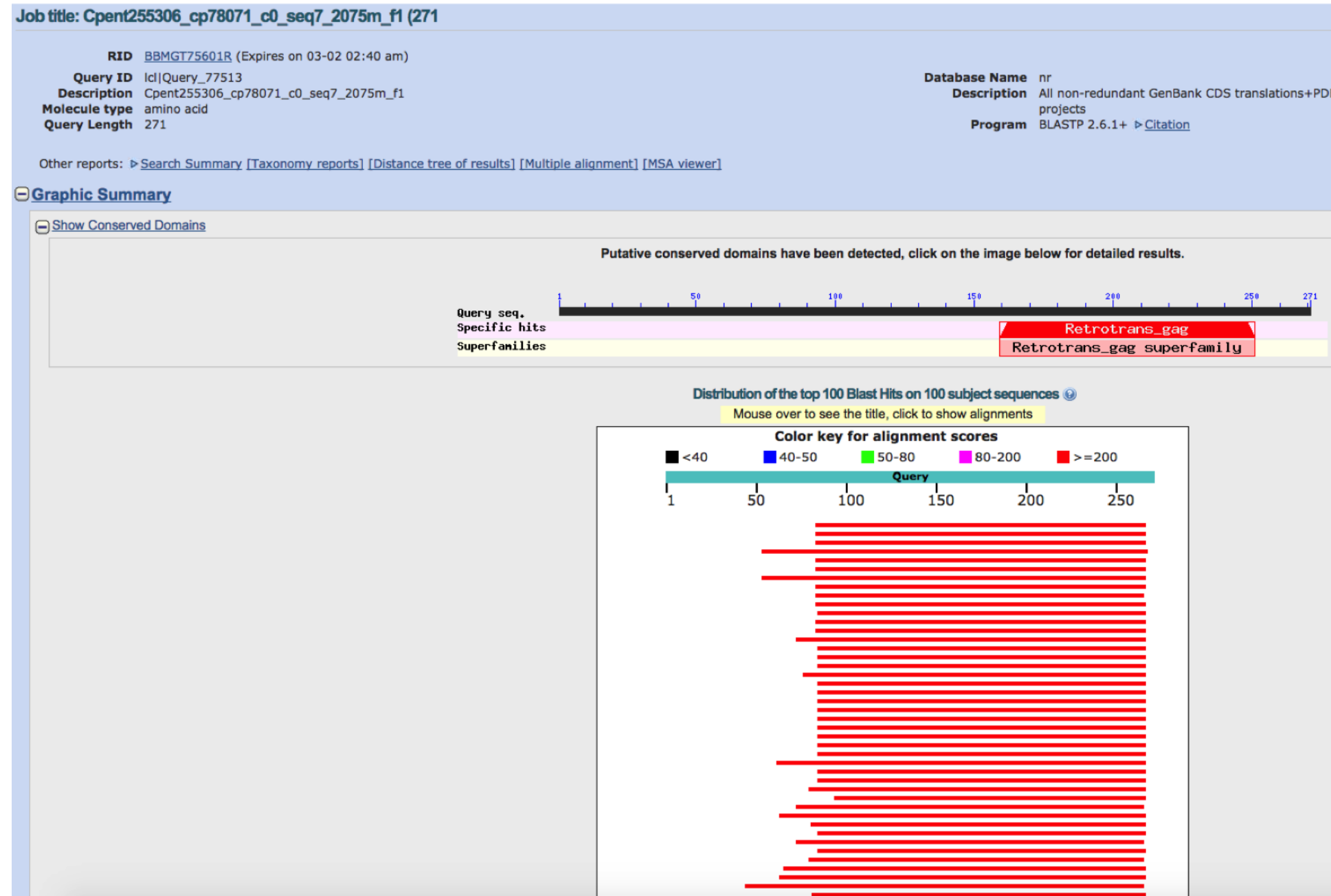


**HGT of both functional and nonfunctional copies in retrotransposon - orthofinder group 54**



Orthogroup 54 gene tree supports HGT in *Cuscuta* from *Gossypium*

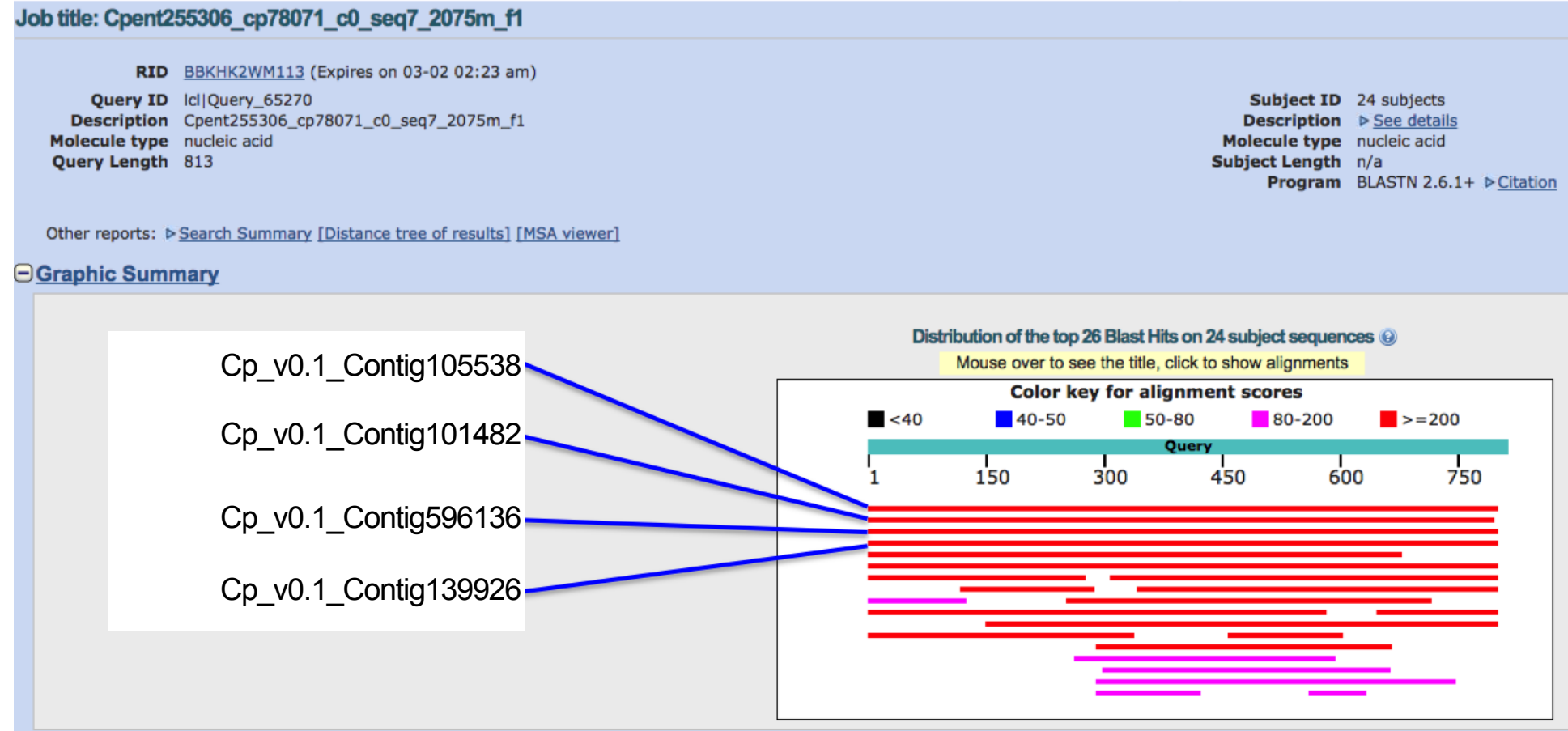
**NR blastp shows that it's a retrotransposon**



**NR blastp shows top hits from Gossypium**

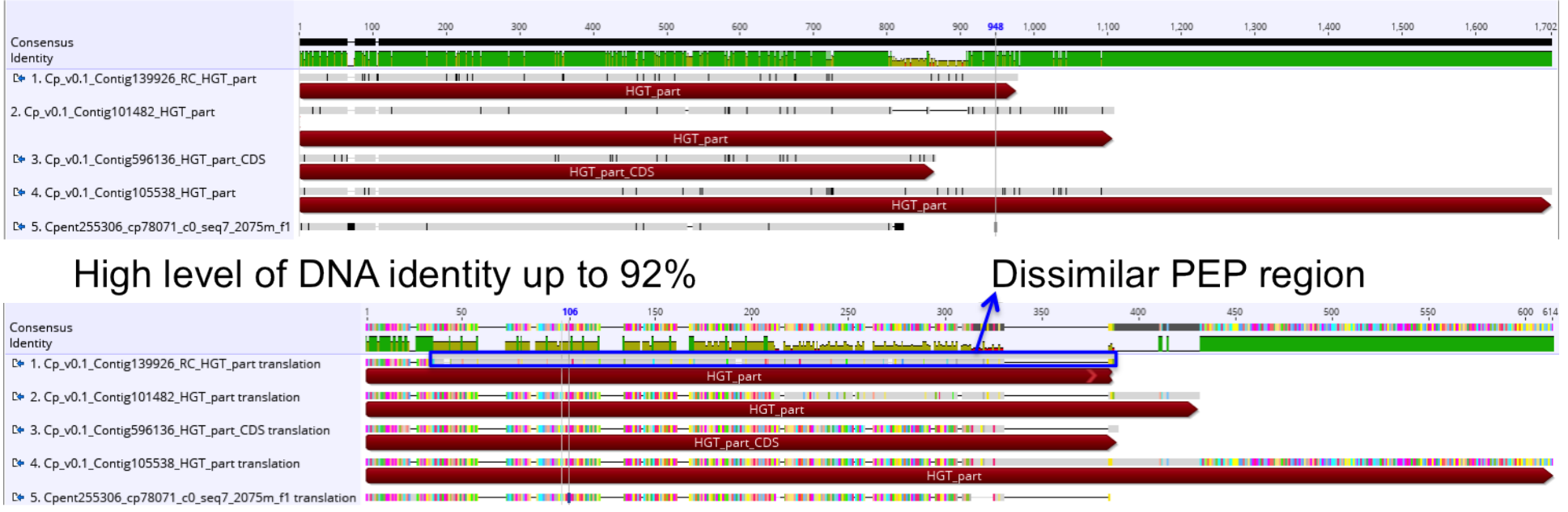
	Max score	Total score	Query cover	E value	Ident	Accession
<input type="checkbox"/> <a href="#">PREDICTED: uncharacterized protein LOC105788207 [Gossypium raimondii]</a>	293	293	67%	6e-96	72%	<a href="#">XP_012470434.1</a>
<input type="checkbox"/> <a href="#">PREDICTED: uncharacterized protein LOC107889793 [Gossypium hirsutum]</a>	294	294	67%	8e-96	71%	<a href="#">XP_016669844.1</a>
<input type="checkbox"/> <a href="#">PREDICTED: uncharacterized protein LOC105786894 [Gossypium raimondii]</a>	298	298	67%	5e-95	71%	<a href="#">XP_012468822.1</a>
<input type="checkbox"/> <a href="#">PREDICTED: uncharacterized protein LOC107900138 [Gossypium hirsutum]</a>	291	291	78%	1e-94	64%	<a href="#">XP_016681329.1</a>
<input type="checkbox"/> <a href="#">PREDICTED: uncharacterized protein LOC105771574 isoform X1 [Gossypium raimondii]</a>	290	290	67%	3e-94	72%	<a href="#">XP_012448460.1</a>
<input type="checkbox"/> <a href="#">PREDICTED: uncharacterized protein LOC107921572 [Gossypium hirsutum]</a>	295	295	67%	2e-92	71%	<a href="#">XP_016706896.1</a>
<input type="checkbox"/> <a href="#">PREDICTED: LOW QUALITY PROTEIN: uncharacterized protein LOC107943328 [Gossypium hirsutum]</a>	298	298	78%	4e-92	65%	<a href="#">XP_016732564.1</a>
<input type="checkbox"/> <a href="#">PREDICTED: uncharacterized protein LOC105775226 [Gossypium raimondii]</a>	298	298	67%	4e-91	72%	<a href="#">XP_012453209.1</a>
<input type="checkbox"/> <a href="#">PREDICTED: uncharacterized protein LOC105795765 [Gossypium raimondii]</a>	282	282	67%	4e-91	70%	<a href="#">XP_012480878.1</a>
<input type="checkbox"/> <a href="#">PREDICTED: uncharacterized protein LOC105772005 [Gossypium raimondii]</a>	292	292	67%	8e-91	70%	<a href="#">XP_012448819.1</a>
<input type="checkbox"/> <a href="#">hypothetical protein BVRB_5g116180 [Beta vulgaris subsp. vulgaris]</a>	278	278	67%	9e-91	69%	<a href="#">KMT10494.1</a>
<input type="checkbox"/> <a href="#">PREDICTED: uncharacterized protein LOC107907935 [Gossypium hirsutum]</a>	282	282	67%	1e-90	69%	<a href="#">XP_016690722.1</a>
<input type="checkbox"/> <a href="#">PREDICTED: uncharacterized protein LOC107962773 [Gossypium hirsutum]</a>	278	278	67%	8e-90	69%	<a href="#">XP_016754806.1</a>
<input type="checkbox"/> <a href="#">PREDICTED: uncharacterized protein LOC105786732 [Gossypium raimondii]</a>	296	296	71%	1e-88	70%	<a href="#">XP_012468678.1</a>

**Alignment of genomic hits against CDS sequence of Cpent255306\_cp78071\_c0\_seq7\_2075m\_f1**

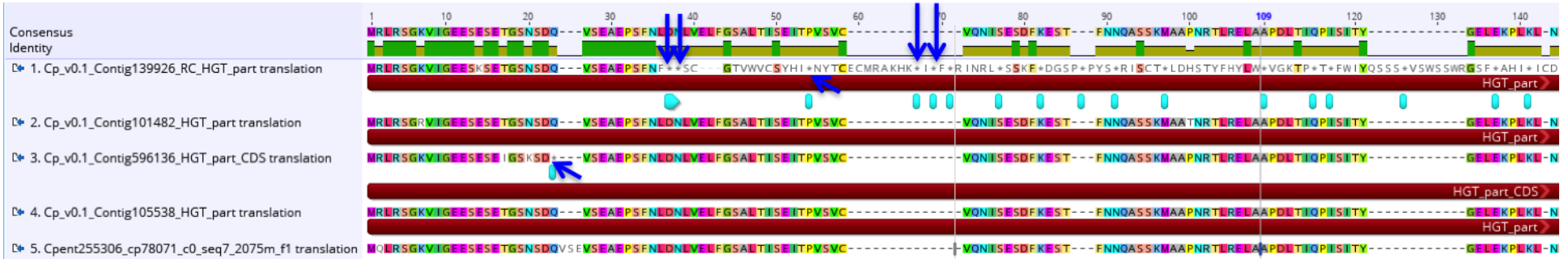


Contig596136 top BLASTN best hits against angiosperms in Phytozome are from *Gossypium* too

**HGT resulting in functional genes and nonfunctional pseudogene copies**



Internal stop codons in Cp\_v0.1\_Contig596136 and Cp\_v0.1\_Contig139926 suggesting pseudogenes



Still, no evidence of RT leading to pseudogene copies – gene without introns, cannot support RT

**Fig. S11. Analysis workflow illustrates HGT of a retrotransposon gene family containing functional and nonfunctional HGT genes in *Cuscuta* from an *Gossypium* ancestor.** It is assumed that HGT via RT may lead to pseudogenes, however, in this example, functional HGTs and HGT pseudogenes coexist, and the absence of introns in the donor gene fails to support RT. Thus no evidence is found that RT leads to HGT pseudogenes in *Cuscuta*. a, Phylogenetic tree of OrthoFinder group 54 supports HGT in *Cuscuta* genus from a putative ancestor of *Gossypium*. A BLASTp search of the *Cuscuta* HGT sequence against the NR database (b) shows the top hits are from *Gossypium* (c) and that it is a retrotransposon. (d) shows alignment between the HGT gene CDS and the genomic hits indicating that this retrotransposon gene has no introns. It also shows that there are multiple copies in the genome with similarity to the HGT gene Cpent255306\_cp78071\_c0\_seq7\_2075m\_f1. (e) alignment of the HGT gene and its genomic hits shows high level of DNA identity, but when translated into peptide sequences, the Cp\_v0.1\_Contig139926 gene shows premature stop codon which disrupts the reading frame and causes dissimilarity in inferred peptide sequence alignment. This suggests that functional and nonfunctional copies of HGT gene coexist in the *Cuscuta campestris* genome.