homomine report

July 01, 2024

Homomine report of Zm00001eb000510

o Basic information of Zm00001eb000510 from B73

chr	start	end	strand	gene
chr1	2144315	2148163	-	Zm00001eb000510

o Target hit in A188

Note: Below chromosomal interval might not cover the whole gene.

chr	start	end	strand	gene	transcript
chr1	2366471	2370330	-	Zm00056a000060	Zm00056a000060_T001

o Visualization of Nucmer alignments

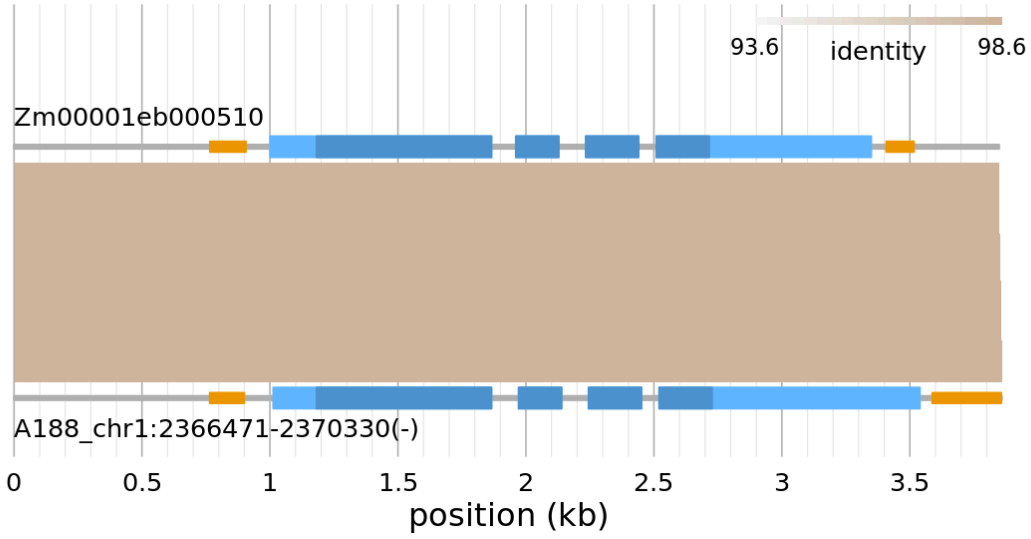

Fig 1. Nucmer alignment.

Nucmer was used to align sequences of the two sequences. Only uniquely aigned regions are displayed. Orange: repetitive sequences; light blue: untranslated regions; blue: coding regions.

qstart	qend	sstart	send	qmatch	smatch	identity	qlen	slen	qry	subj
1	3849	1	3860	3849	3860	98.58	3849	3860	Zm00001eb000510	A188_chr1:2366471-2370330(-)

o Genomic variants with high or moderate impacts

gene	pos	B73	A188	transcript	effect	impact	protVar
Zm00001eb000510	1744	TT	CC	Zm00001eb000510_T001	missense_variant	MODERATE	Phe188Ser
Zm00001eb000510	2435	T	C	Zm00001eb000510_T001	stop_lost	HIGH	Ter352Argext*?

gene	pos	B73	A188	transcript	effect	impact	protVar
Zm00001eb000510	1744	TT	CC	Zm00001eb000510_T002	missense_variant	MODERATE	Phe188Ser

o Structural variation used B73 as the reference

SV was defined if either REF or ALT allele has at least 50 bp and the length difference of two alleles are at least 30 bp.
No SVs identified

o Structural variation used A188 as the reference

No SVs identified

o All polymorphisms identified

Variants on the sequence from A188

seqname	pos	REF	ALT
A188_chr1:2366471-2370330(-)	1744	CC	TT
A188_chr1:2366471-2370330(-)	1908	ACTGTACTCTGT	A
A188_chr1:2366471-2370330(-)	2193	T	C
A188_chr1:2366471-2370330(-)	2446	C	T
A188_chr1:2366471-2370330(-)	3016	TA	T
A188_chr1:2366471-2370330(-)	3112	T	G
A188_chr1:2366471-2370330(-)	3126	T	C
A188_chr1:2366471-2370330(-)	3143	C	G
A188_chr1:2366471-2370330(-)	3245	CATGCAATGCA	C
A188_chr1:2366471-2370330(-)	3275	A	G
A188_chr1:2366471-2370330(-)	3378	A	T
A188_chr1:2366471-2370330(-)	3381	T	C
A188_chr1:2366471-2370330(-)	3439	T	TGACCGCTCCAATCCG
A188_chr1:2366471-2370330(-)	3564	T	C

seqname	pos	REF	ALT
A188_chr1:2366471-2370330(-)	3576	TTACTC	T
A188_chr1:2366471-2370330(-)	3583	AG	TA
A188_chr1:2366471-2370330(-)	3665	A	AC
A188_chr1:2366471-2370330(-)	3769	G	T
A188_chr1:2366471-2370330(-)	3776	G	A

Variants on the sequence from B73

seqname	pos	REF	ALT
Zm00001eb000510	1744	TT	CC
Zm00001eb000510	1908	A	ACTGTACTCTGT
Zm00001eb000510	2182	C	T
Zm00001eb000510	2435	T	C
Zm00001eb000510	3005	T	TA
Zm00001eb000510	3100	G	T
Zm00001eb000510	3114	C	T
Zm00001eb000510	3131	G	C
Zm00001eb000510	3233	C	CATGCAATGCA
Zm00001eb000510	3253	G	A
Zm00001eb000510	3356	T	A
Zm00001eb000510	3359	C	T
Zm00001eb000510	3417	TGACCGCTCCAATCCG	T
Zm00001eb000510	3557	C	T
Zm00001eb000510	3569	T	TTACTC
Zm00001eb000510	3571	TA	AG
Zm00001eb000510	3653	AC	A
Zm00001eb000510	3758	T	G
Zm00001eb000510	3765	A	G

o Query sequence from B73

>Zm00001eb000510
GAGAATCAGGCAGGAAGCCATGTAGTAGATTTCTAGCCAAGAGCCCTGTACTTGTTTTTTTTTTGGGTCTGAGATGTAATTGTCATGT
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o Target sequence from A188

>A188_chr1:2366471-2370330(-)
GAGAATCAGGCAGGAAGCCATGTAGTAGATTTCTAGCCAAGAGCCCTGTACTTGTTTTTTTTTTGGGTCTGAGATGTAATTGTCATGT
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