

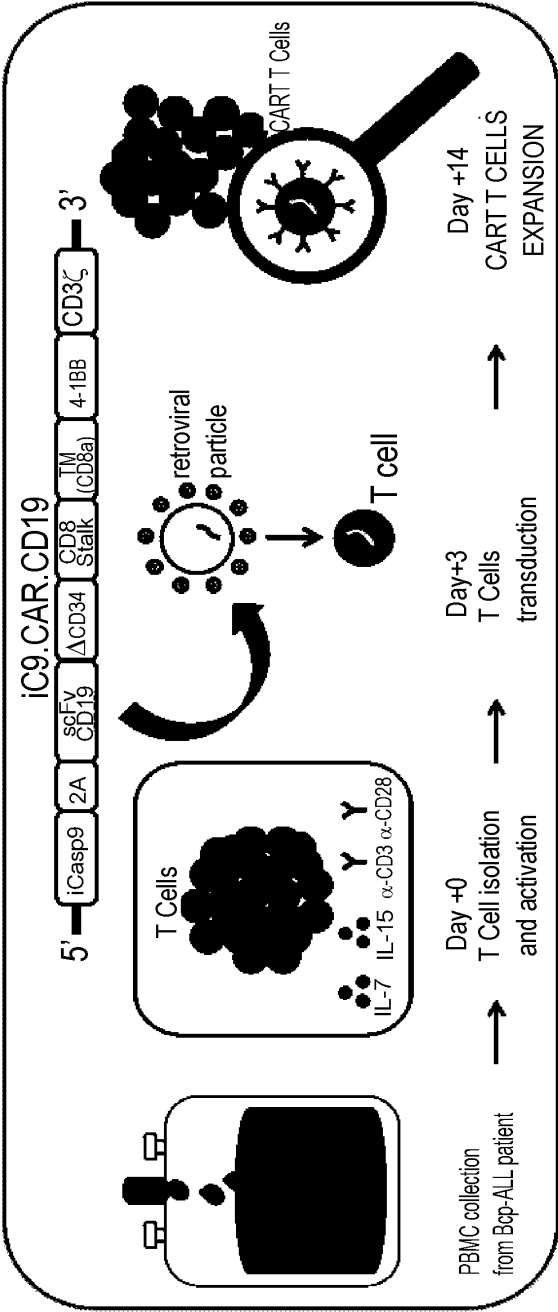


Fig. 1A

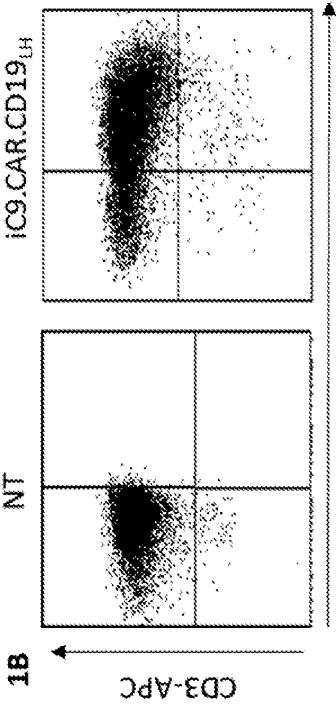


Fig. 1B CAR-CD34 PE (Qbend)

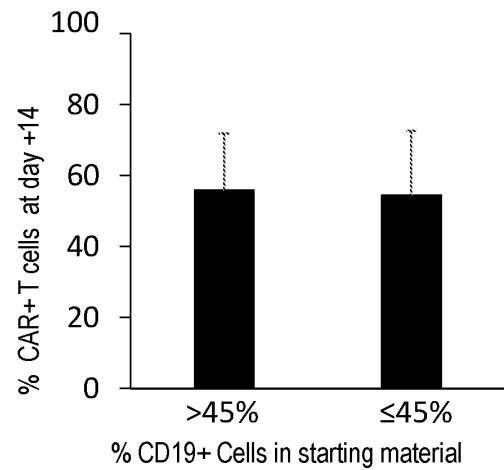


Fig. 1C

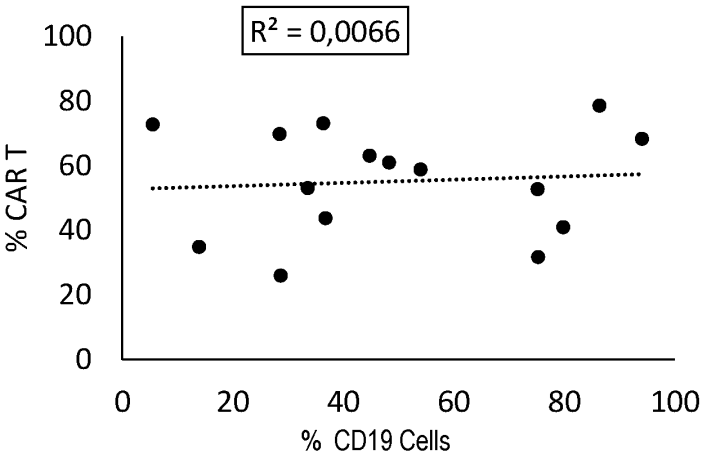


Fig. 1D

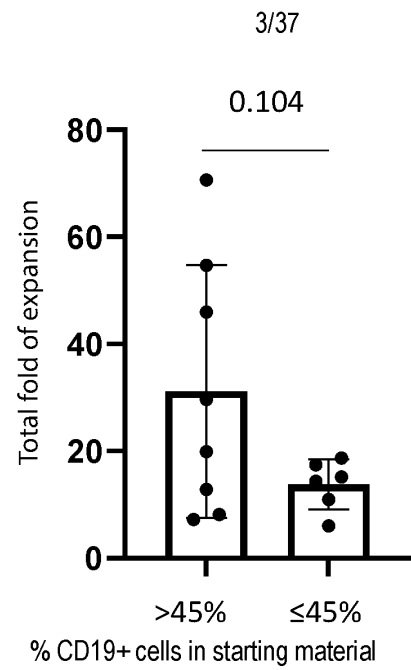
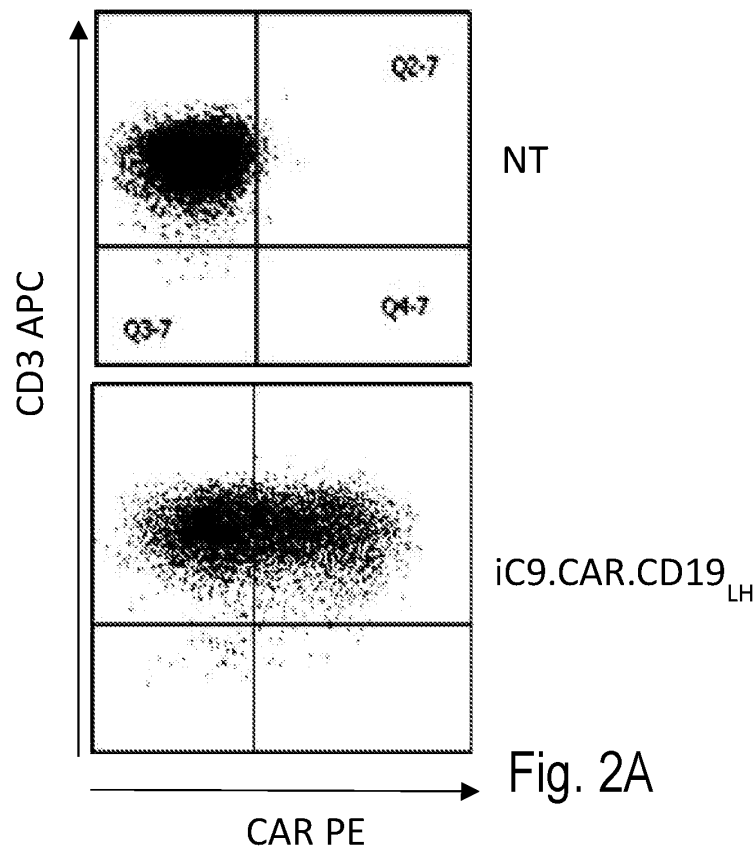


Fig. 1E



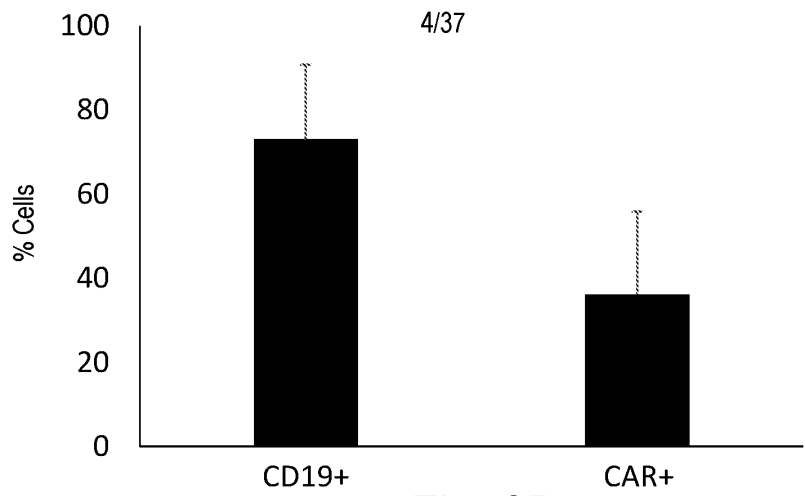


Fig. 2B

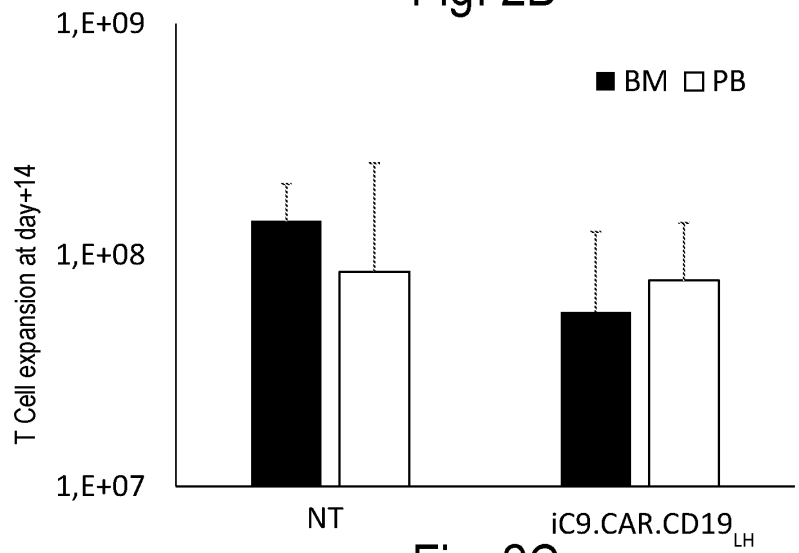


Fig. 2C

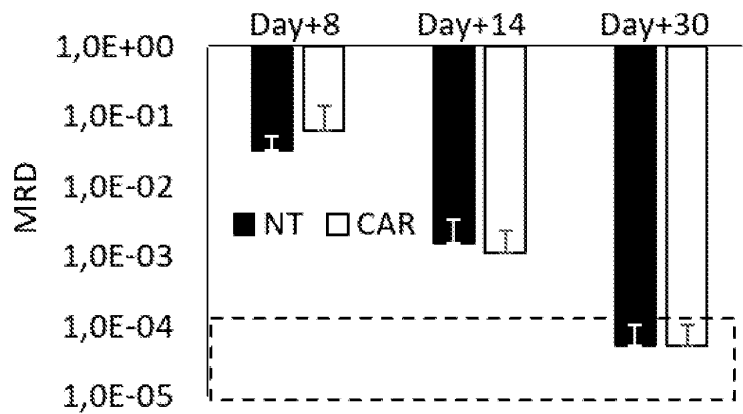


Fig. 3A

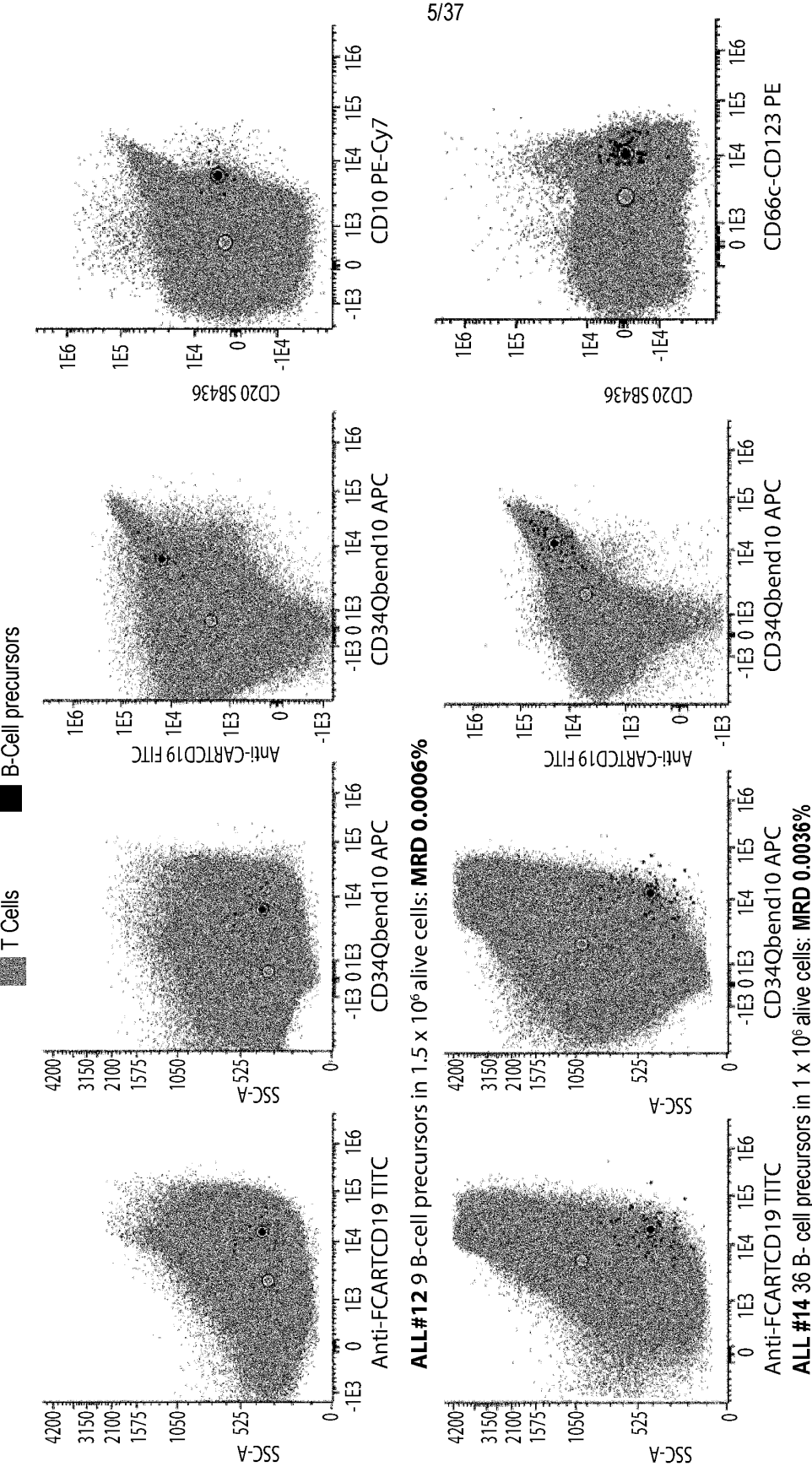
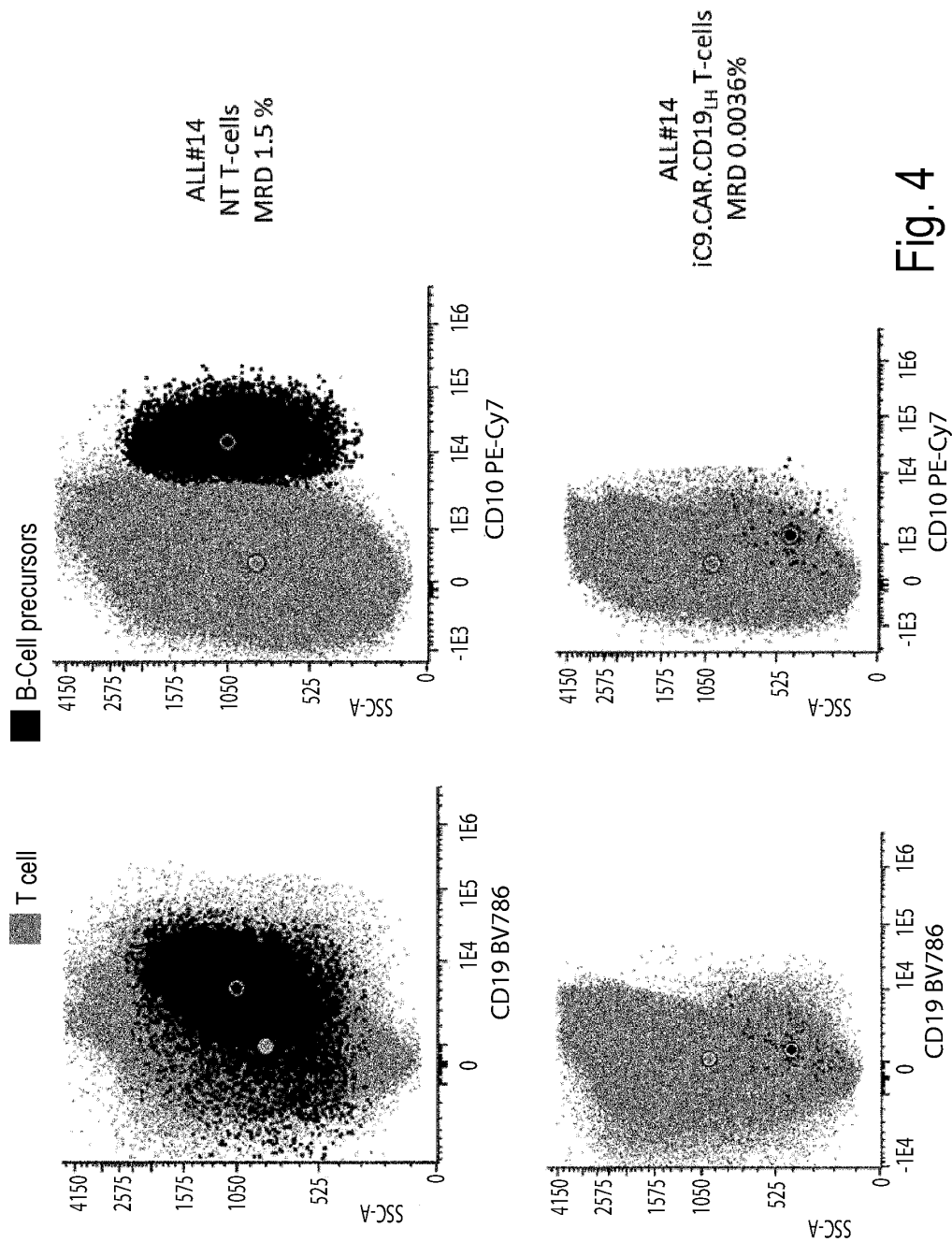


Fig. 3B



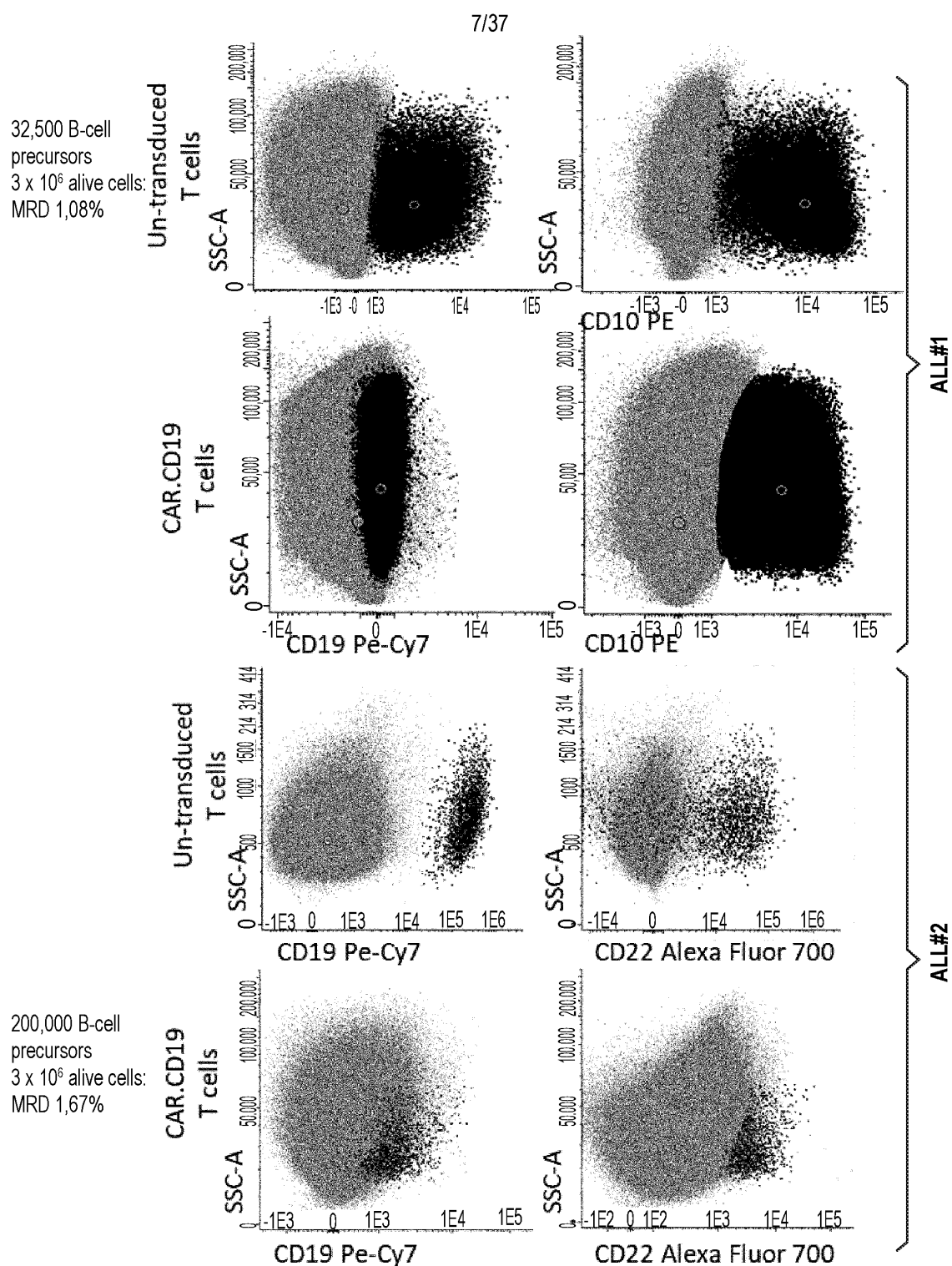


Fig. 5

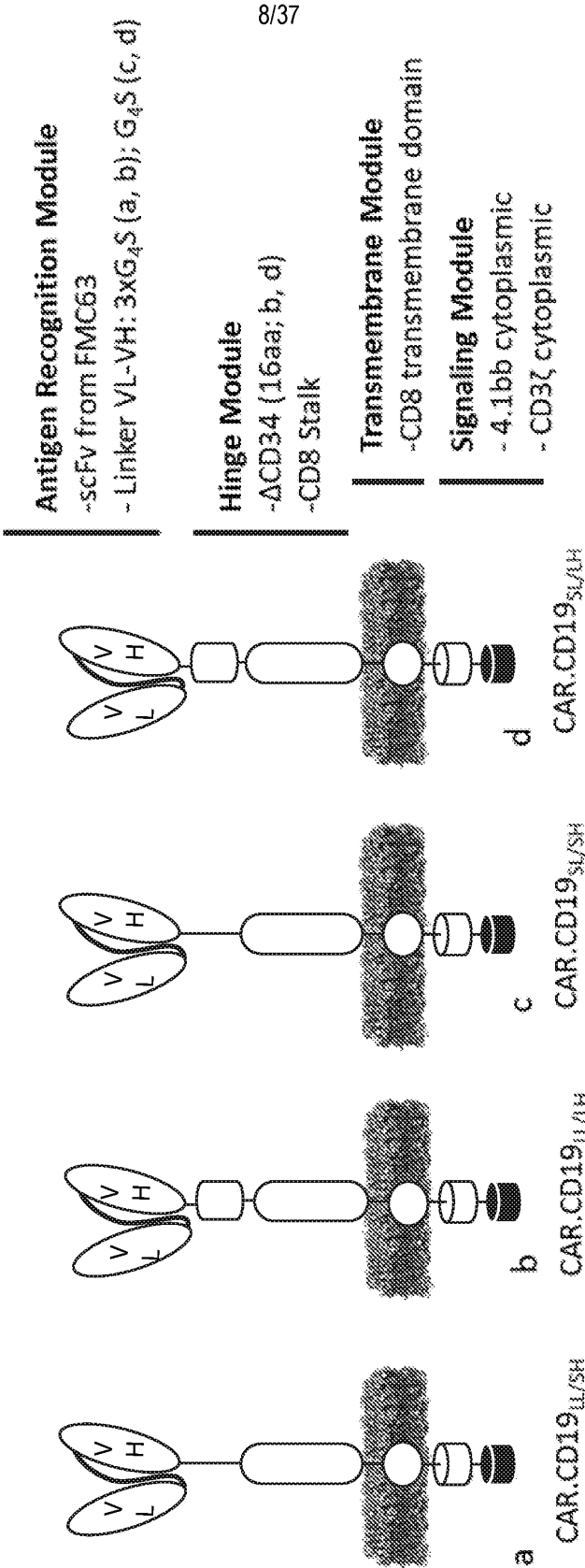


Fig. 6A

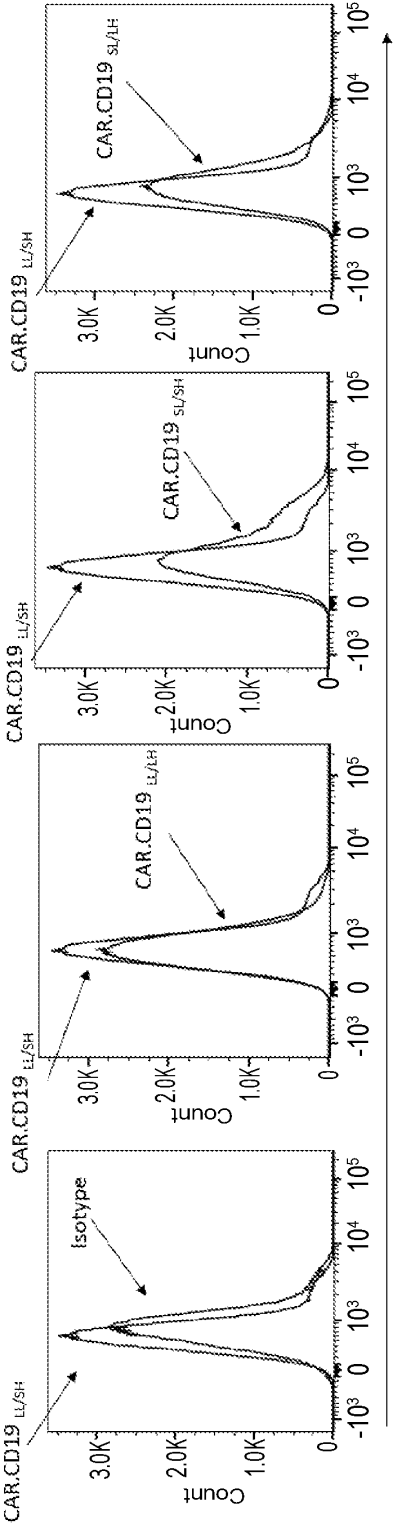


Fig. 6B

Fig. 6C

Fig. 6D

Fig. 6F

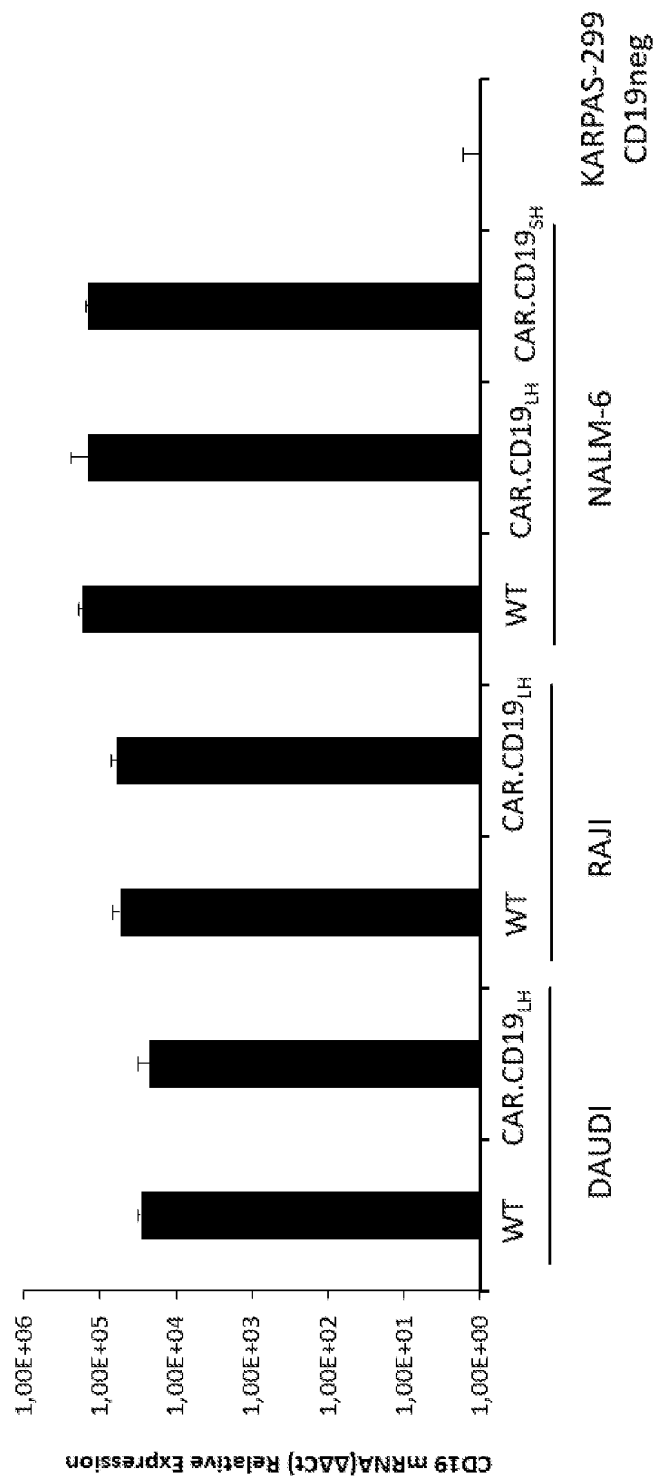


Fig. 7A

□ Isotype Control
■ CD19 Expressor

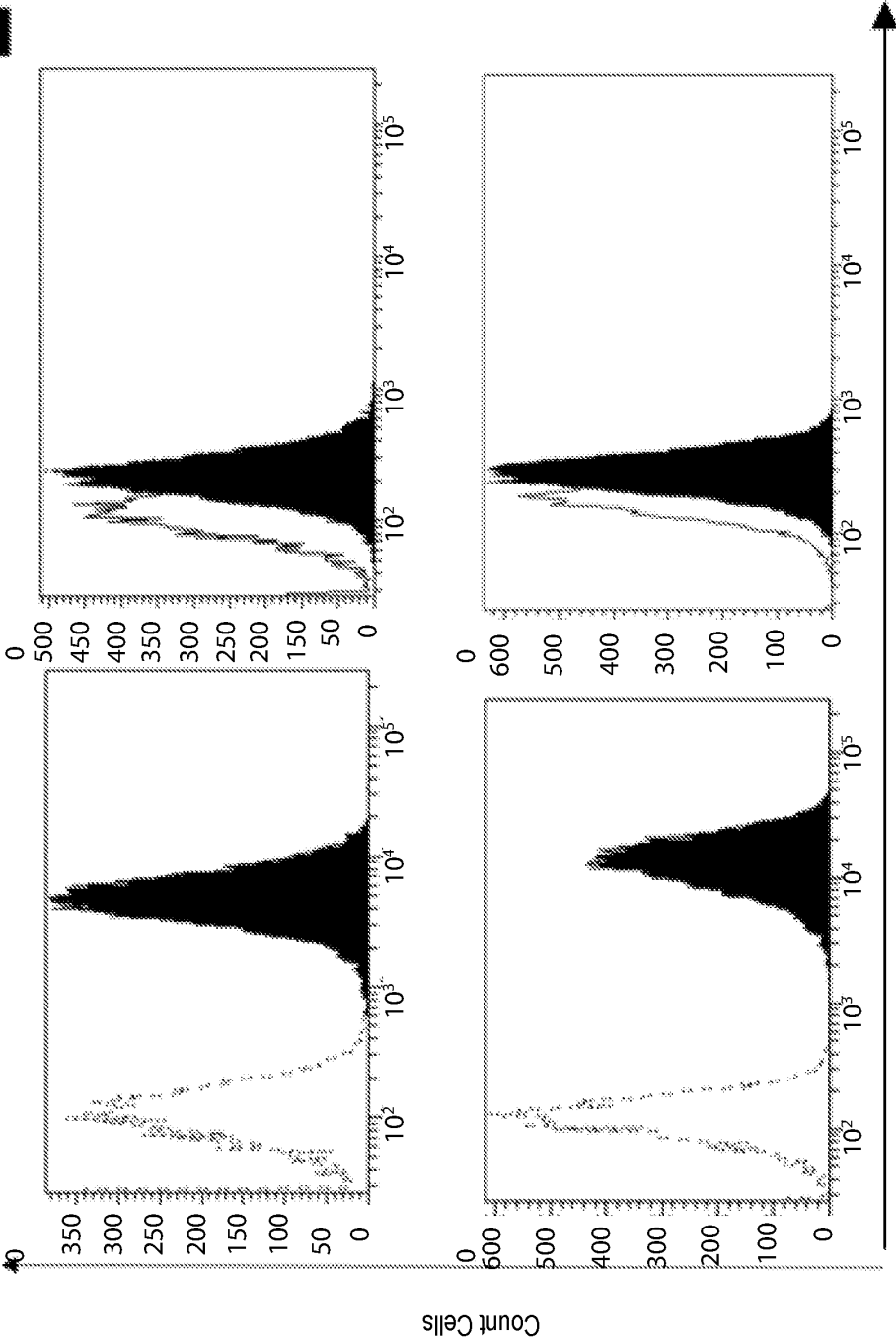


Fig. 7B

Anti-CD19 BV421 (clone HIB19)

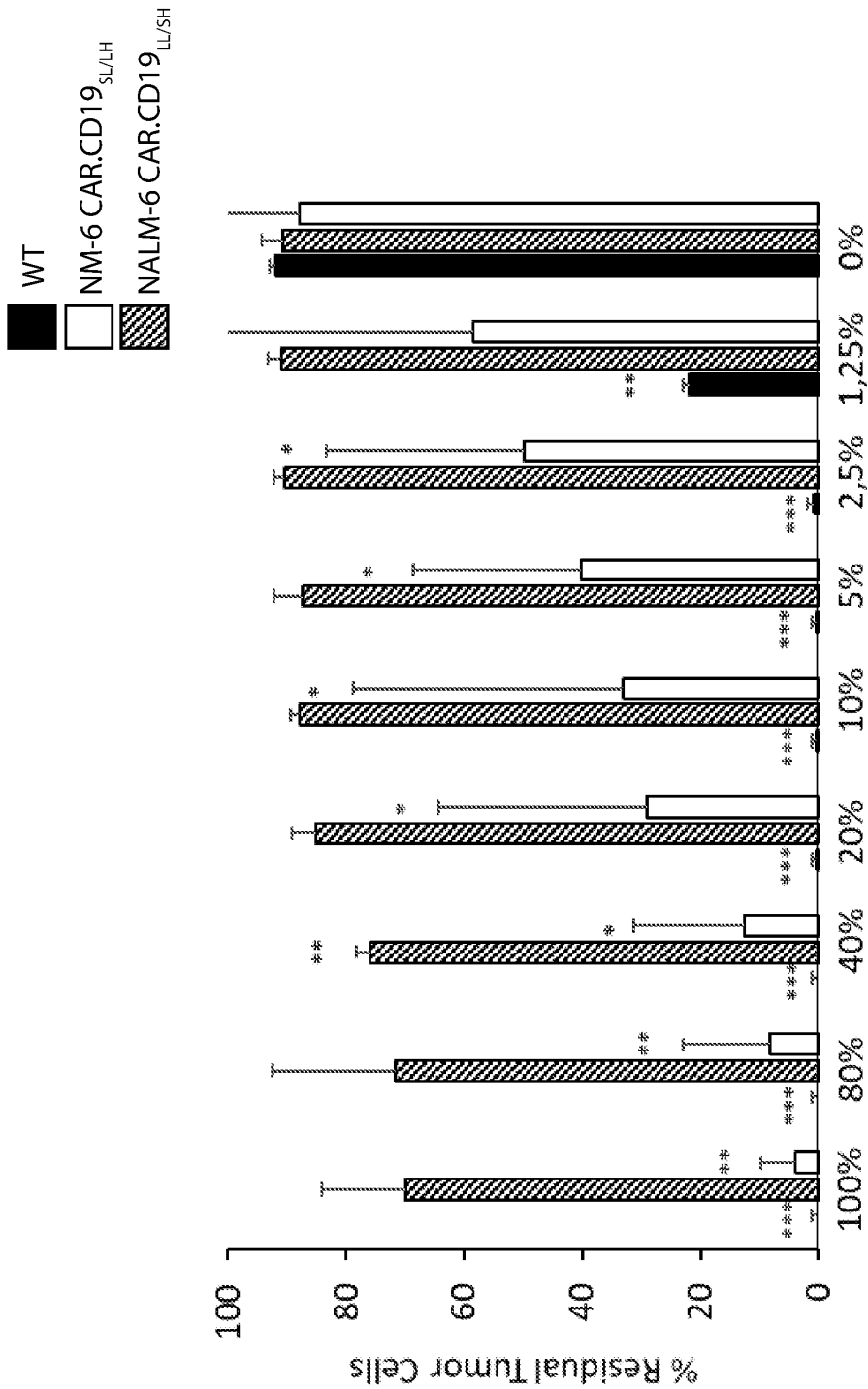


Fig. 7C

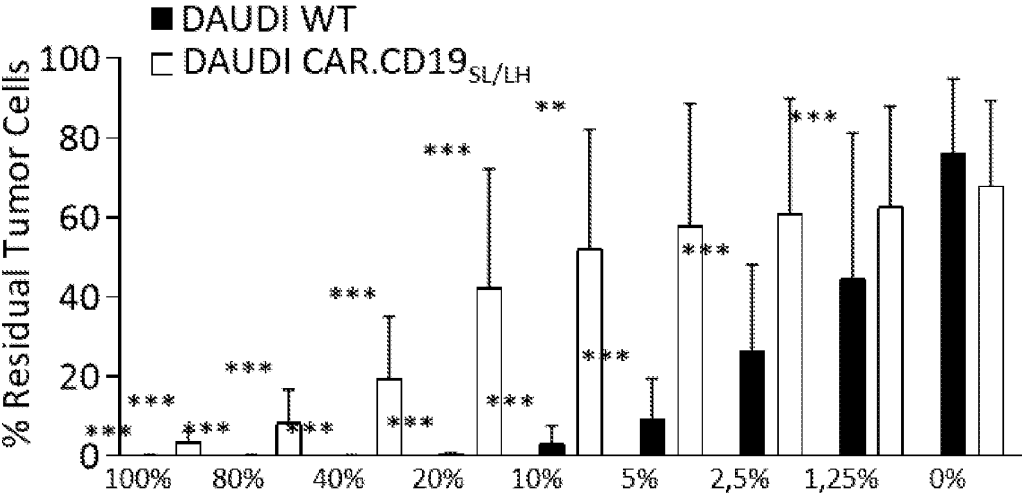


Fig. 8A

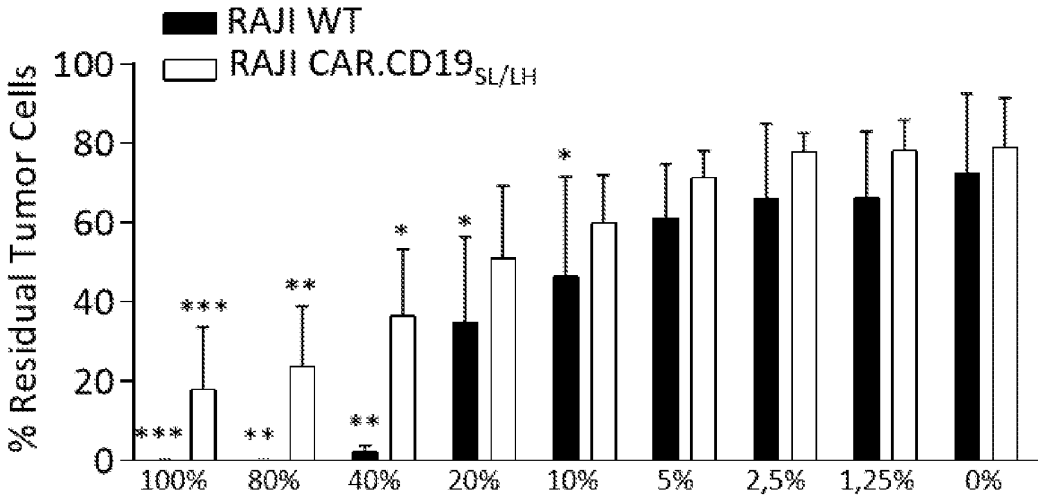


Fig. 8B

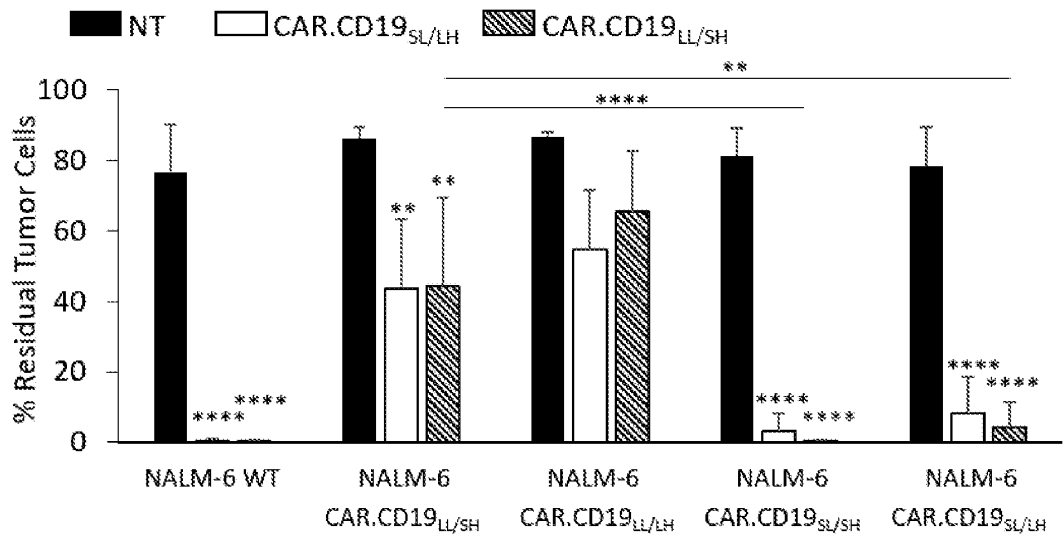


Fig. 8C

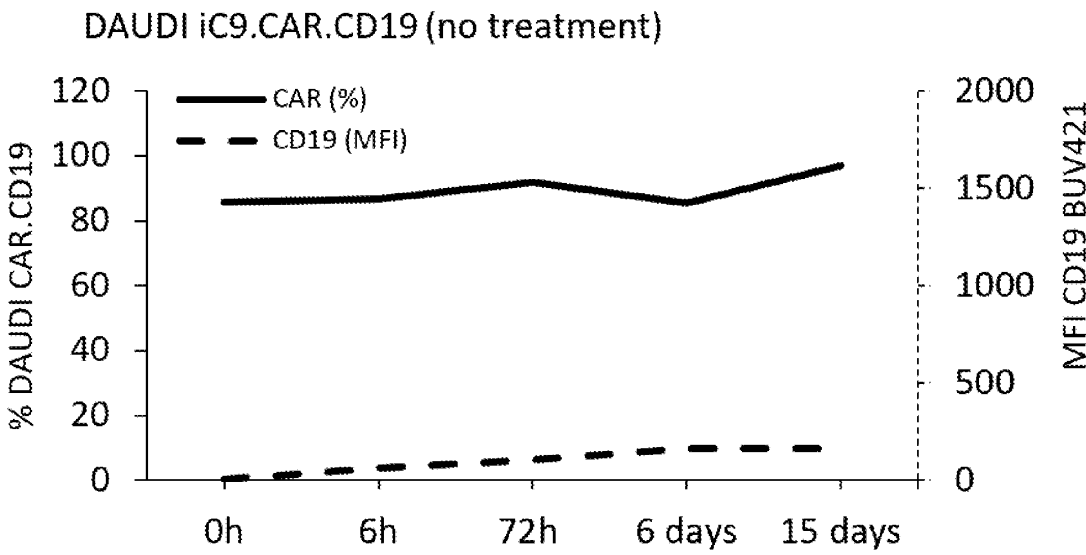


Fig. 8D

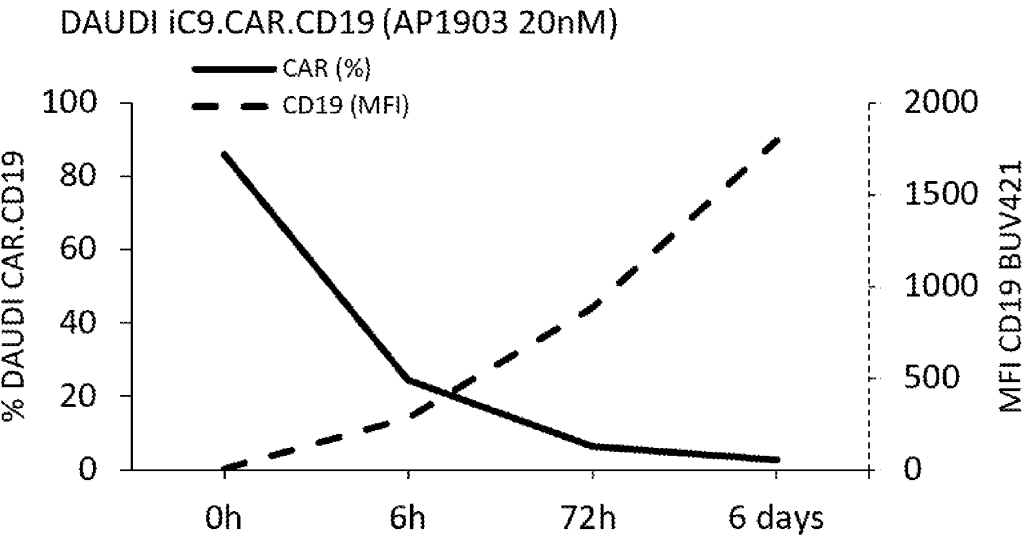


Fig. 8E

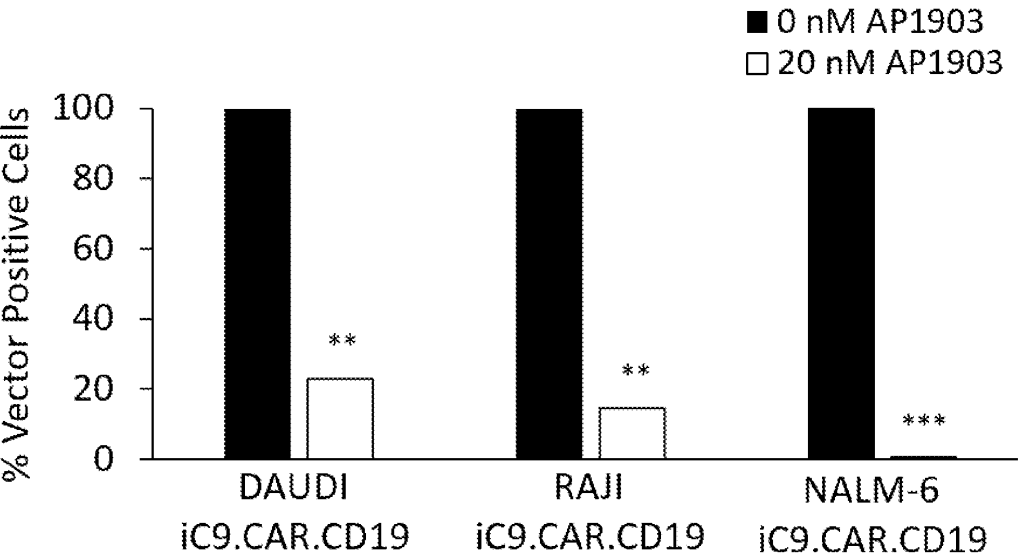


Fig. 8F

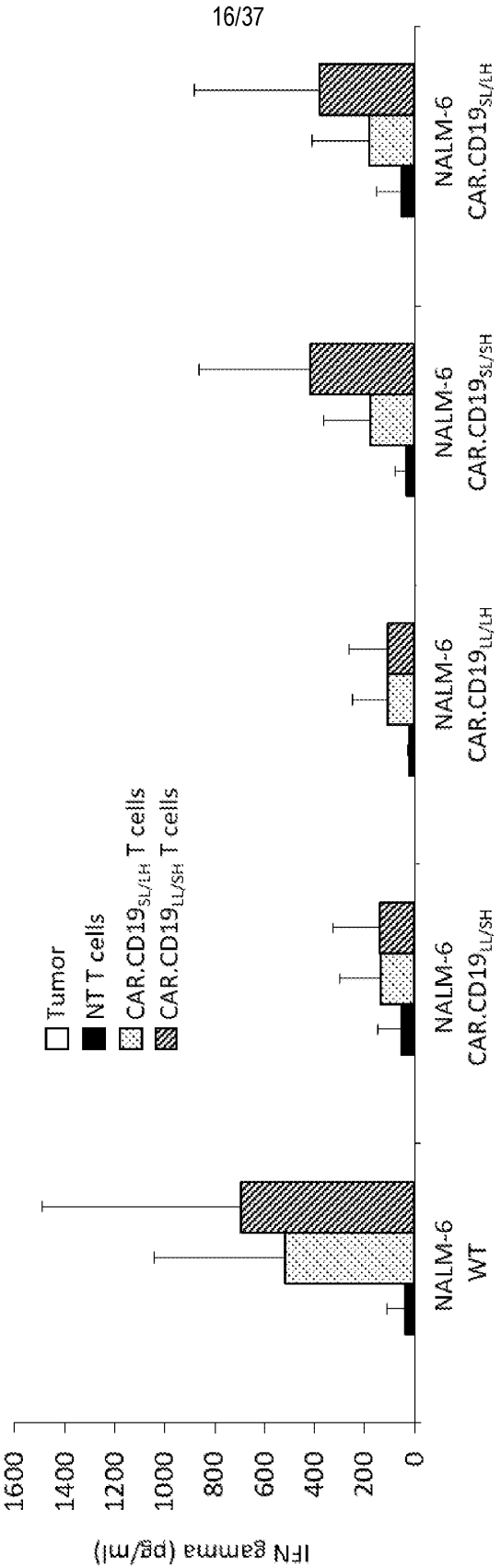


Fig. 9A

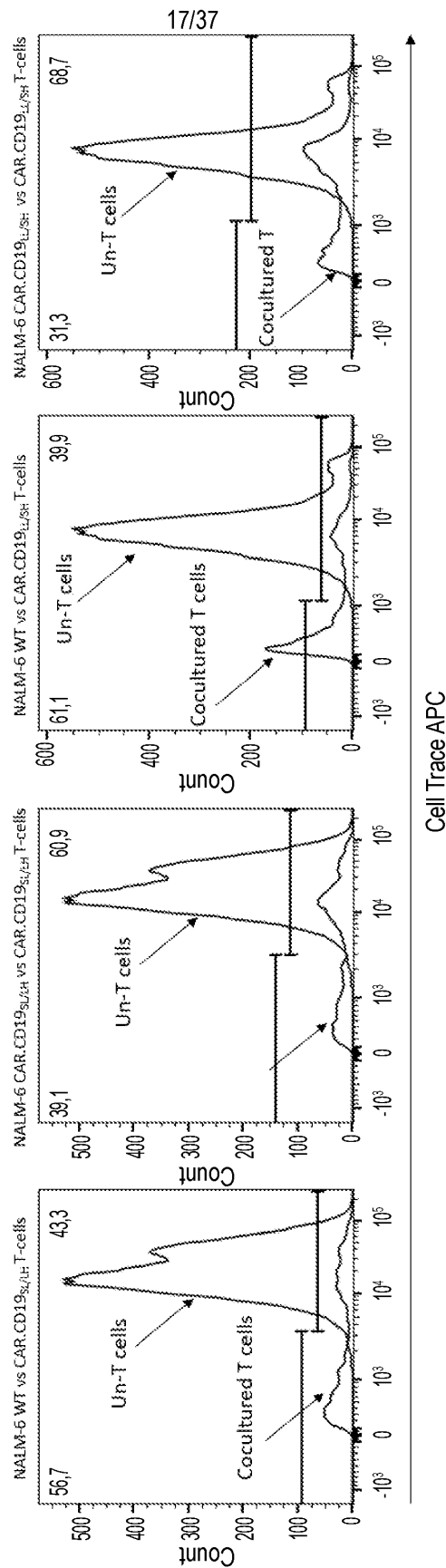


Fig. 9B

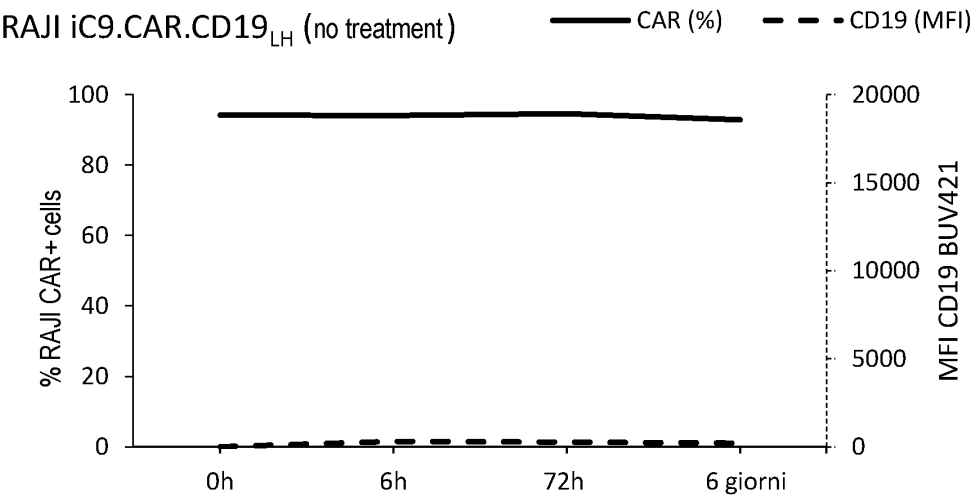


Fig. 10A

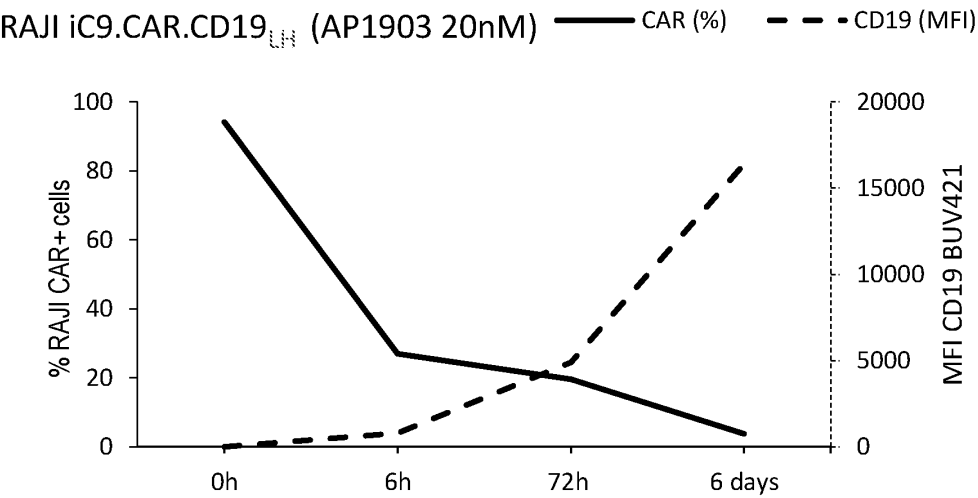


Fig. 10B

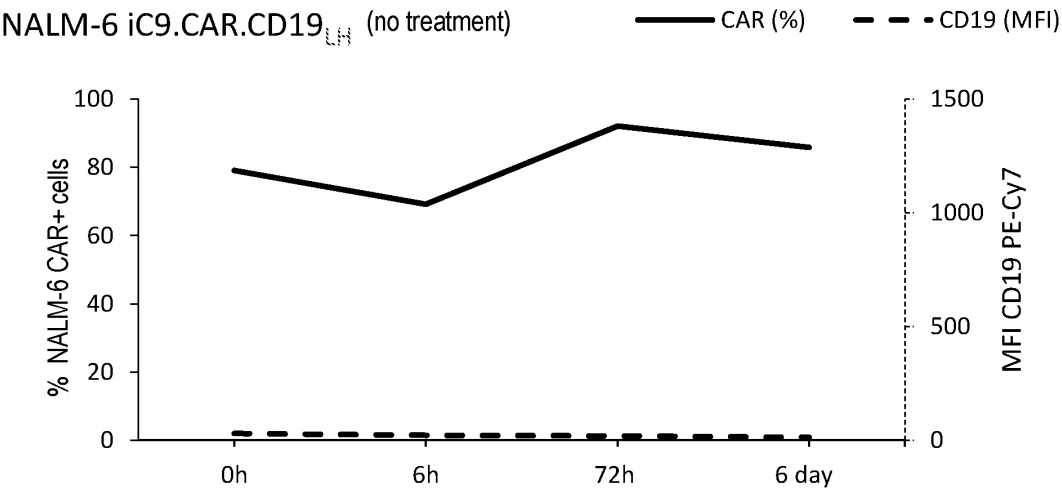


Fig. 10C

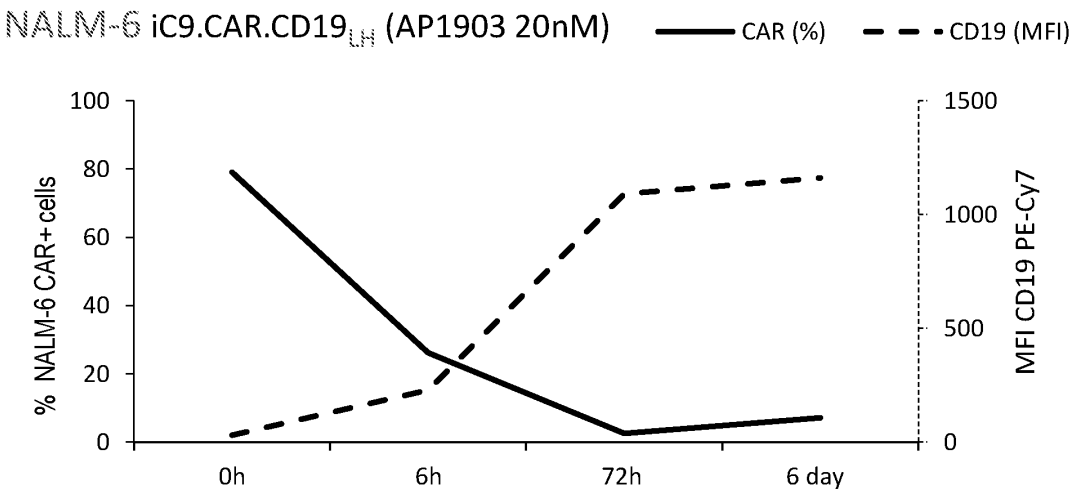


Fig. 10D

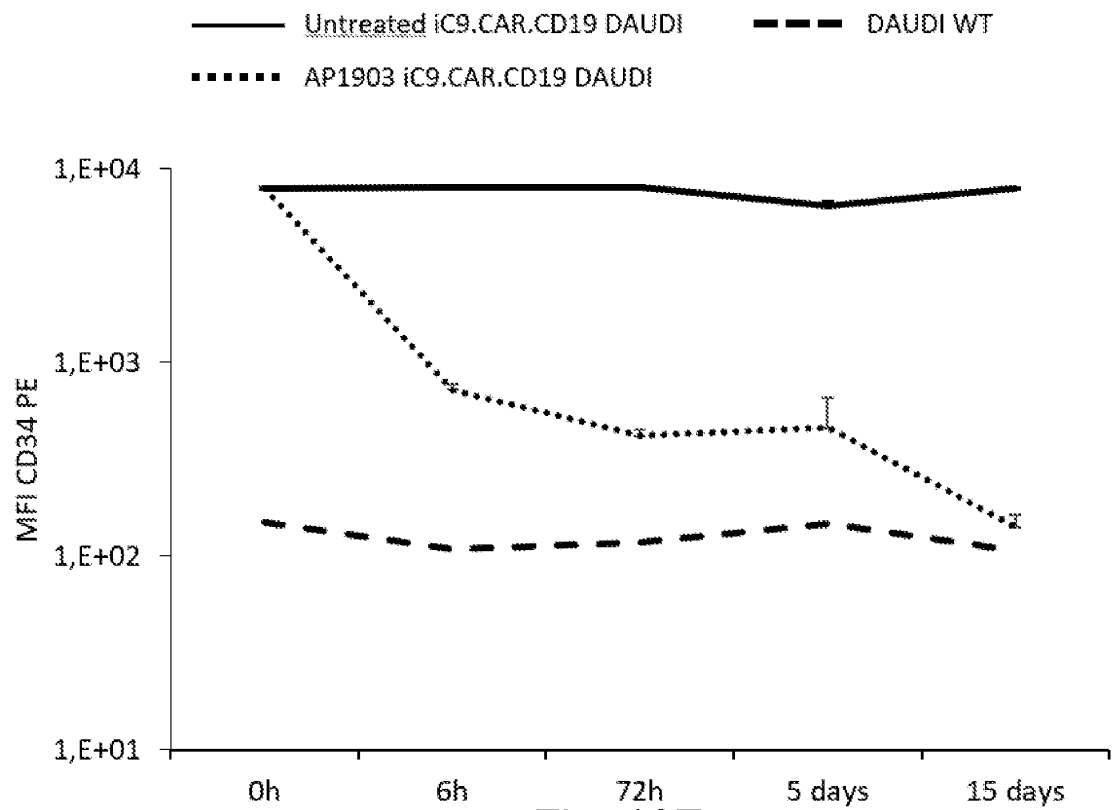


Fig. 10E

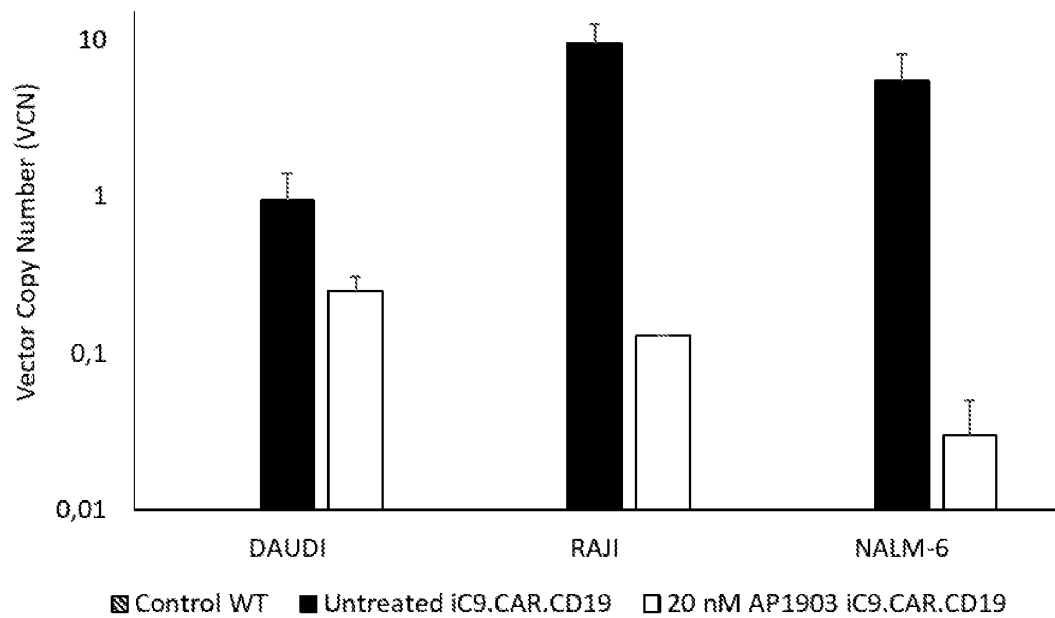


Fig. 10F

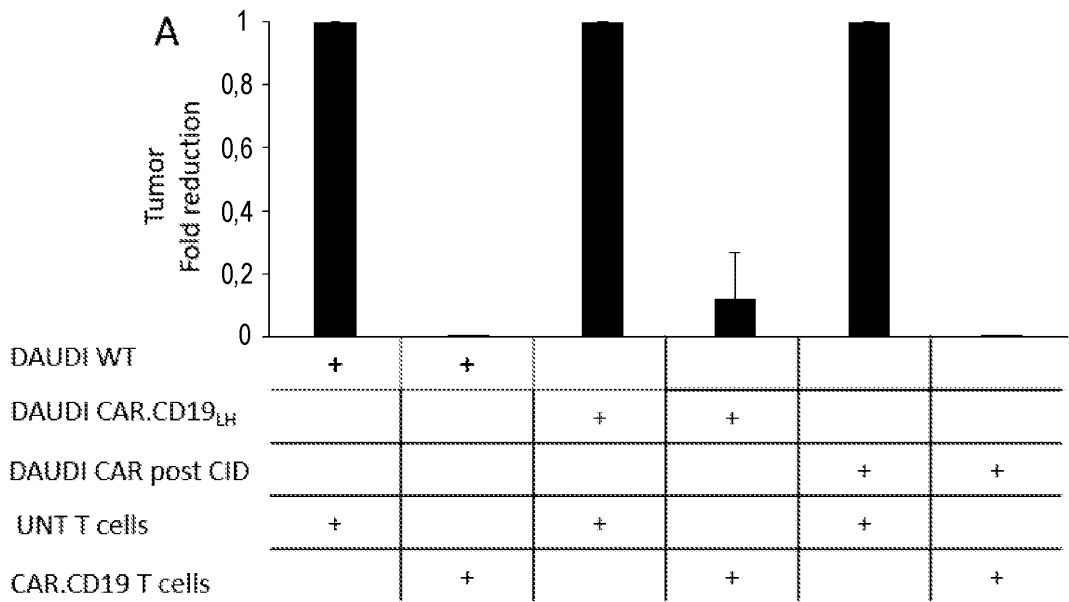


Fig. 11A

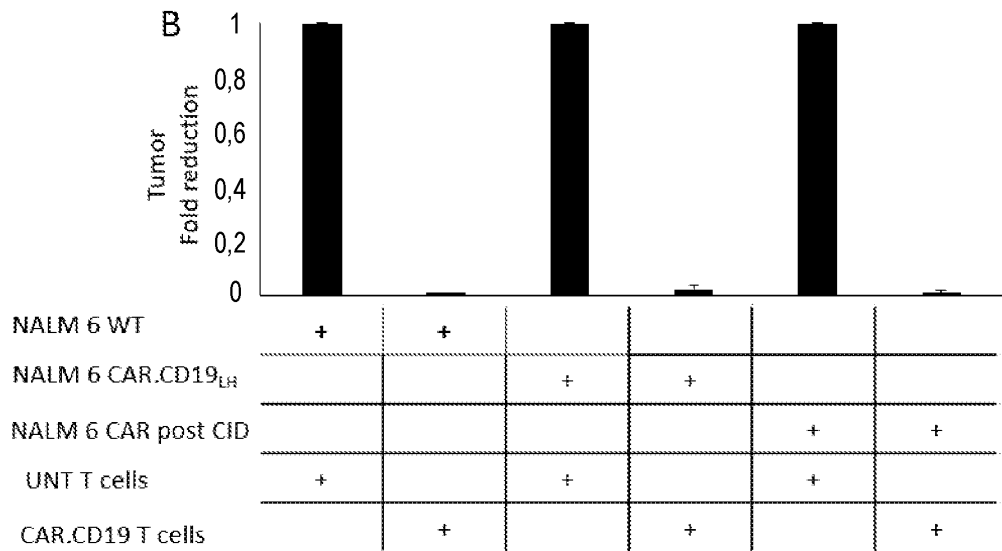


Fig. 11B

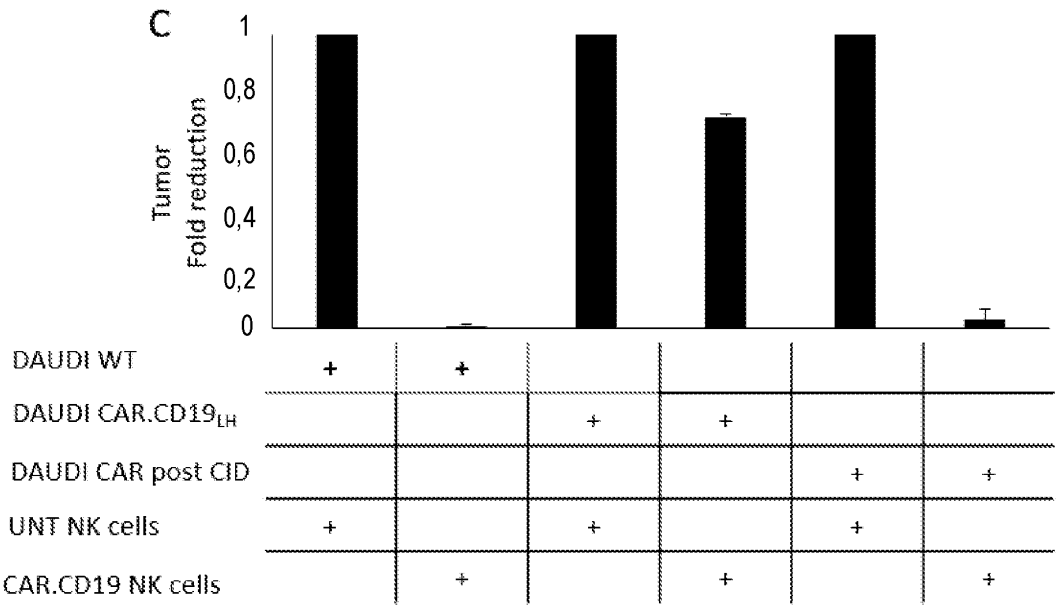


Fig. 11C

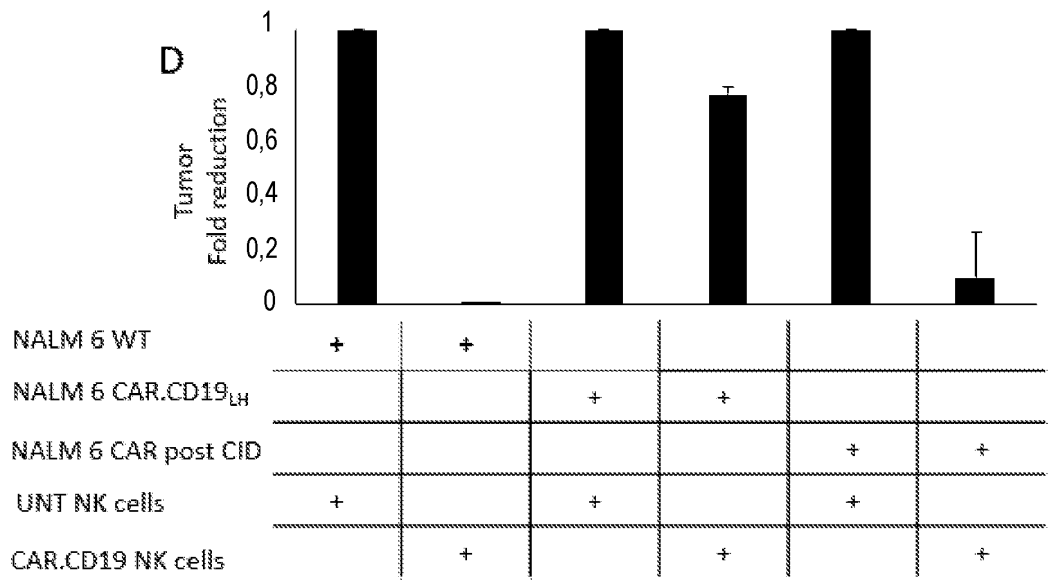


Fig. 11D

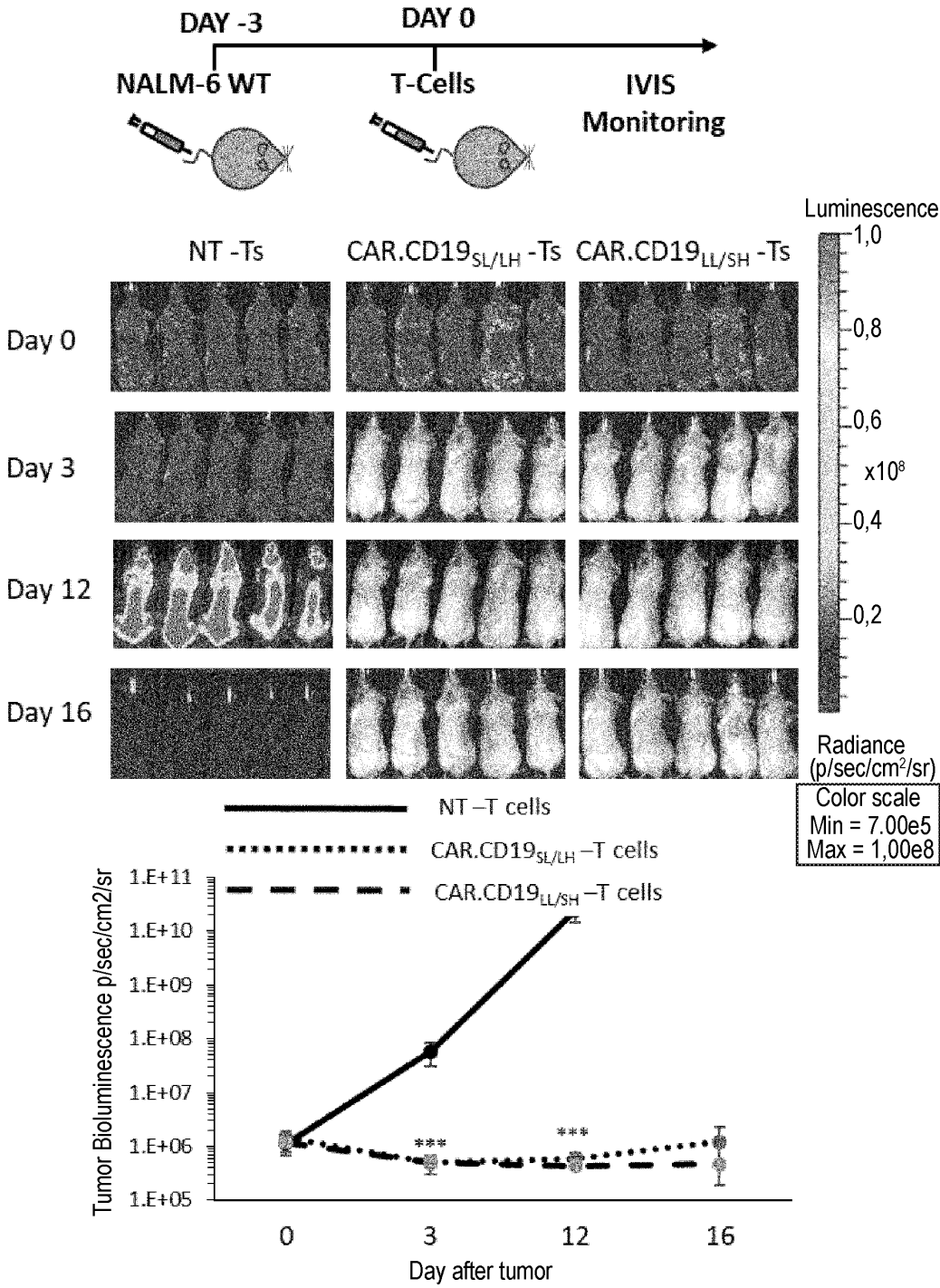


Fig. 12A

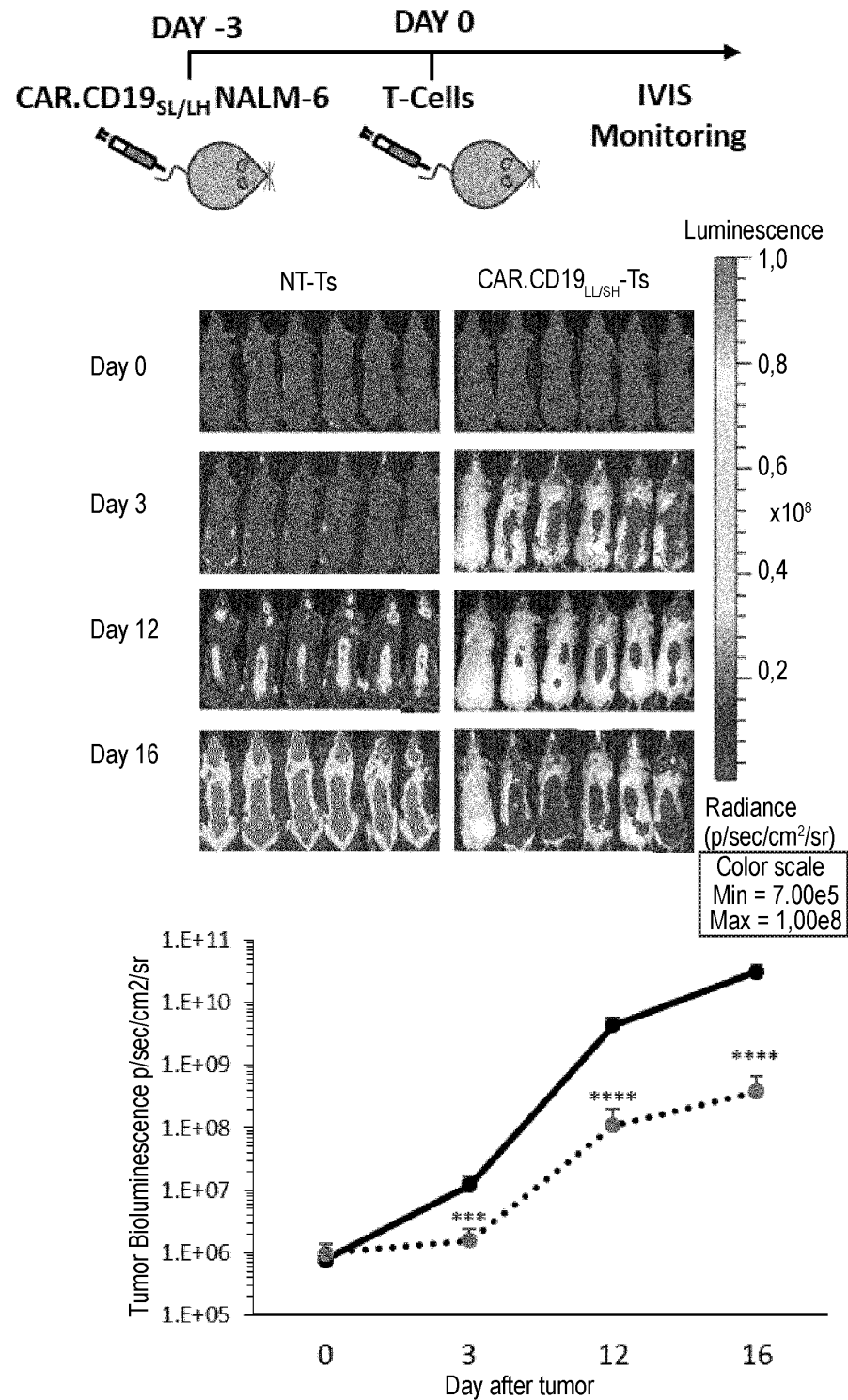


Fig. 12B

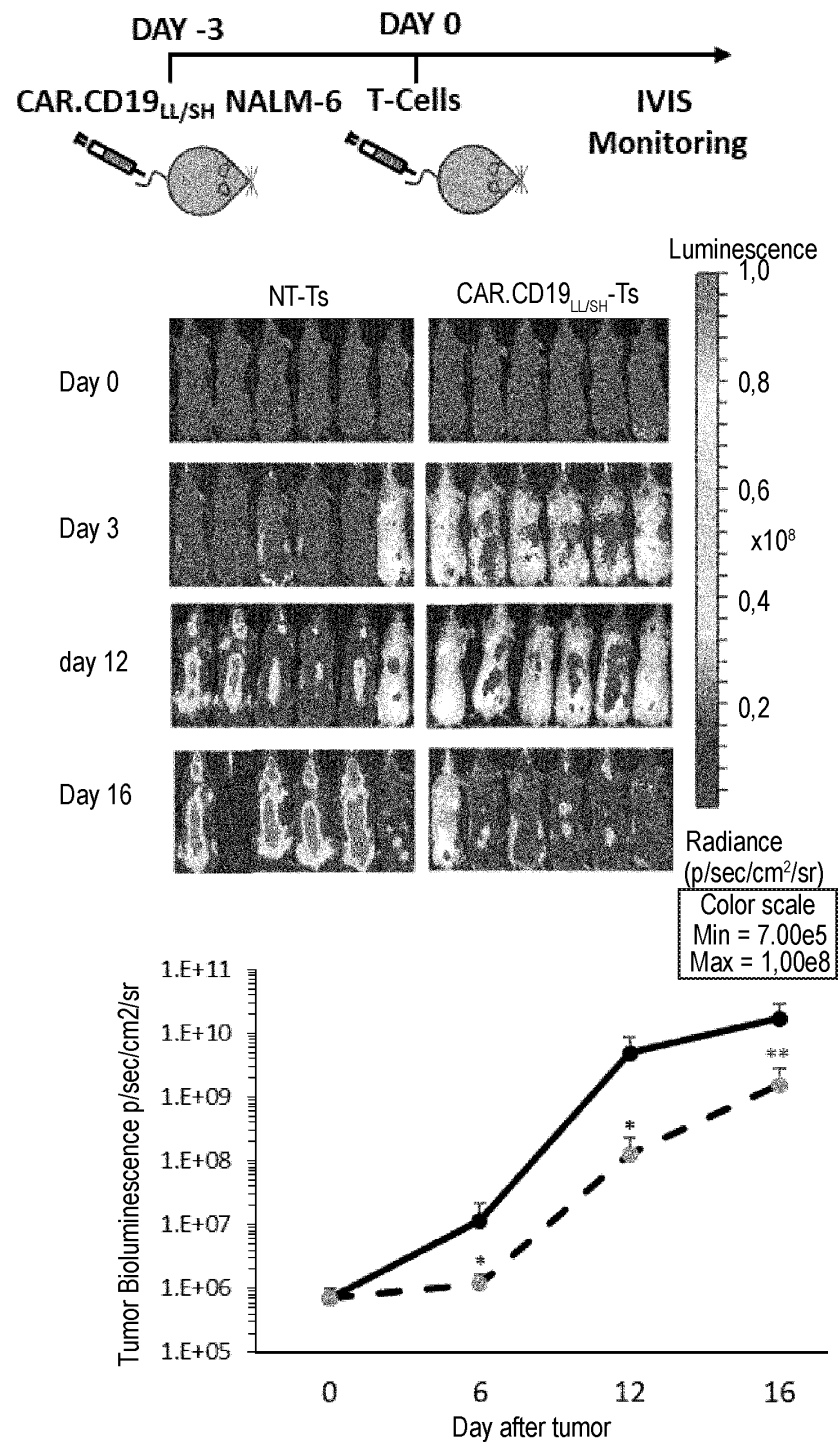


Fig. 12C

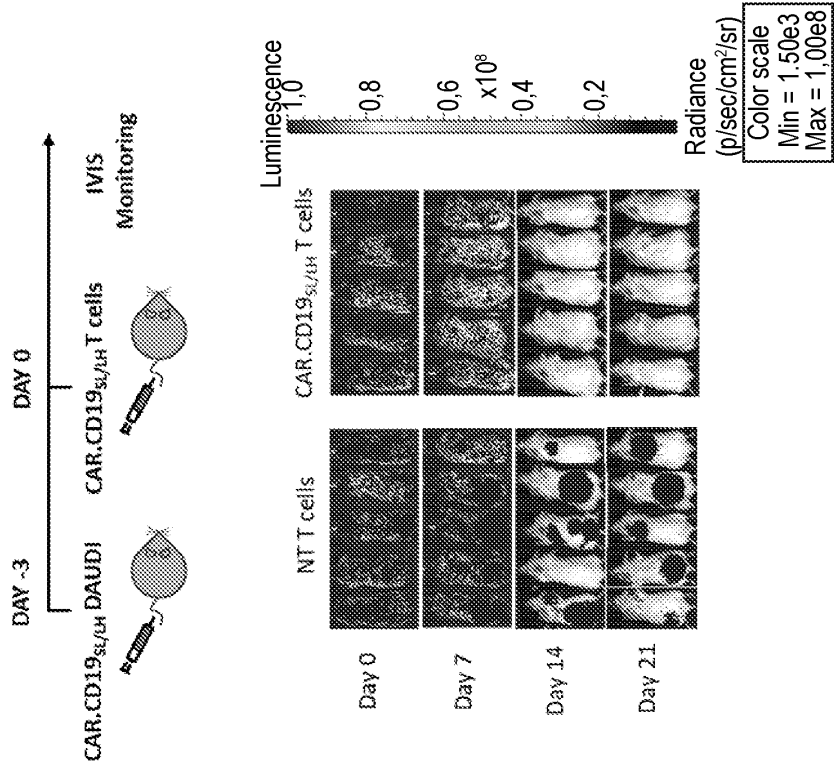
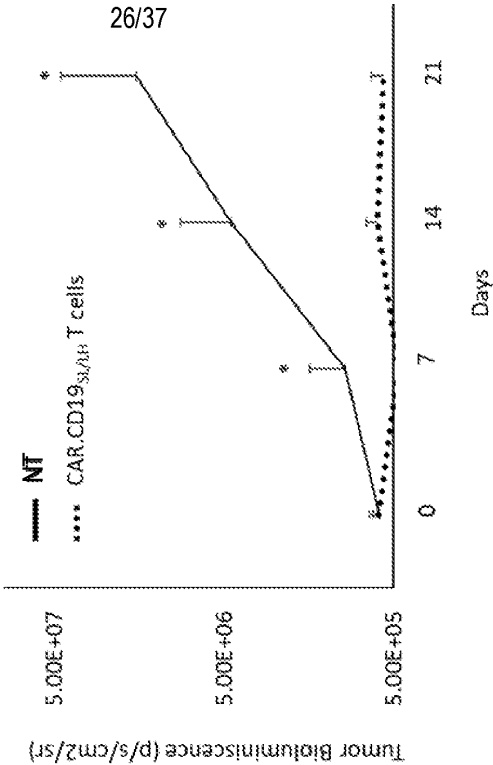


Fig. 12D



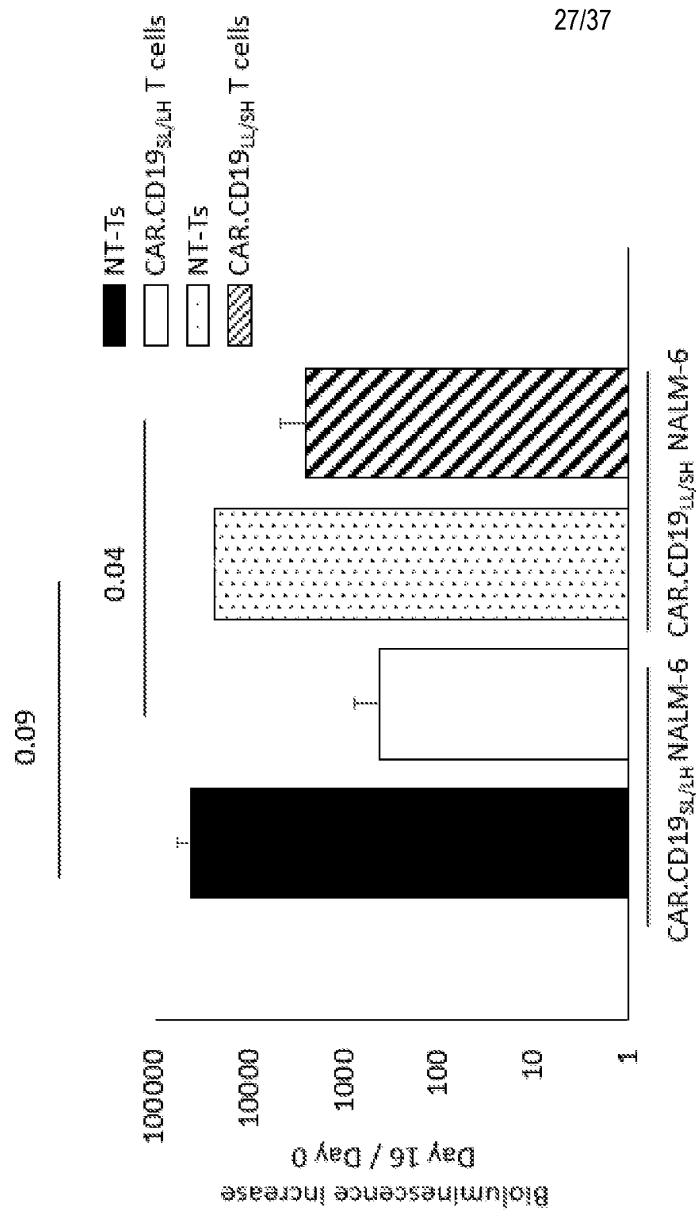


Fig. 12E

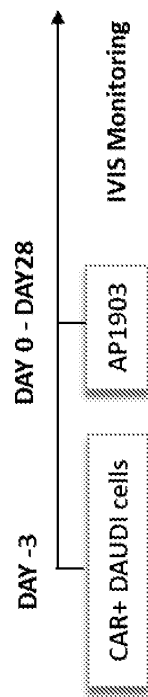


Fig. 13A

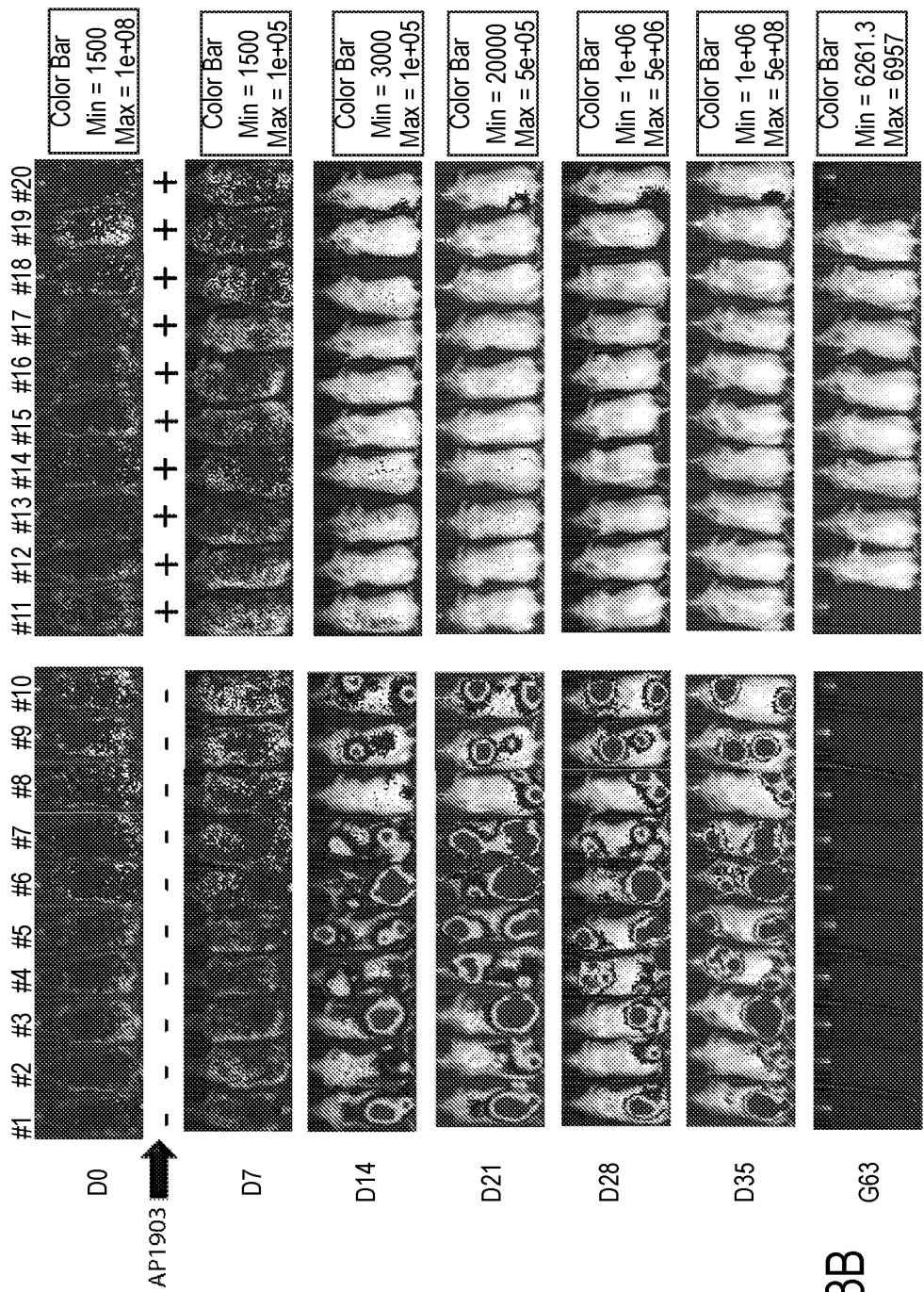


Fig. 13B

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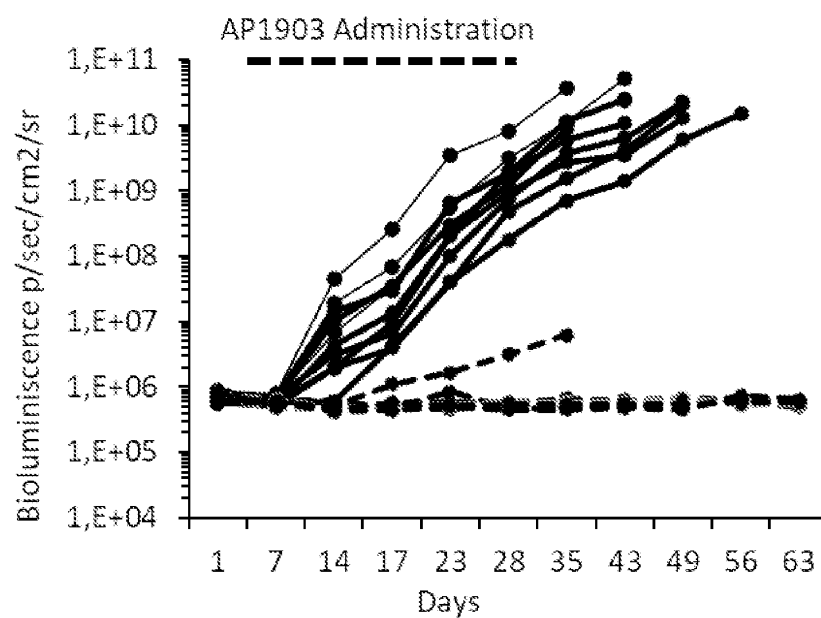


Fig. 13C

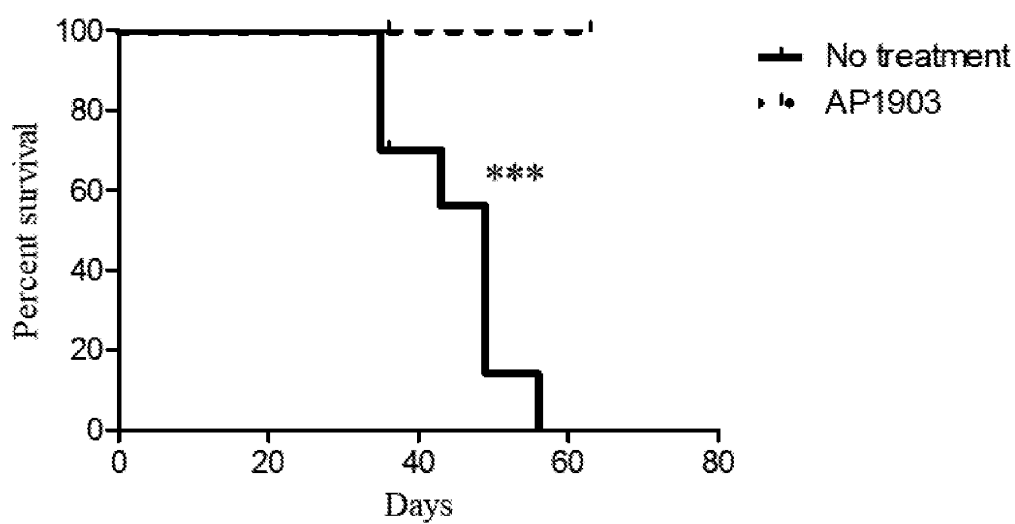
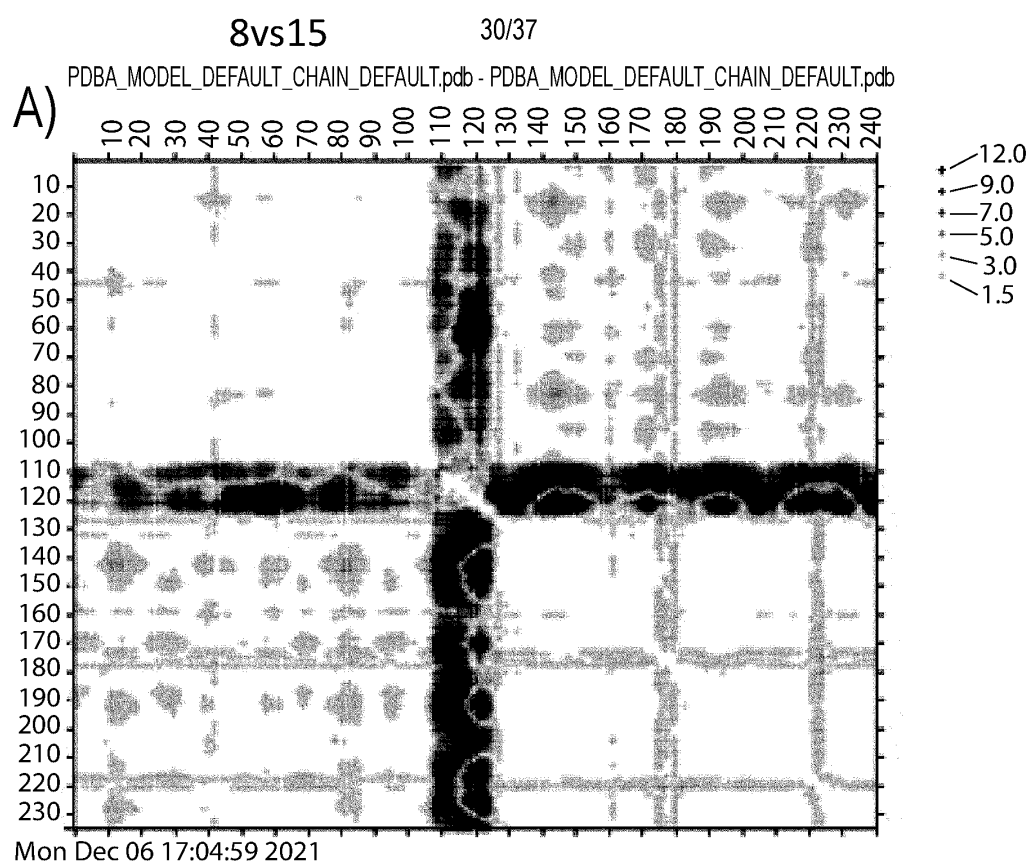


Fig. 13D



8vs15

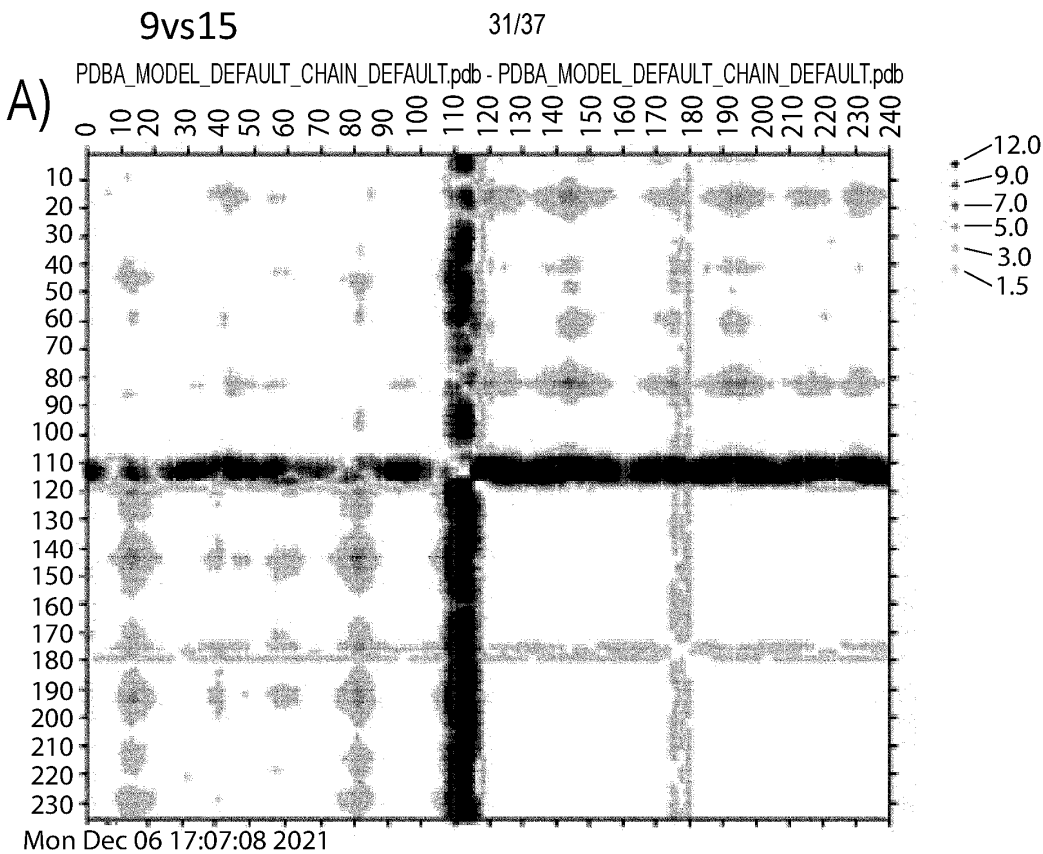
SuperPose used a structural alignment to guide the superposition.

B)

Local RMSD				
	<u>Alpha Carbons</u>	<u>Back Bone</u>	<u>Heavy</u>	<u>All</u>
<u>RMSD</u>	0.81	0.91	1.33	1.33
<u>Atoms</u>	105	420	809	809
<u>Structure</u>	<u>Residues</u>			
PDBA	1-105			
PDBB	1-105			

Global RMSD				
	<u>Alpha Carbons</u>	<u>Back Bone</u>	<u>Heavy</u>	<u>All</u>
<u>RMSD</u>	5.56	5.54	5.61	5.61
<u>Atoms</u>	234	936	1785	1785
<u>Structure</u>	<u>Residues</u>			
PDBA	2-107, 115-242			
PDBB	2-107, 108-235			

Fig. 14



9vs15

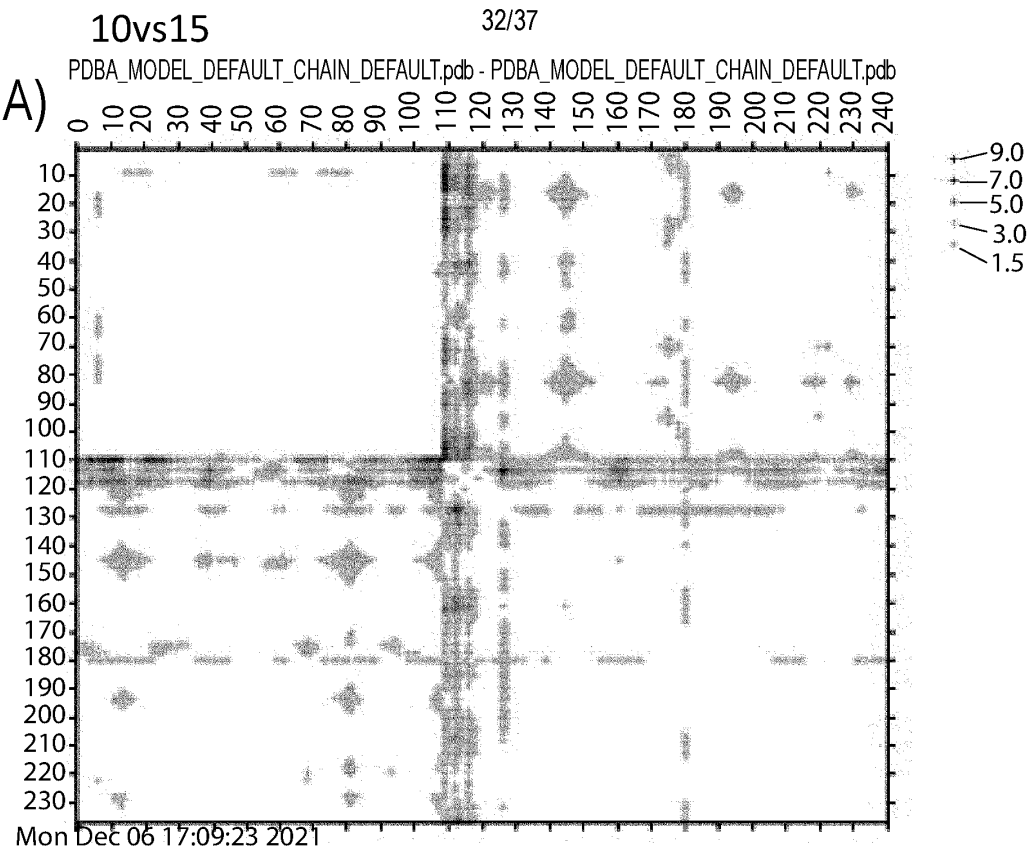
SuperPose used a structural alignment to guide the superposition.

B)

Local RMSD				
	<u>Alpha Carbons</u>	<u>Back Bone</u>	<u>Heavy</u>	<u>All</u>
<u>RMSD</u>	1.02	1.15	1.48	1.48
<u>Atoms</u>	106	424	817	817
<u>Structure</u>		<u>Residues</u>		
PDBA		1-106		
PDBB		1-106		

Global RMSD				
	<u>Alpha Carbons</u>	<u>Back Bone</u>	<u>Heavy</u>	<u>All</u>
<u>RMSD</u>	5.03	5.01	4.45	4.45
<u>Atoms</u>	235	940	1791	1791
<u>Structure</u>		<u>Residues</u>		
PDBA		2-113, 120-242		
PDBB		2-113, 114-236		

Fig. 15



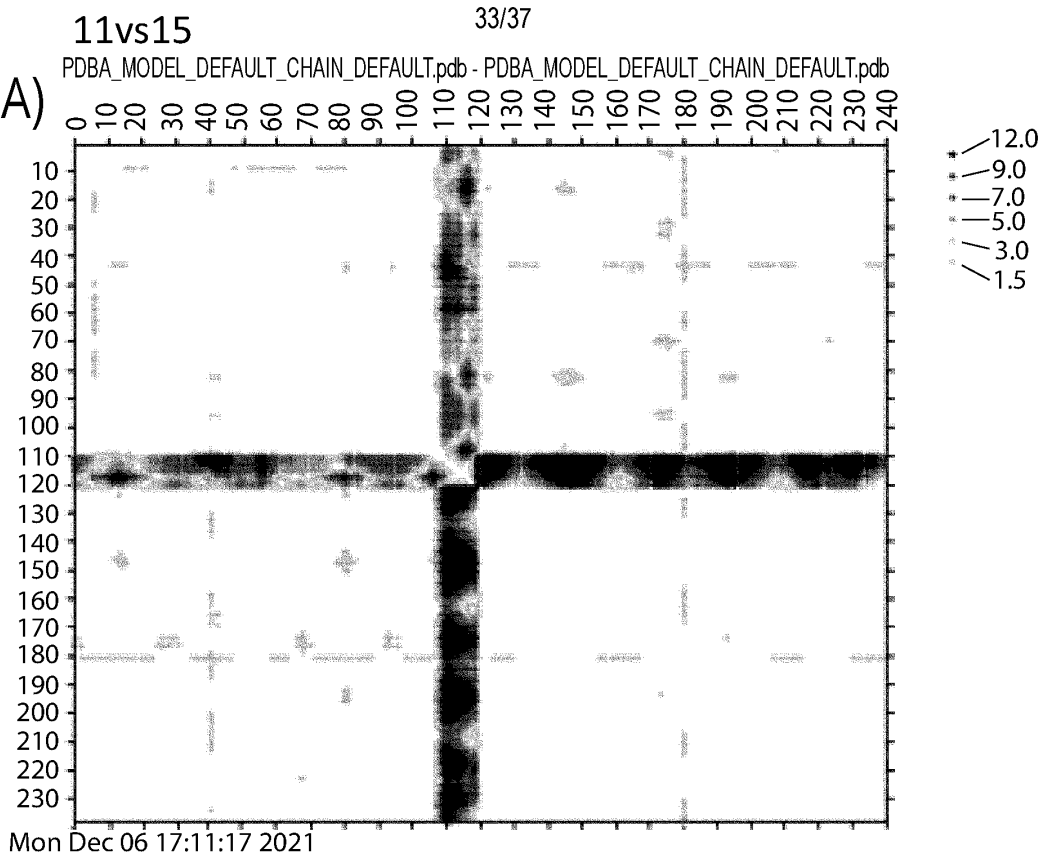
10vs15

B) SuperPose used the sequence alignment to guide the supersposition.

Local RMSD				
	<u>Alpha Carbons</u>	<u>Back Bone</u>	<u>Heavy</u>	<u>All</u>
<u>RMSD</u>	1.40	1.40	1.62	1.62
<u>Atoms</u>	237	948	1803	1803
<u>Structure</u>	<u>Residues</u>			
PDBA	1-107, 113-242			
PDBB	1-107, 108-237			

Global RMSD				
	<u>Alpha Carbons</u>	<u>Back Bone</u>	<u>Heavy</u>	<u>All</u>
<u>RMSD</u>	1.40	1.40	1.62	1.62
<u>Atoms</u>	237	948	1803	1803
<u>Structure</u>	<u>Residues</u>			
PDBA	1-107, 113-242			
PDBB	1-107, 108-237			

Fig. 16



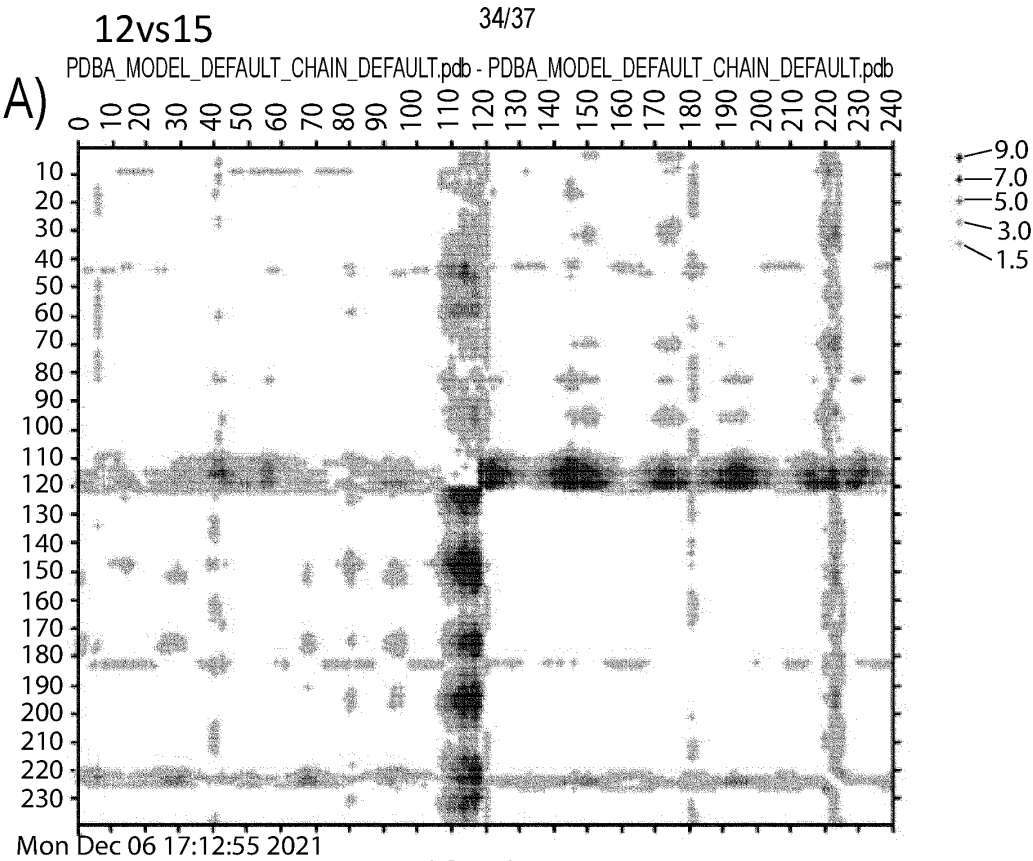
11vs15

B) SuperPose used a structural alignment to guide the superposition.

Local RMSD				
	<u>Alpha Carbons</u>	<u>Back Bone</u>	<u>Heavy</u>	<u>All</u>
<u>RMSD</u>	0.46	0.57	1.04	1.04
<u>Atoms</u>	106	424	817	817
<u>Structure</u>	<u>Residues</u>			
PDBA	1-106			
PDBB	1-106			

Global RMSD				
	<u>Alpha Carbons</u>	<u>Back Bone</u>	<u>Heavy</u>	<u>All</u>
<u>RMSD</u>	3.60	3.65	3.02	3.02
<u>Atoms</u>	237	948	1801	1801
<u>Structure</u>	<u>Residues</u>			
PDBA	2-118, 123-242			
PDBB	2-118, 119-238			

Fig. 17



12vs15

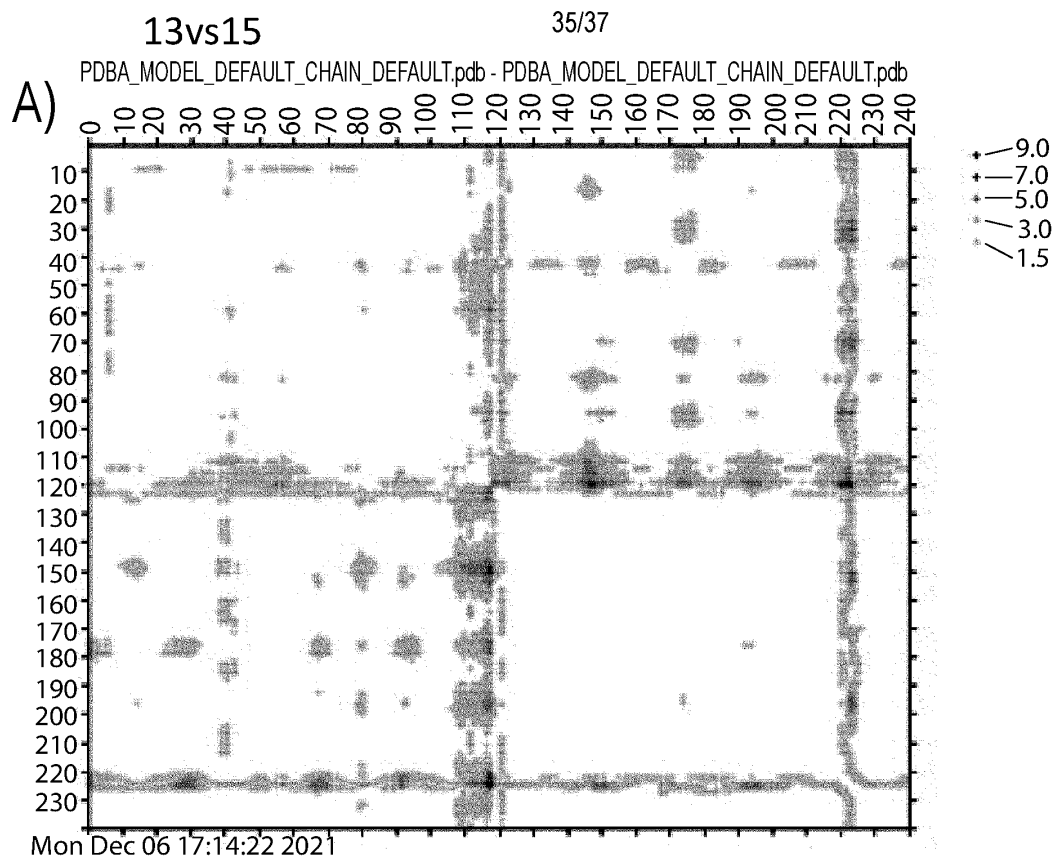
SuperPose used the sequence alignment to guide the supersposition.

B)

Local RMSD				
	Alpha Carbons	Back Bone	Heavy	All
RMSD	2.03	2.03	2.20	2.20
Atoms	239	956	1813	1813
Structure	Residues			
PDBA	1-118, 122-242			
PDBB	1-118, 119-239			

Global RMSD				
	Alpha Carbons	Back Bone	Heavy	All
RMSD	2.03	2.03	2.20	2.20
Atoms	239	956	1813	1813
Structure	Residues			
PDBA	1-118, 122-242			
PDBB	1-118, 119-239			

Fig. 18



13vs15

B) SuperPose used the sequence alignment to guide the supersposition.

Local RMSD				
	Alpha Carbons	Back Bone	Heavy	All
RMSD	1.48	1.48	1.85	1.85
Atoms	240	960	1817	1817
Structure	Residues			
PDBA	1-118, 121-242			
PDBB	1-118, 119-240			

Global RMSD				
	Alpha Carbons	Back Bone	Heavy	All
RMSD	1.48	1.48	1.85	1.85
Atoms	240	960	1817	1817
Structure	Residues			
PDBA	1-118, 121-242			
PDBB	1-118, 119-240			

Fig. 19

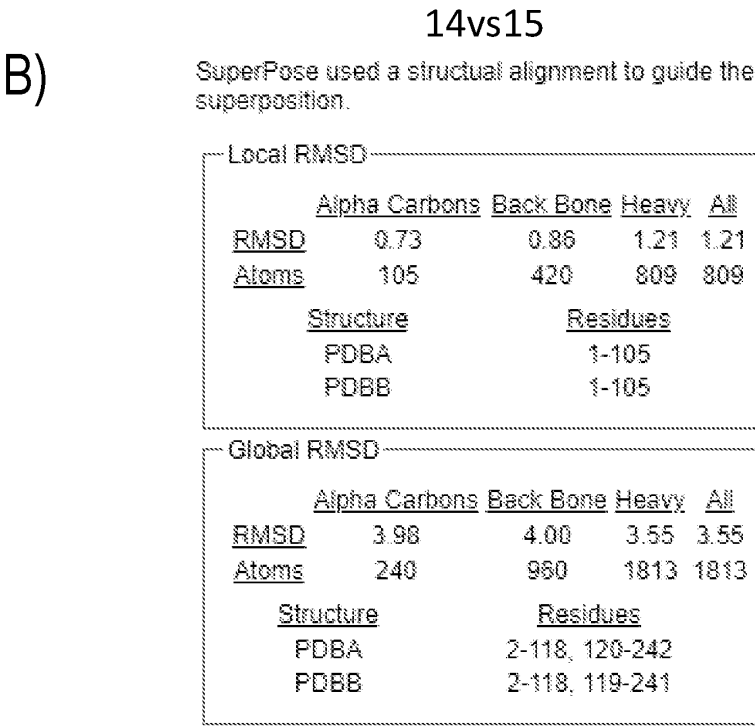
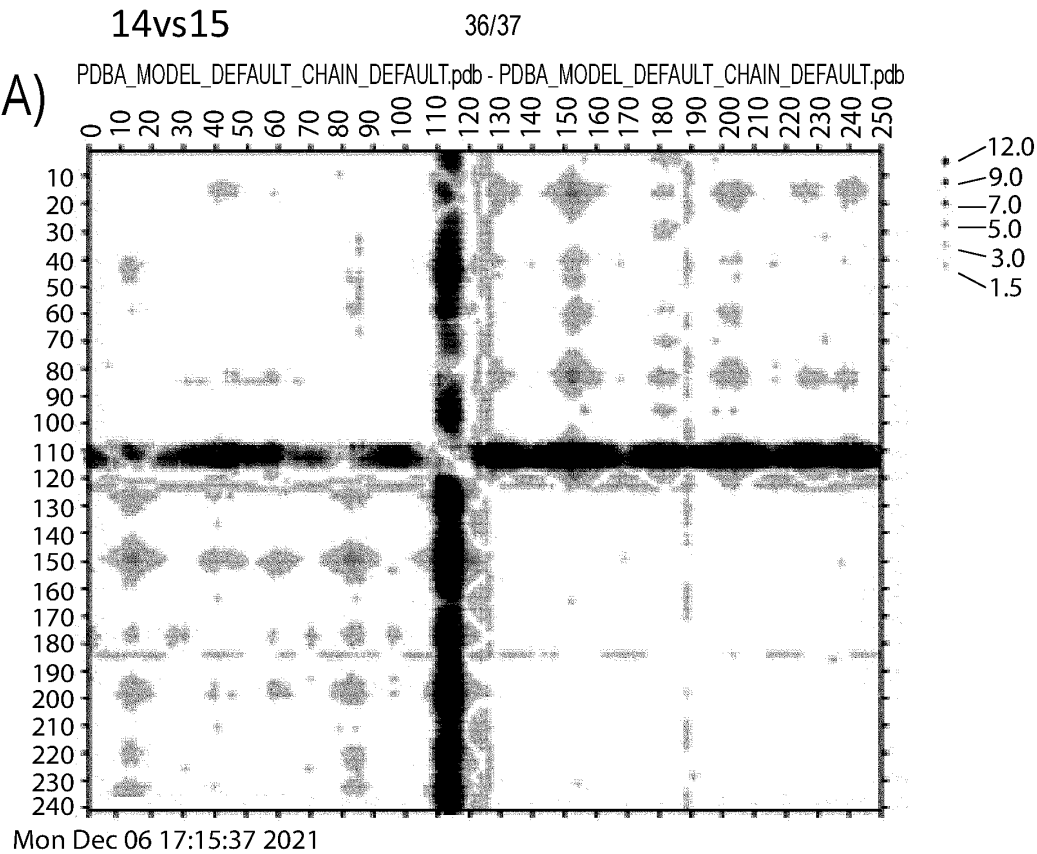
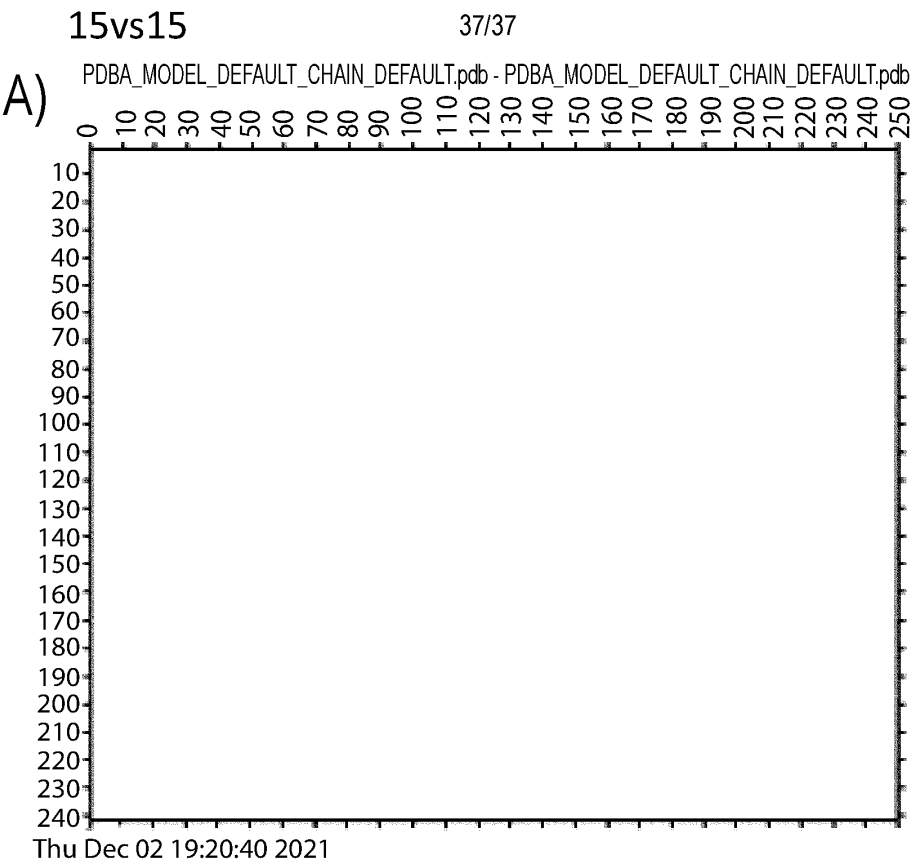


Fig. 20



15vs15

B) SuperPose used the sequence alignment to guide the supersposition.

Local RMSD				
	<u>Alpha</u>	<u>Back</u>	<u>Heavy</u>	<u>All</u>
	<u>Carbons</u>	<u>Bone</u>		
<u>RMSD</u>	0.00	0.00	0.00	0.00
<u>Atoms</u>	242	968	1825	1825
<u>Structure</u>	<u>Residues</u>			
PDBA	1-242			
PDBB	1-242			

Global RMSD				
	<u>Alpha</u>	<u>Back</u>	<u>Heavy</u>	<u>All</u>
	<u>Carbons</u>	<u>Bone</u>		
<u>RMSD</u>	0.00	0.00	0.00	0.00
<u>Atoms</u>	242	968	1825	1825
<u>Structure</u>	<u>Residues</u>			
PDBA	1-242			
PDBB	1-242			

Fig. 21