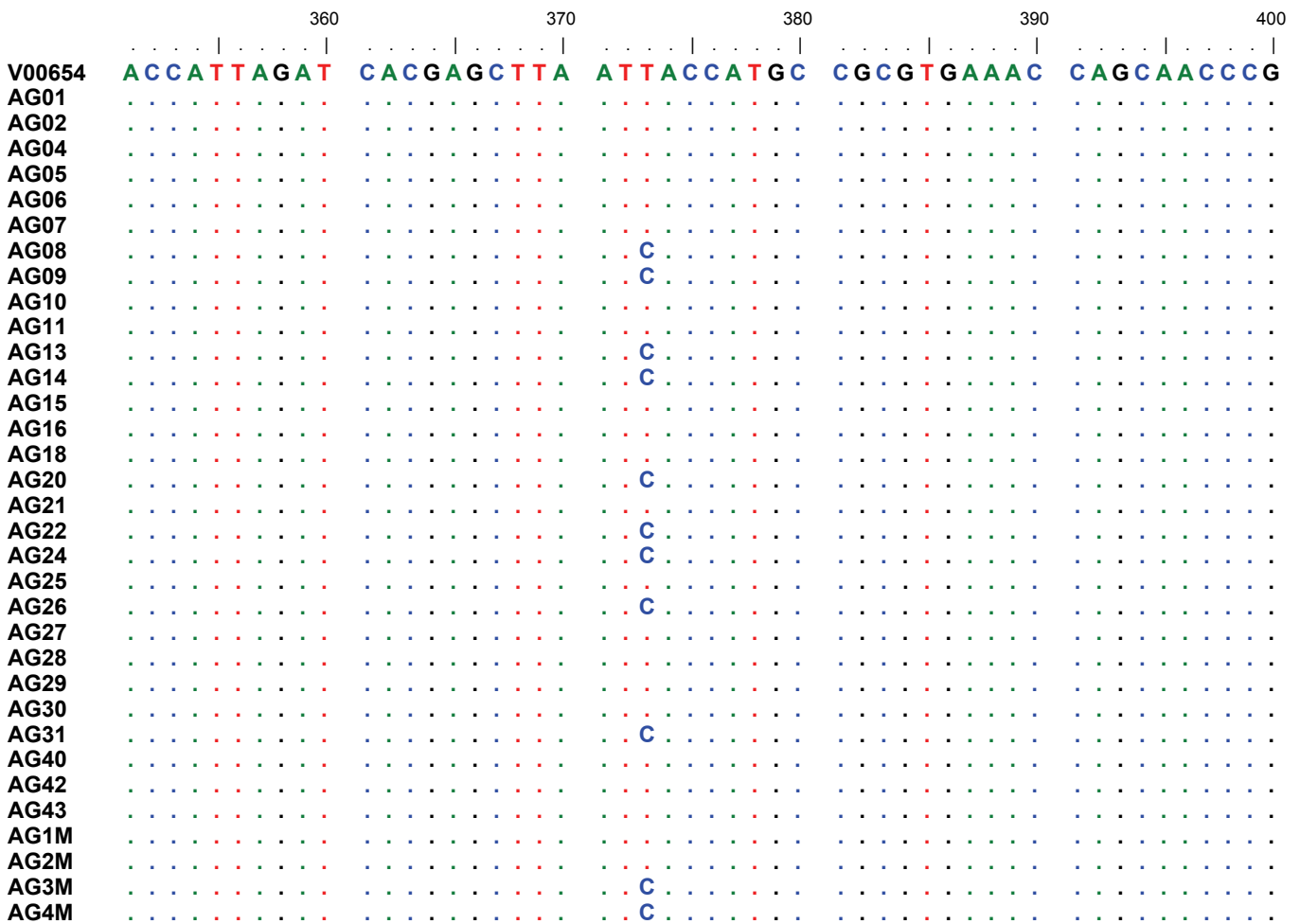
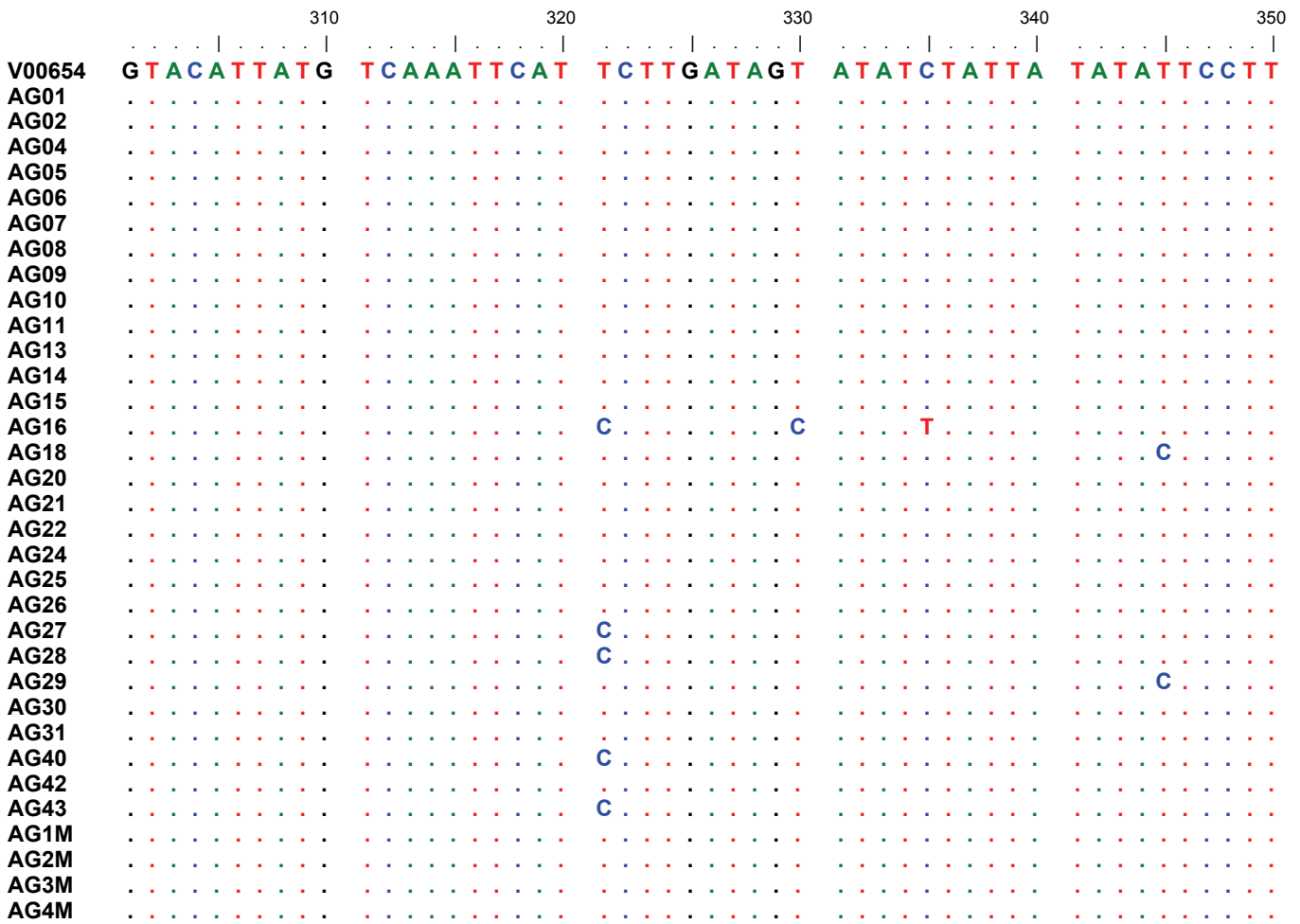


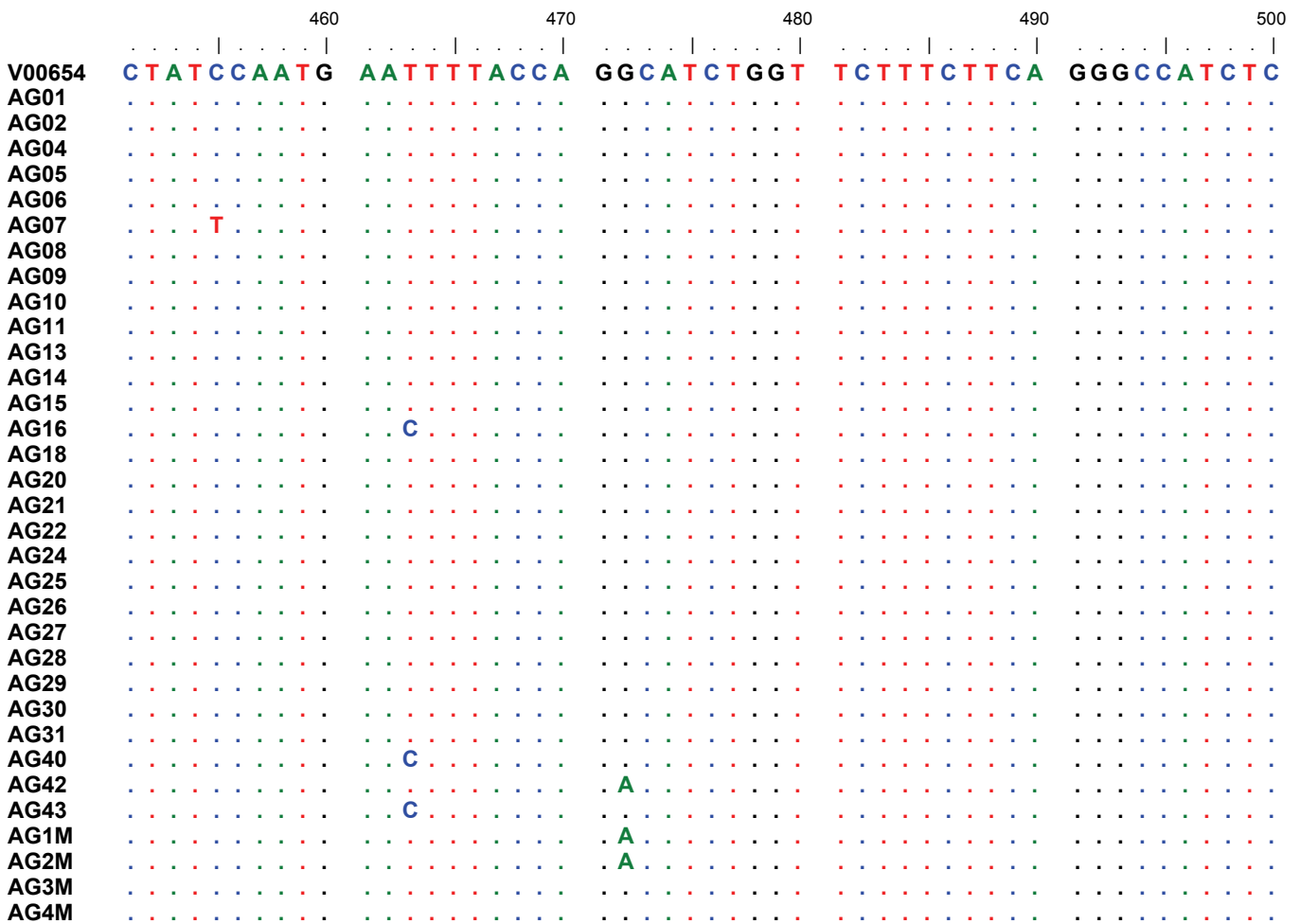
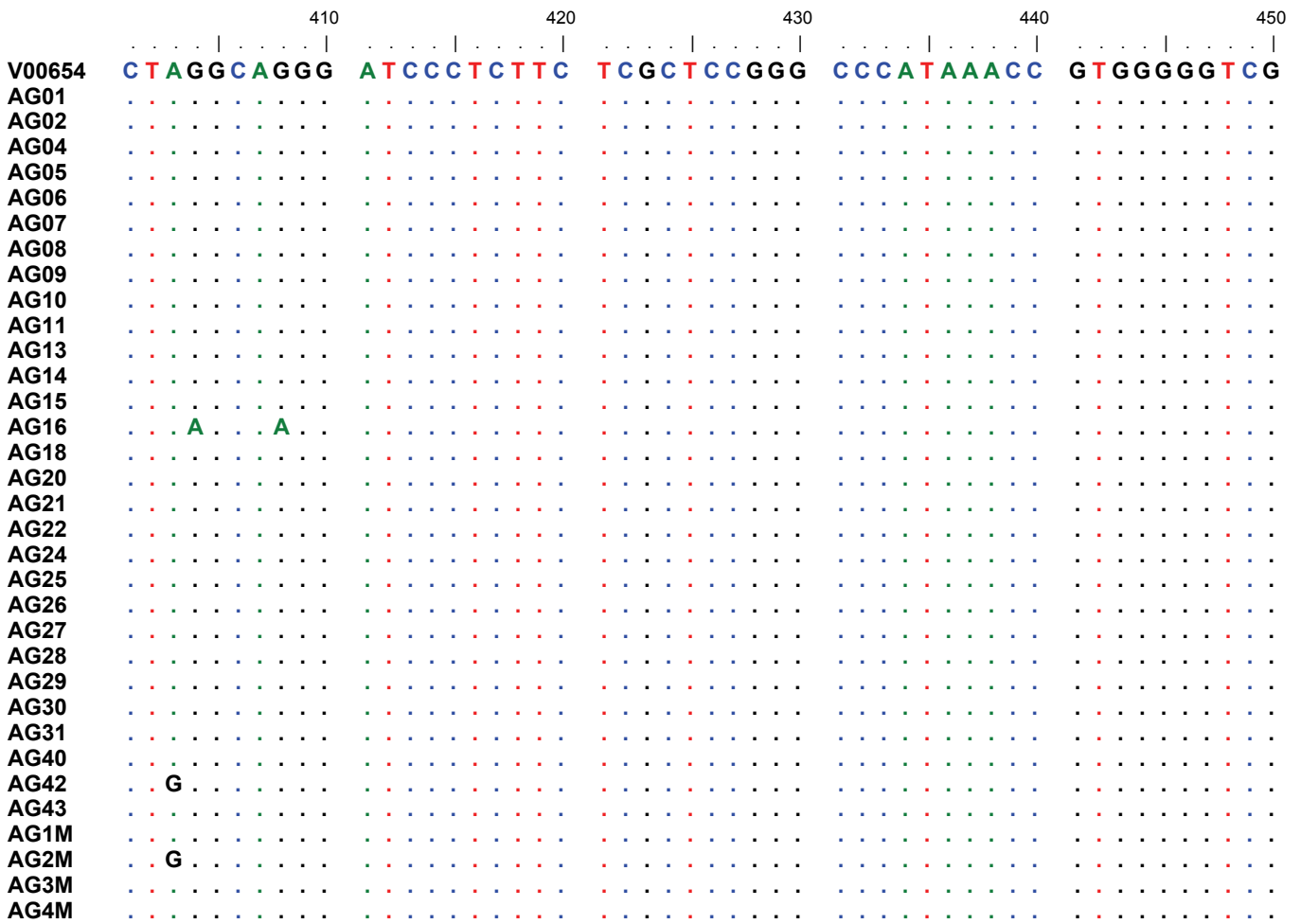
	110	120	130	140	150
V00654	T T A C A A A C A C	C A C T A G C T A A	C A T A A C A C G C	C C A T A C A C A G	A C C A C A G A A T
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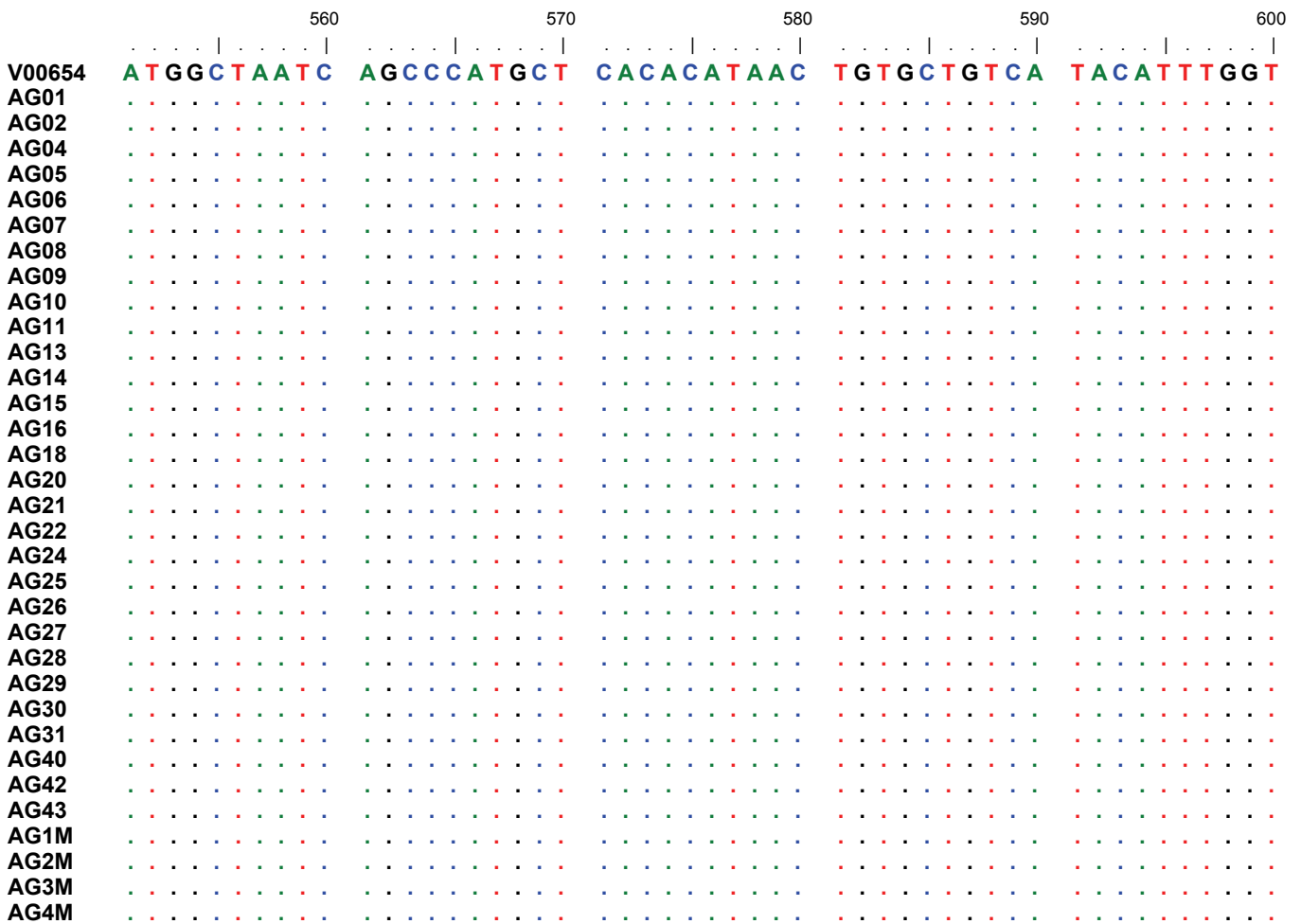
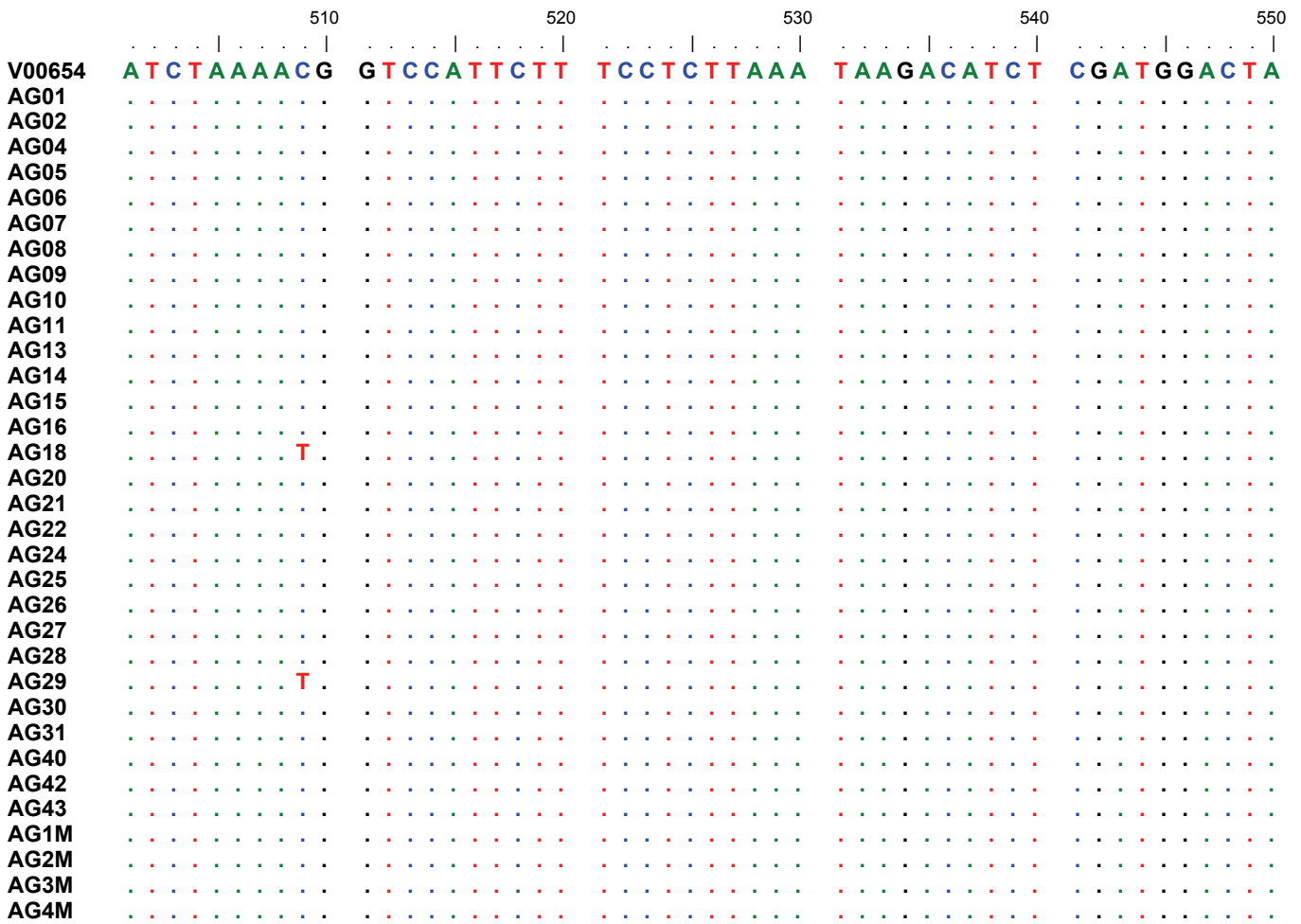
	160	170	180	190	200
V00654	G A A T T A C C T A	C G C A A G G G G T	A A T G T A C A T A	A C A T T A A T G T	A A T A A A G A C A
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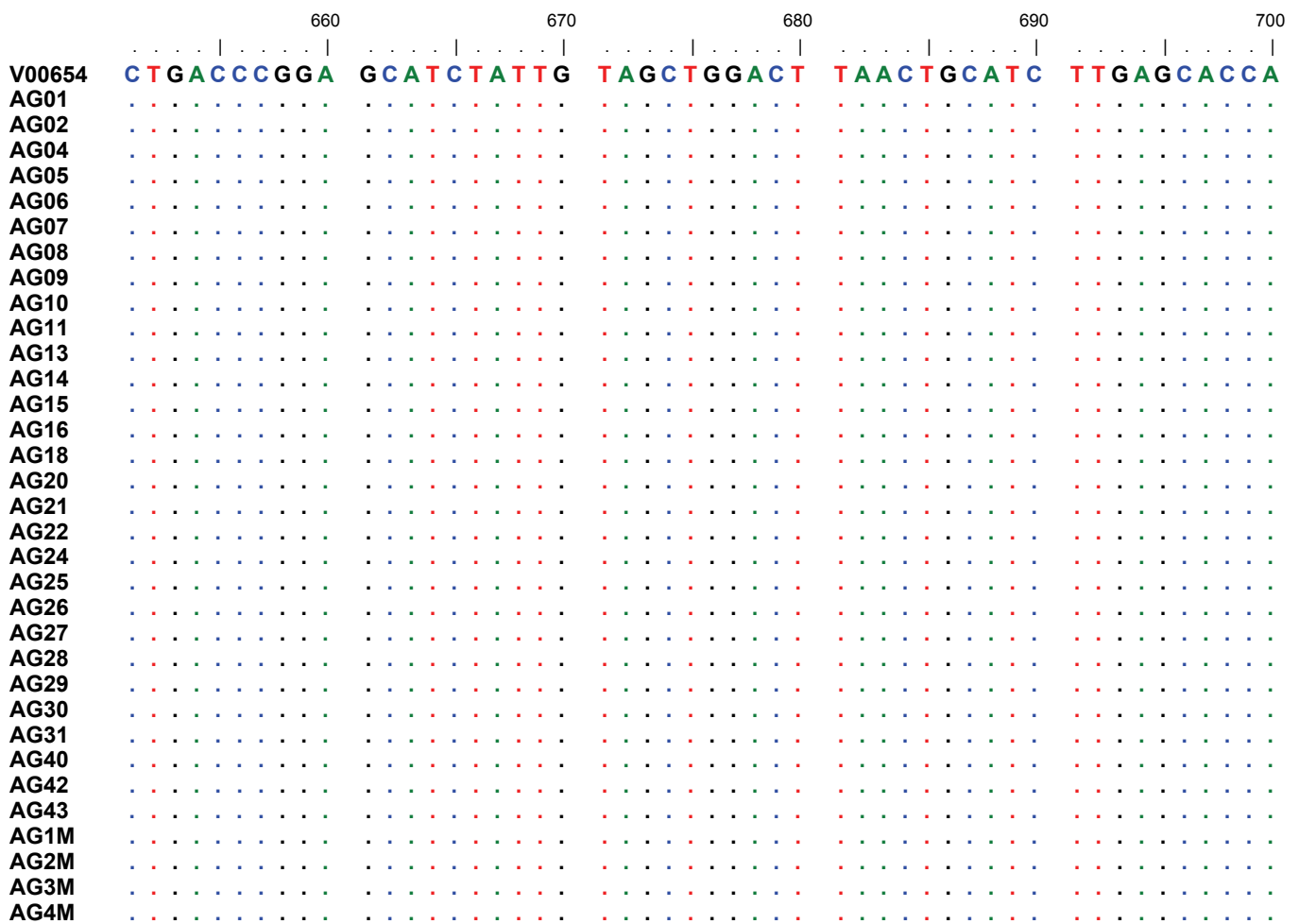
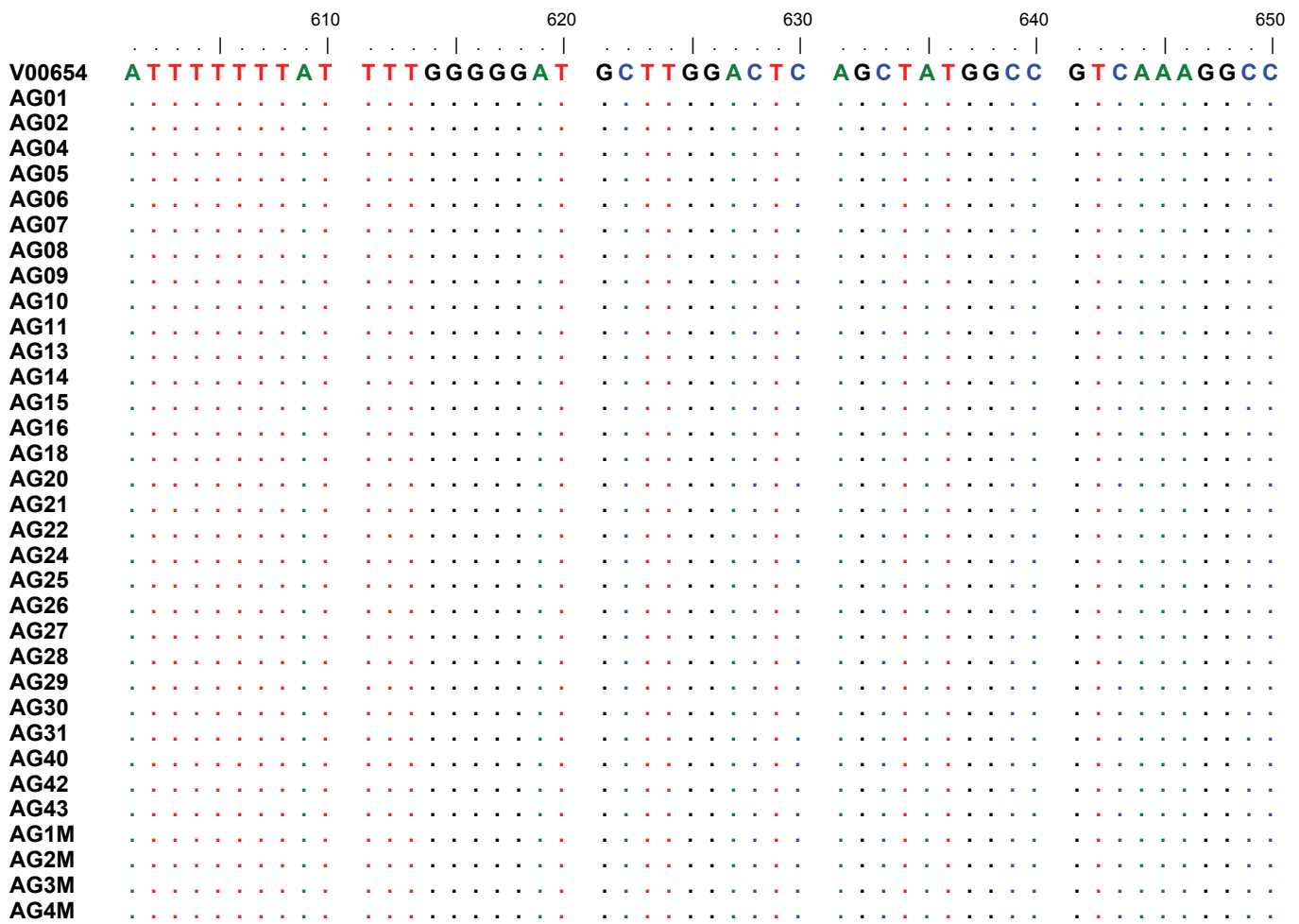
	210	220	230	240	250
V00654	T A A T A T G T A T	A T A G T A C A T T	A A A T T A T A T G	C C C C A T G C A T	A T A A G C A A G T
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	260	270	280	290	300
V00654	A C A T G A C C T C	T A T A G C A G T A	C A T A A T A C A T	A T A A T T A T T G	A C T G T A C A T A
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	710	720	730	740	750
V00654	GCATAATGAT	AAGCATGGAC	ATTACAGTCA	ATGGTCACAG	GACATAAATT
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AG06	.	G	.	.	.
AG07	.	G	.	.	.
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AG10	.	G	.	.	.
AG11	.	G	.	.	.
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AG16	.	G	.	.	.
AG18	.	G	G	.	.
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AG21	.	G	.	.	.
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AG27	G
AG28	G
AG29	.	G	G	.	G
AG30	.	G	.	.	.
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AG40	.	G	.	.	.
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AG43	.	G	.	.	.
AG1M	.	G	.	.	.
AG2M	.	G	.	.	.
AG3M
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	760	770	780	790	800
V00654	ATATTATATA	TCCCCCCTT	CATAAAAATT	TCCCCCTTAA	ATATCTACCA
AG01	.	C	.	.	.
AG02	.	C	.	.	.
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AG10	.	C	.	.	.
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AG13	.	C	.	.	.
AG14	.	C	.	.	.
AG15	.	C	.	.	.
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AG18	.	C	.	.	.
AG20	.	C	.	.	.
AG21	.	C	.	.	.
AG22	.	C	.	.	.
AG24	.	C	.	.	.
AG25	.	C	.	.	.
AG26	.	C	.	.	.
AG27	.	C	.	.	.
AG28	.	C	.	.	.
AG29	.	C	.	.	.
AG30	.	C	.	.	.
AG31	.	C	.	.	.
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AG42	.	C	.	.	.
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AG1M	.	C	.	.	.
AG2M	.	C	.	.	.
AG3M	.	C	.	.	.
AG4M	.	C	.	.	.

	810	820	830	840	850
V00654	CCACTTTTAA	CAGACTTTTC	CCTAGATACT	TATTTAAATT	TTTCACGCTT
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	860	870	880	890	900
V00654	TCAATACTCA	ATTTAGCACT	CCAAACAAAG	TCAATATATA	AACGCAGGCC
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