

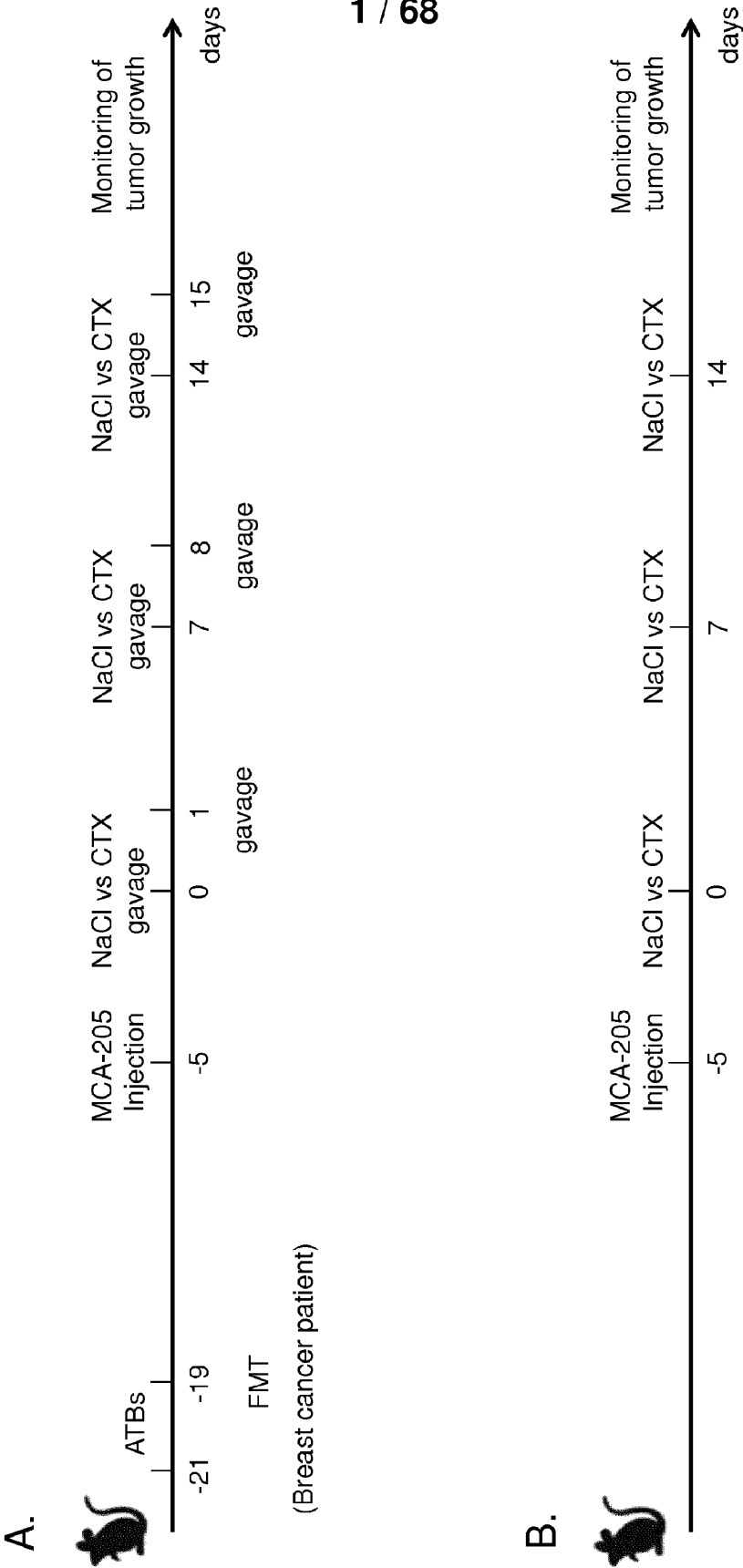


Figure 1

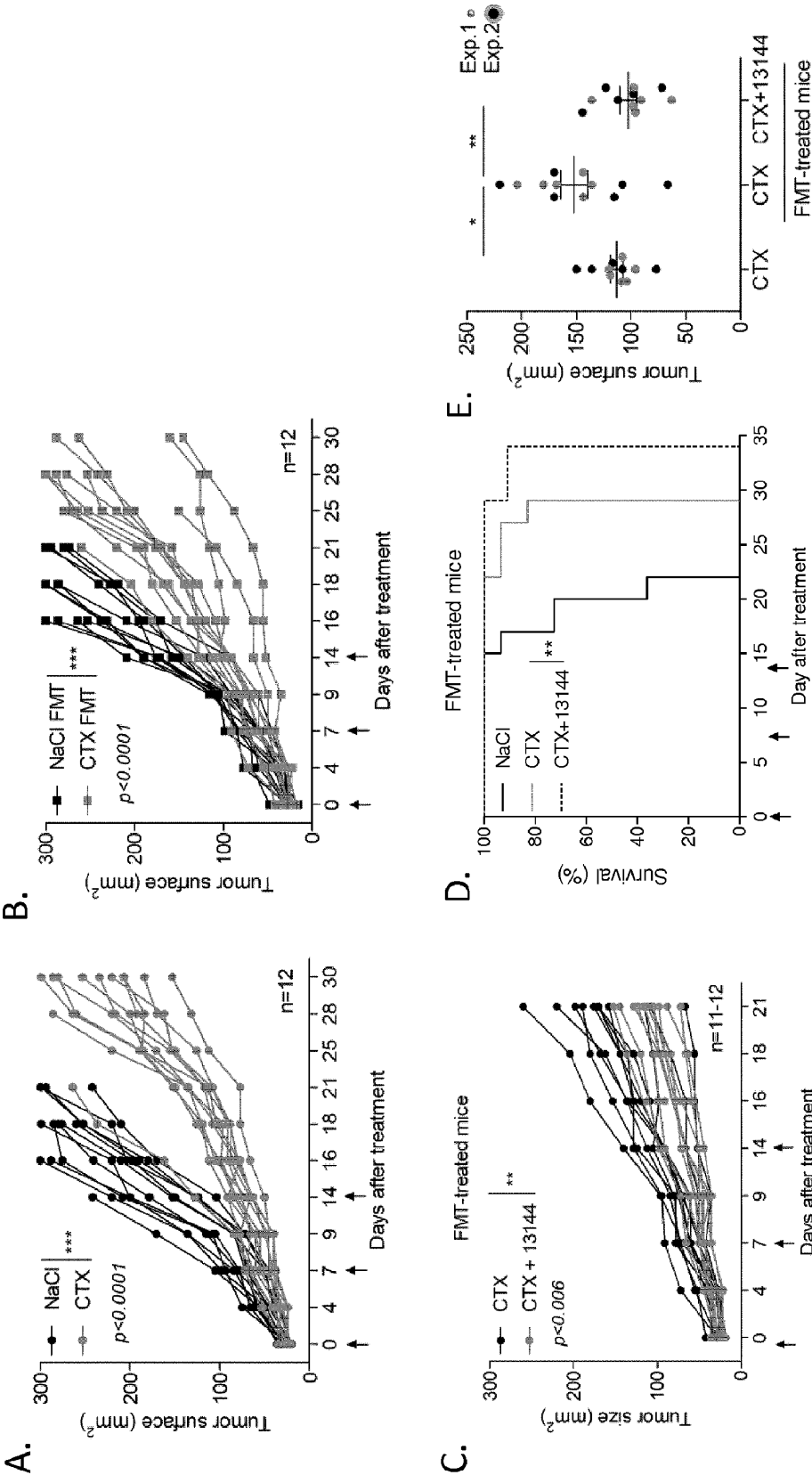
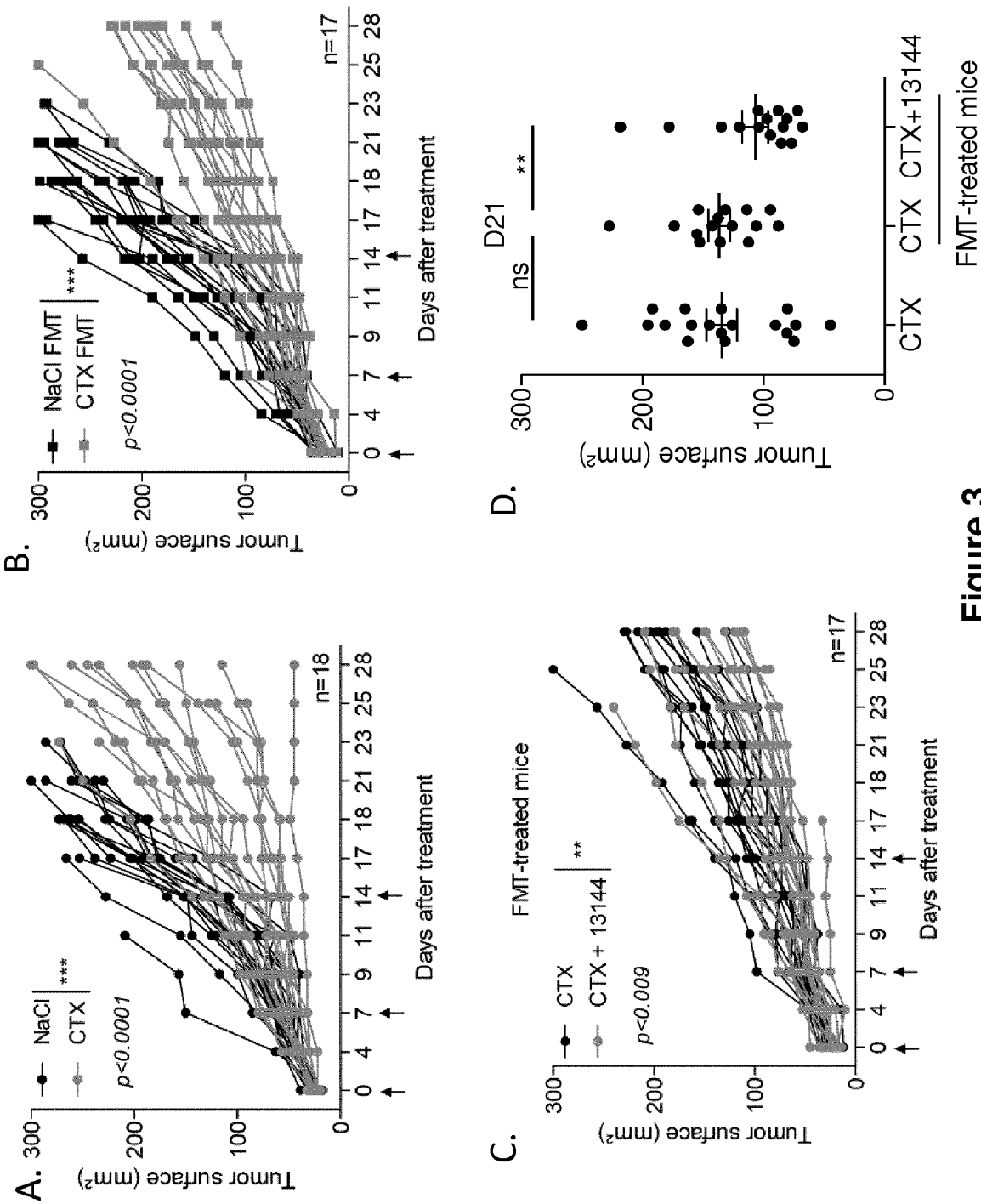


Figure 2



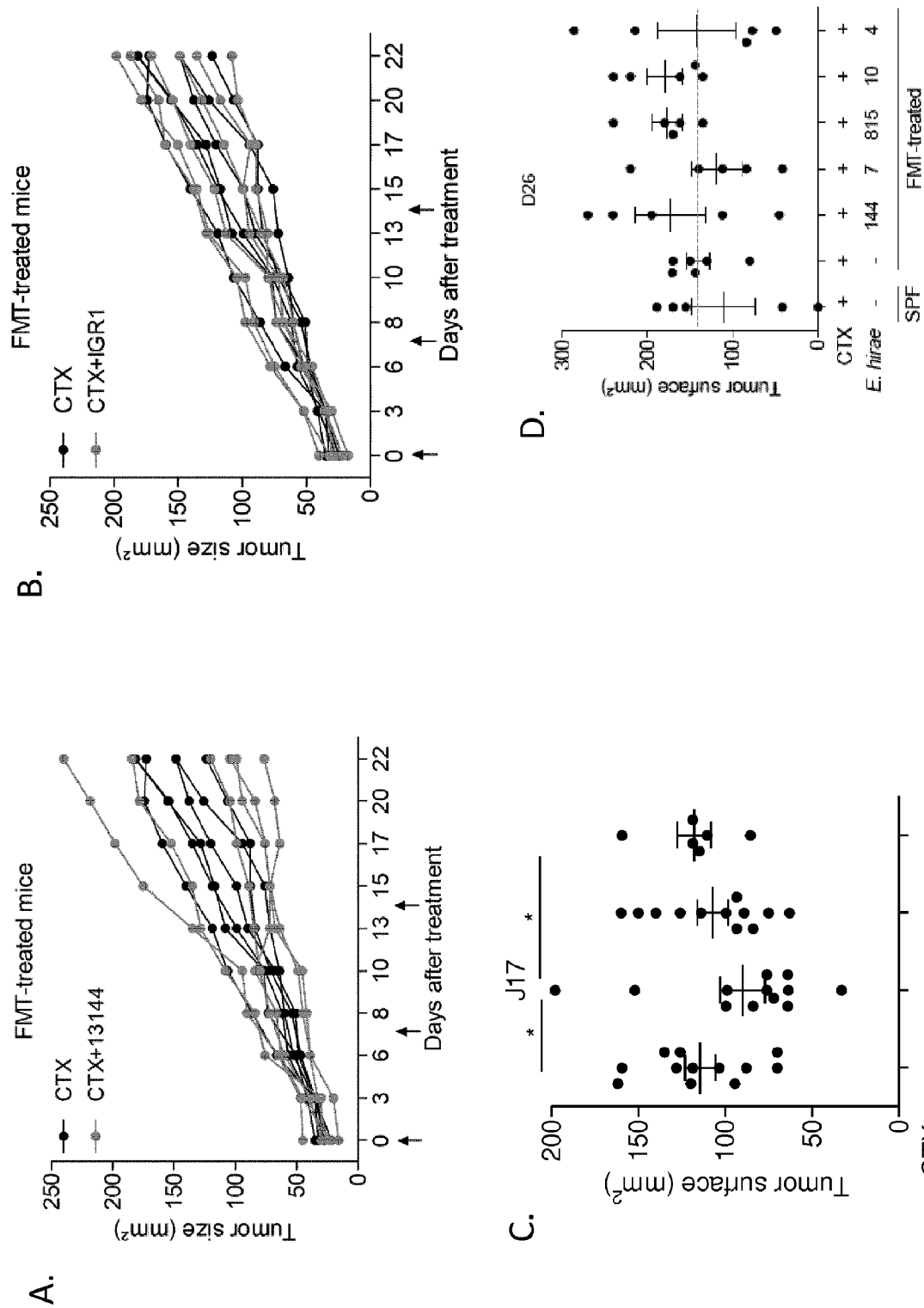


Figure 4

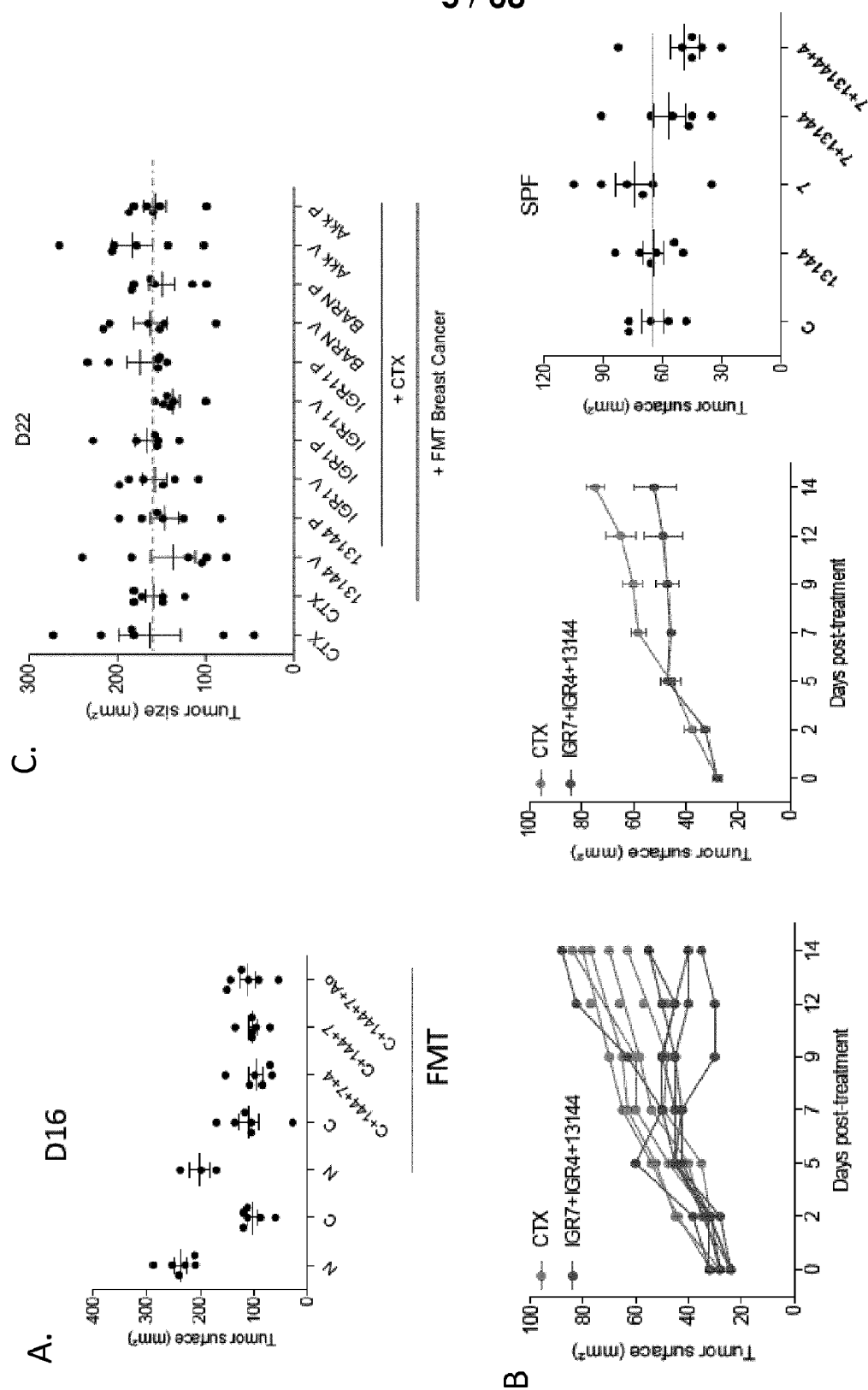


Figure 5

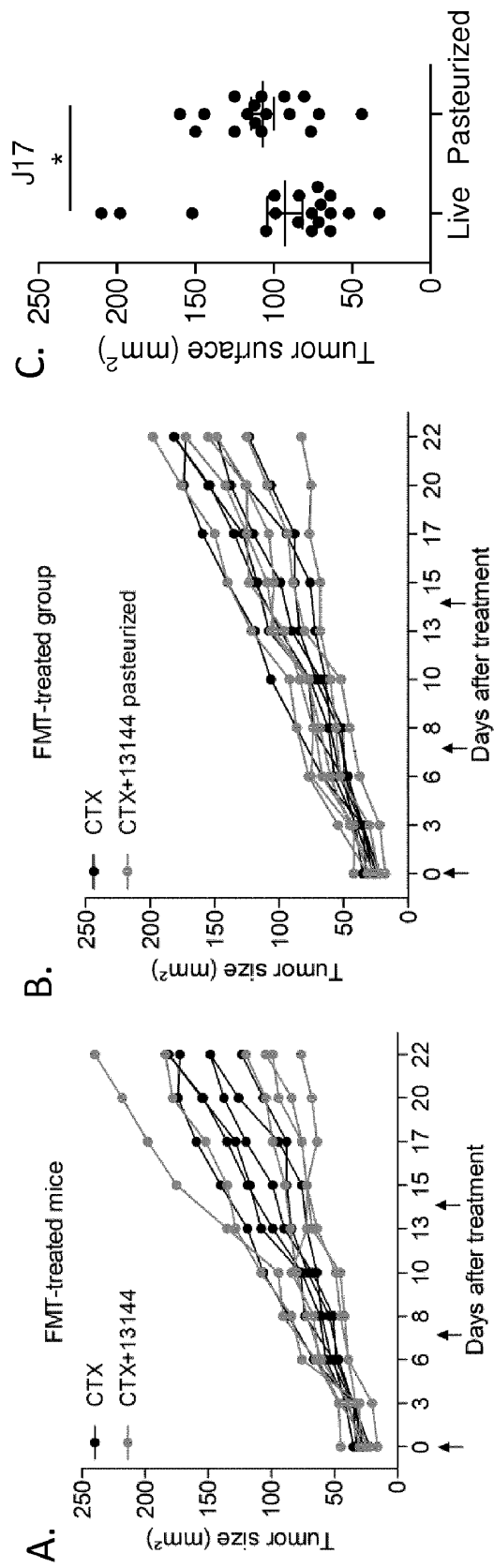


Figure 6

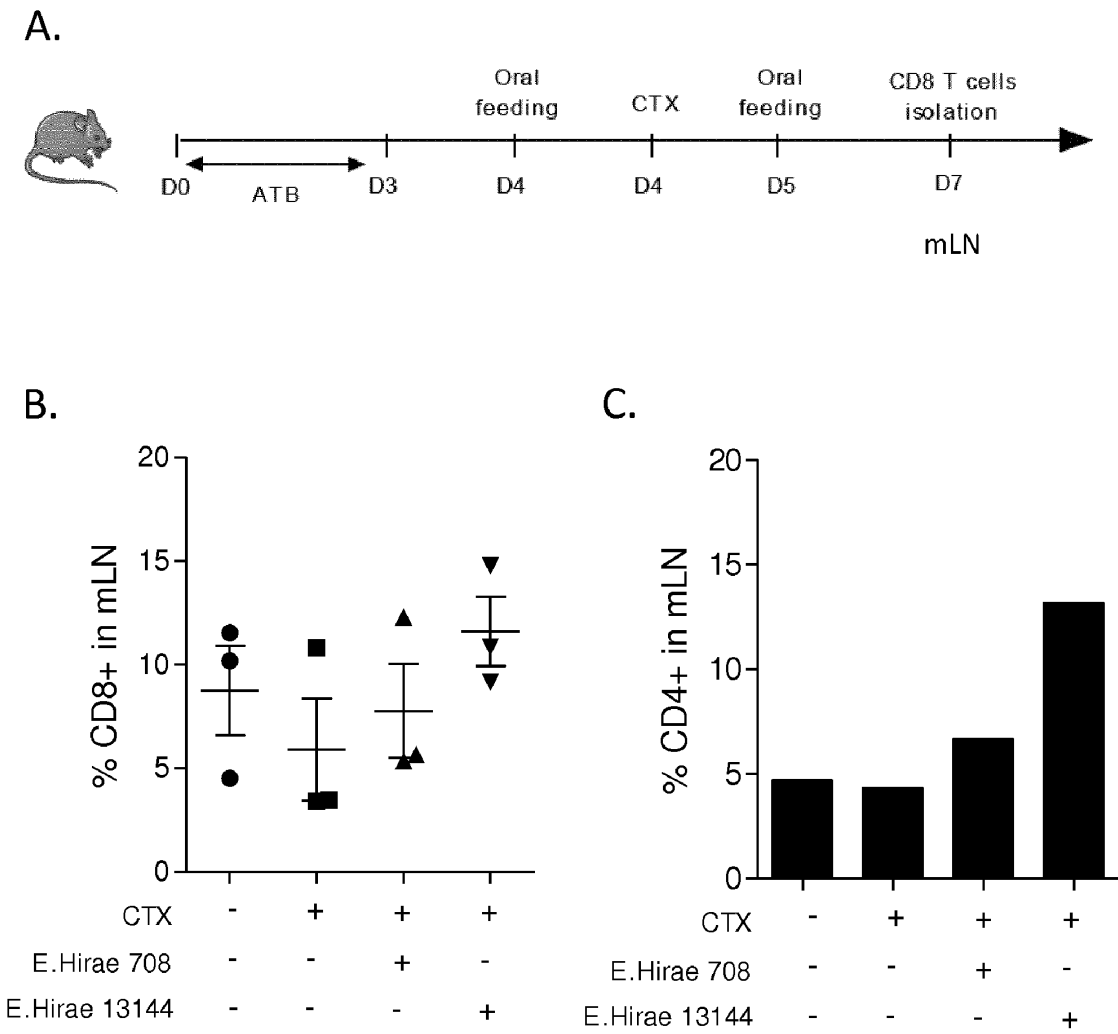
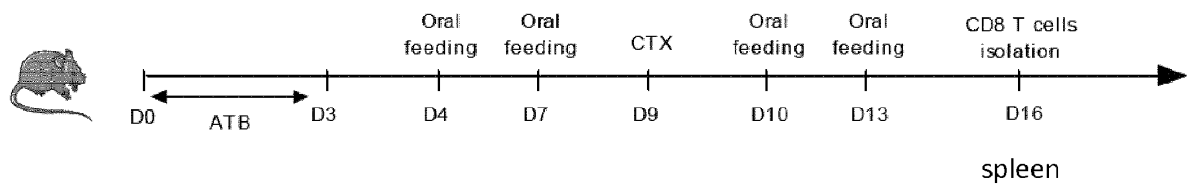
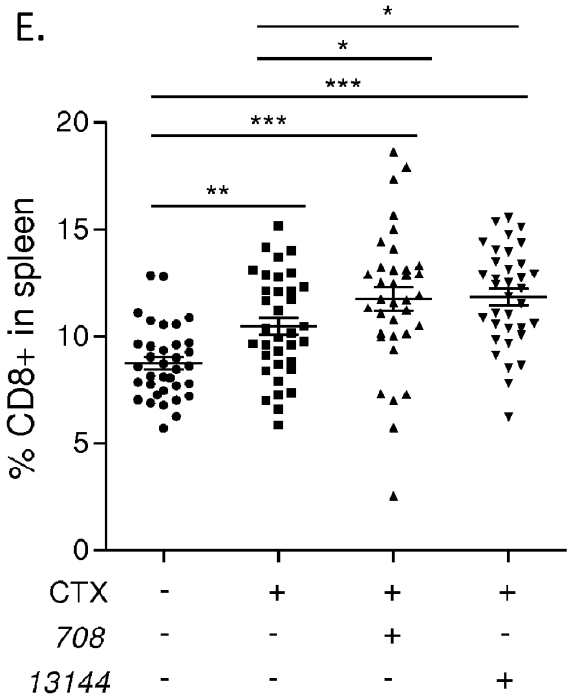


Figure 7A-C

D.



E.



F.

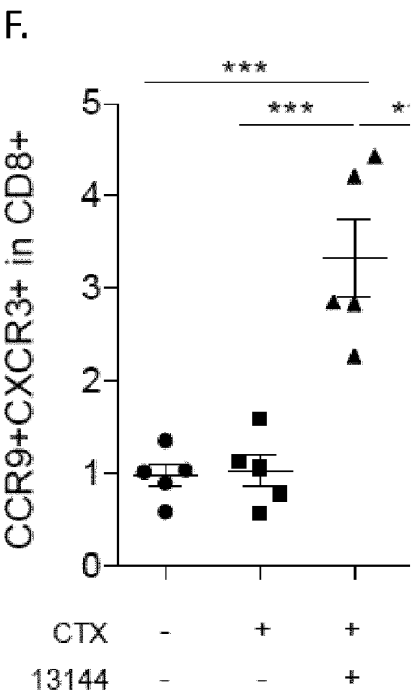
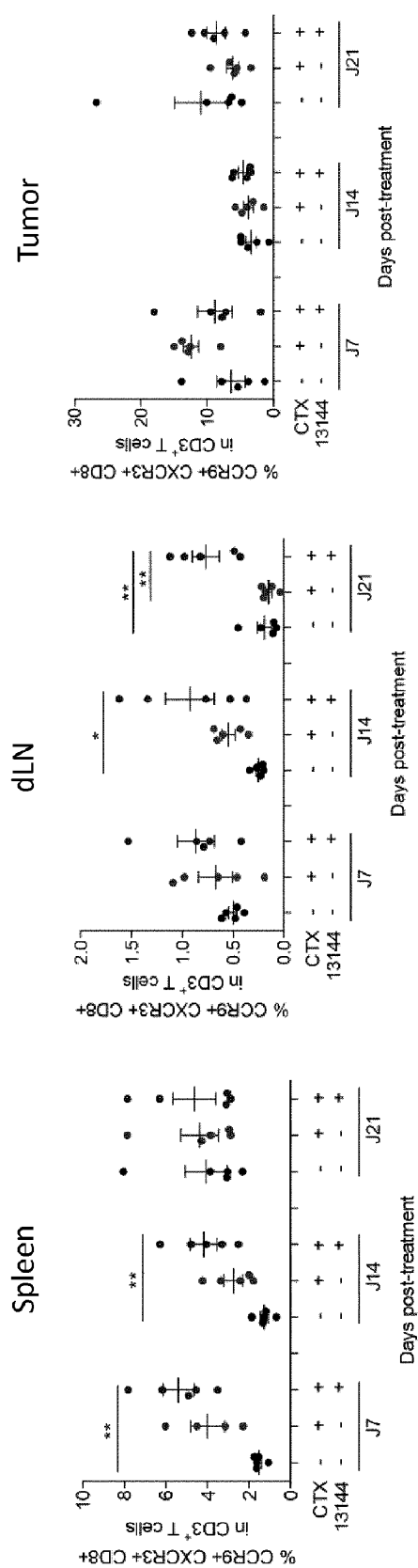


Figure 7D-F

A. Without FMT



B. With FMT

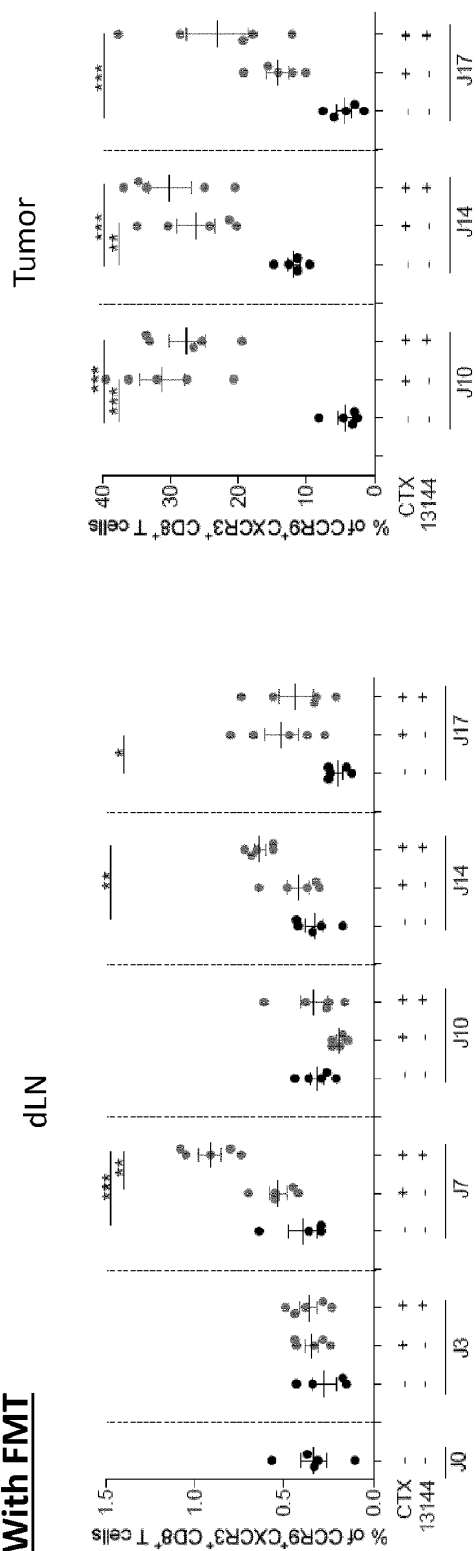


Figure 8

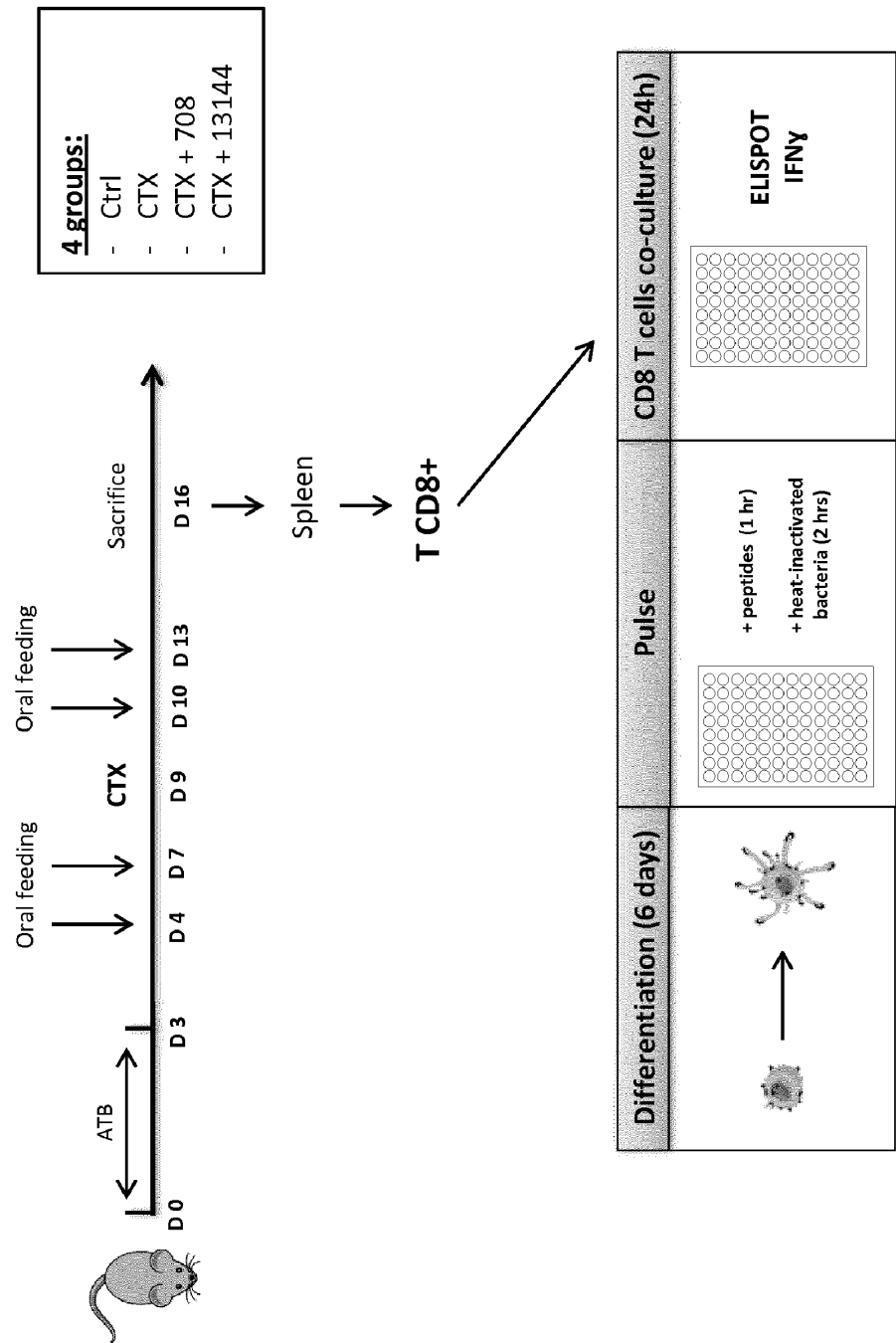


Figure 9

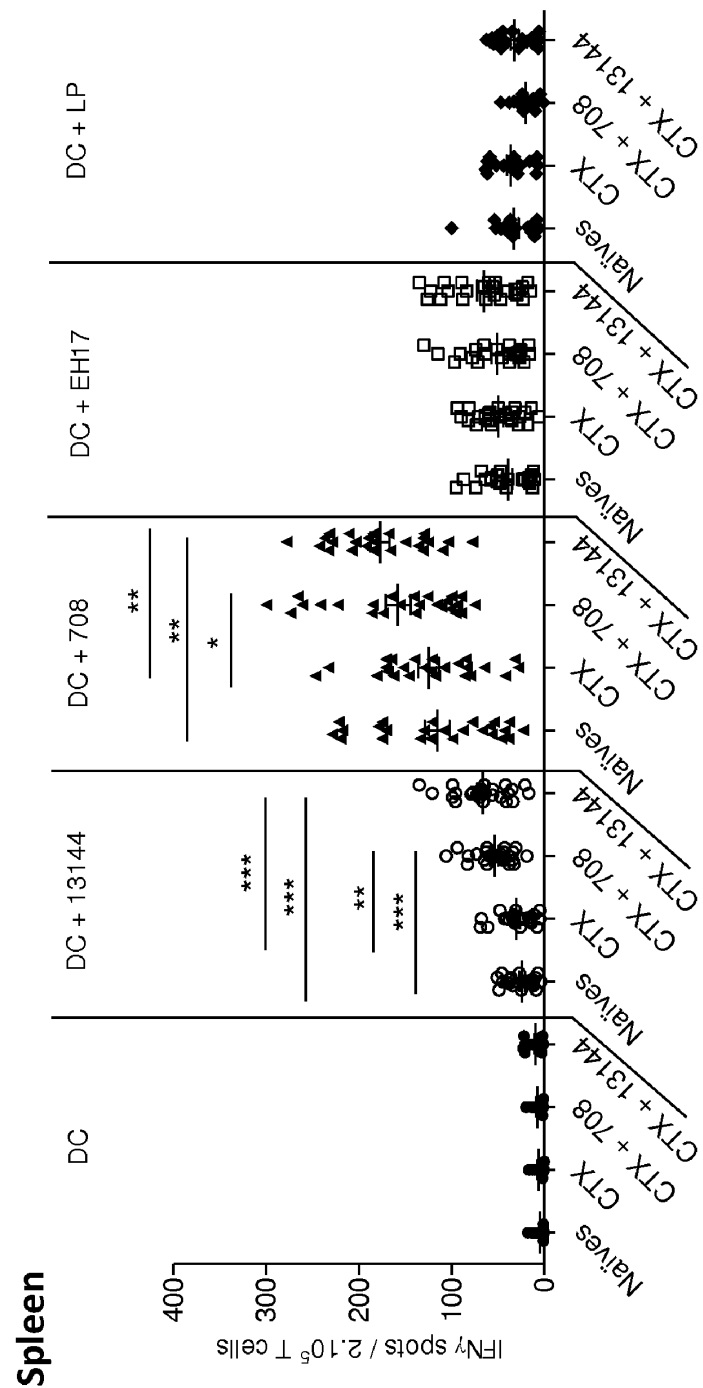


Figure 10

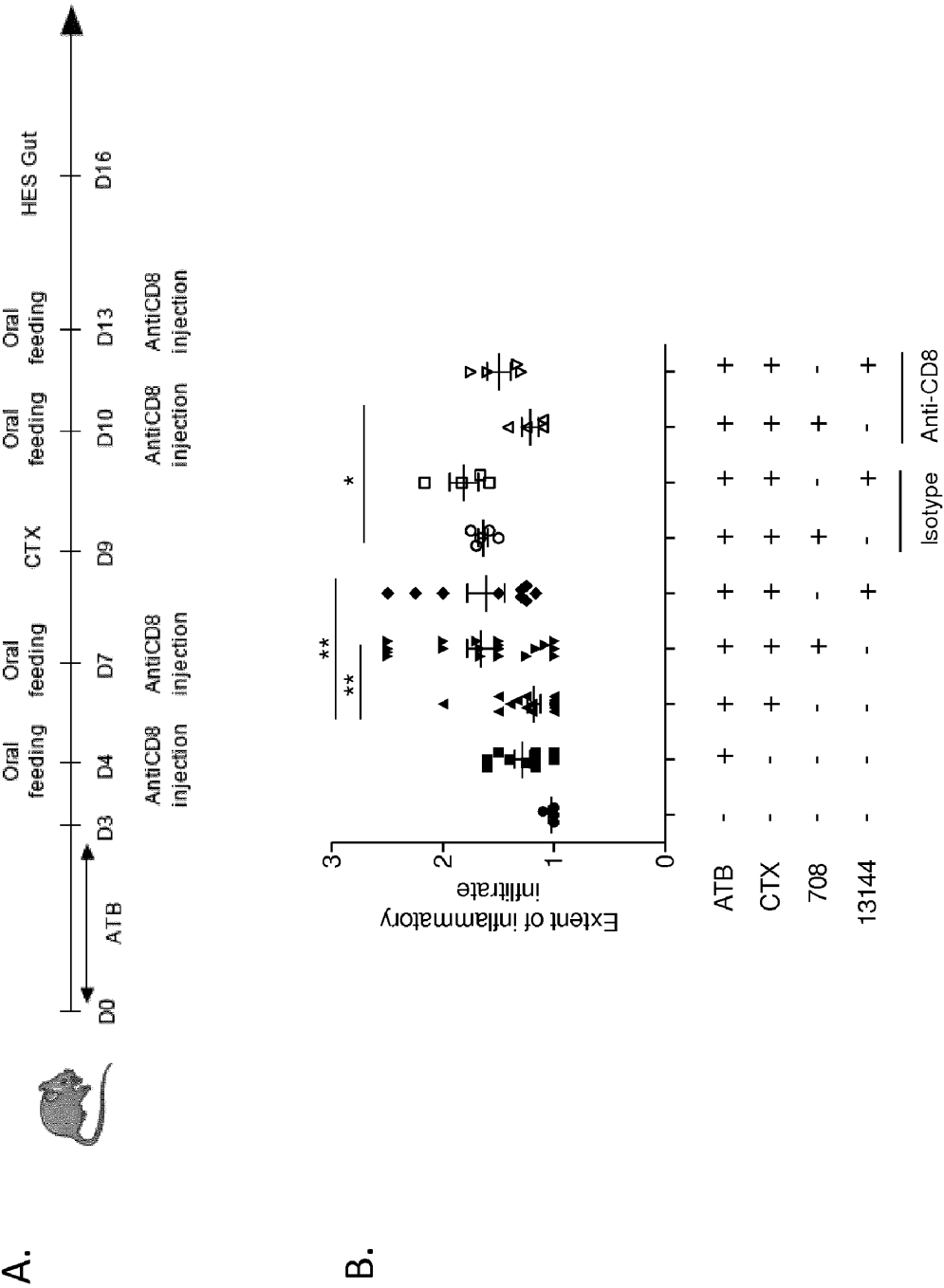


Figure 11

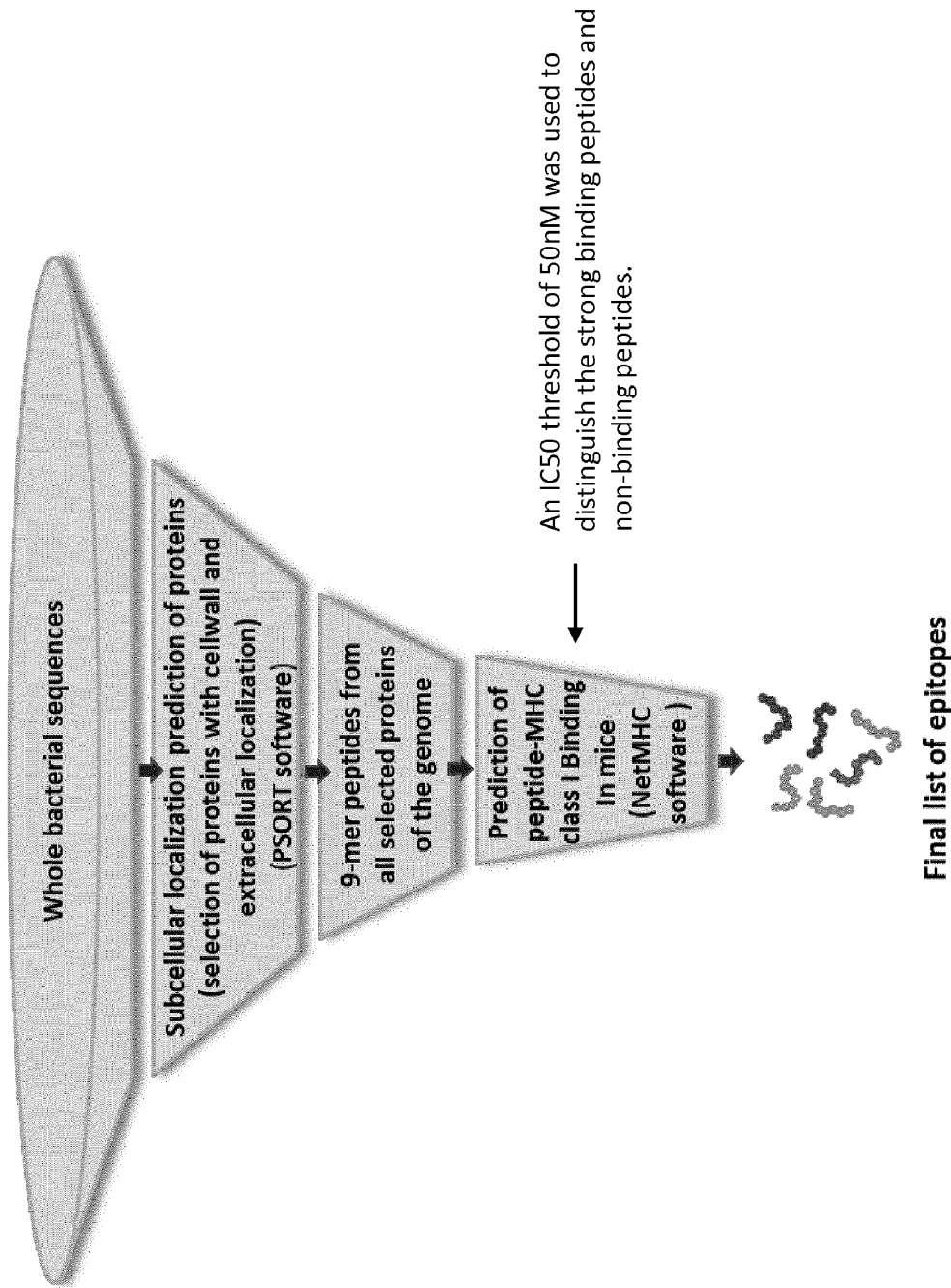


Figure 12

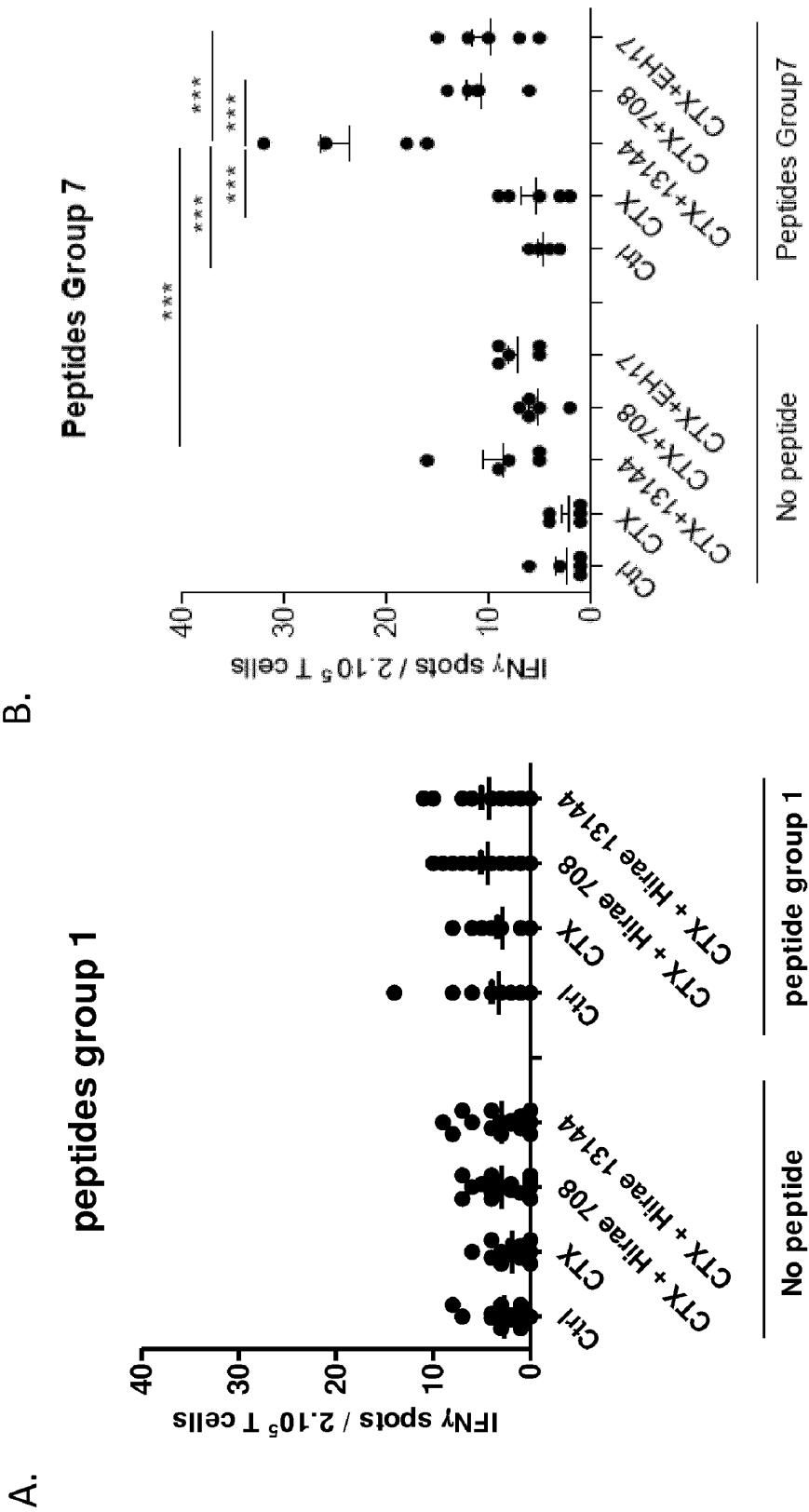


Figure 13A-B

C.

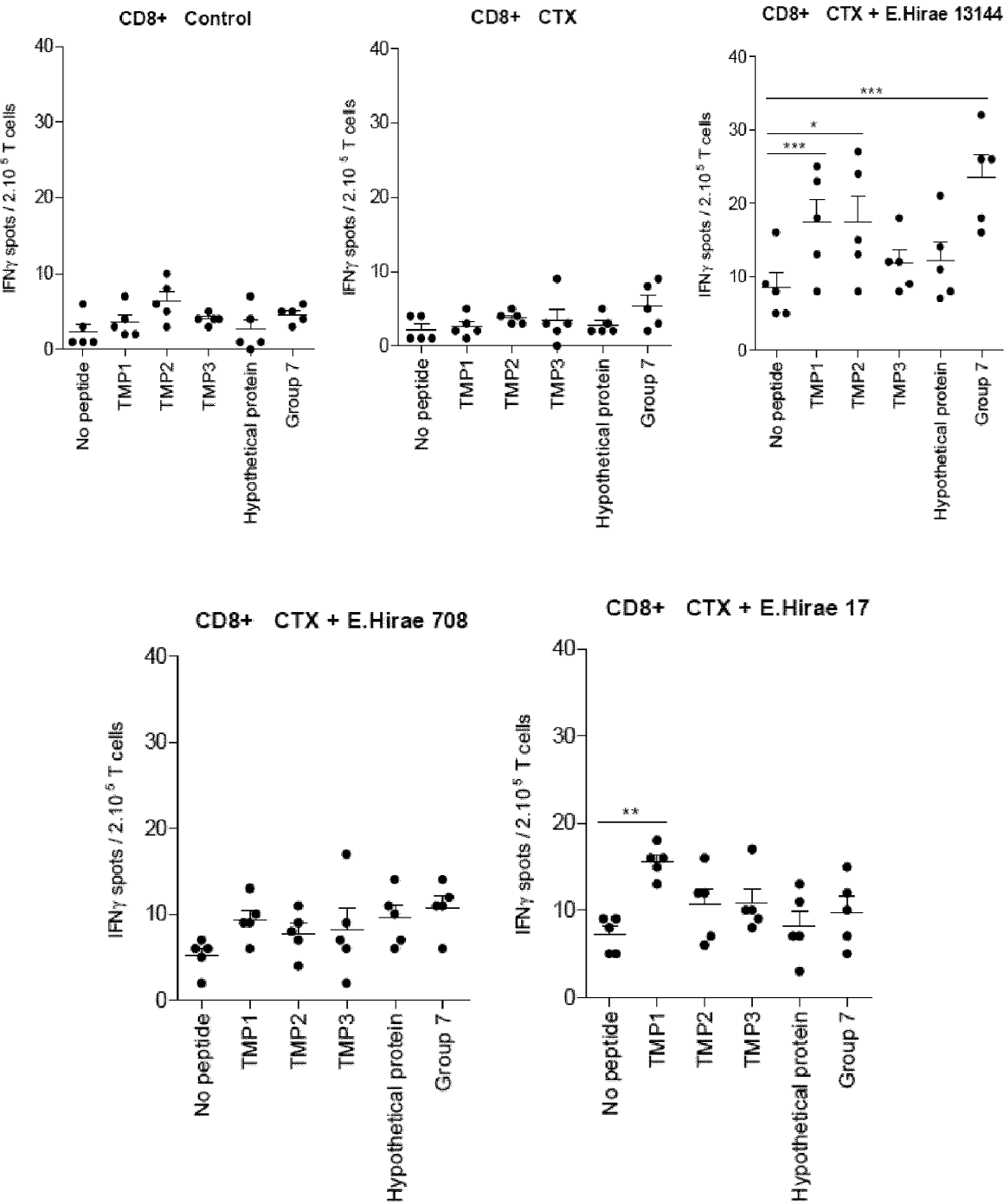


Figure 13C

13144	HLA	peptide	Affinity(nM)
	H-2-Kb	TSLARFANI (TMP1)	7.81

10815	HLA	peptide	Affinity(nM)
	H-2-Kb	TS ^F ARFANI	4.37

13144	HLA	peptide	Affinity(nM)
	H-2-Kb	AMIEFFIOGL (TMP2)	31.25

10815	HLA	peptide	Affinity(nM)
	H-2-Kb	AIIEFIKGL	82.63

Figure 13D

E.

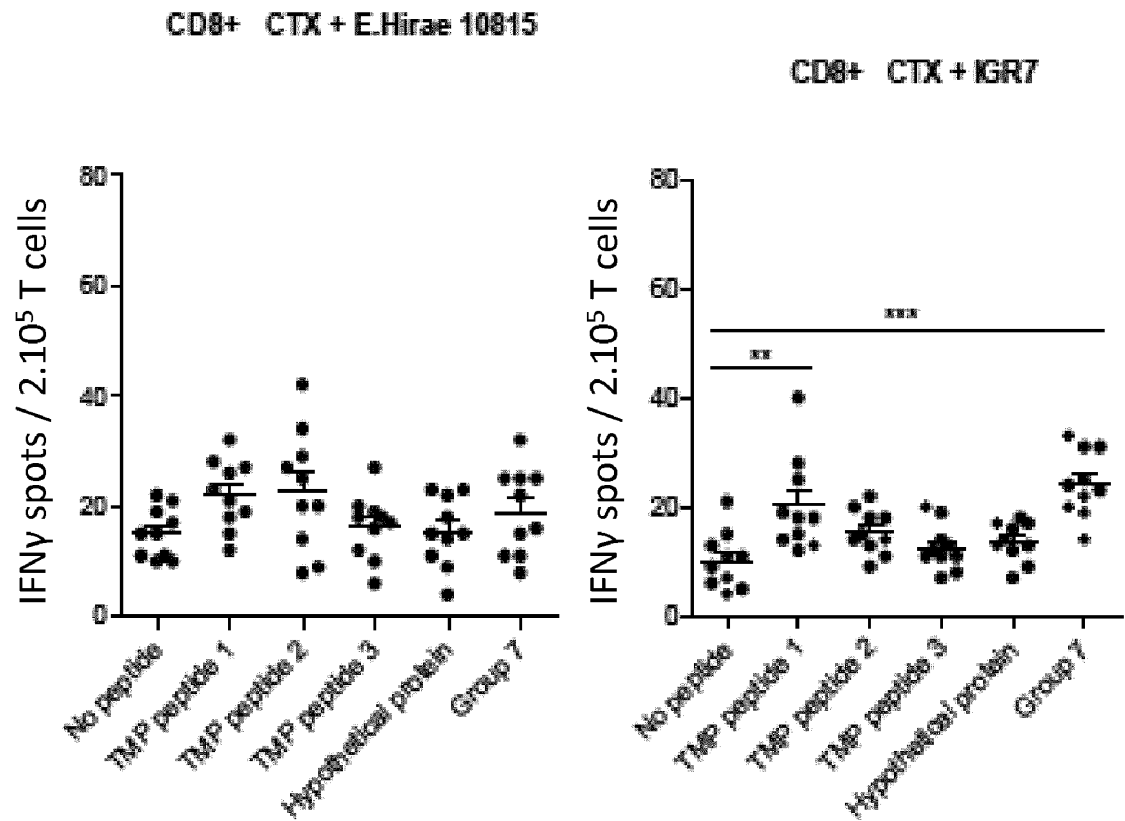
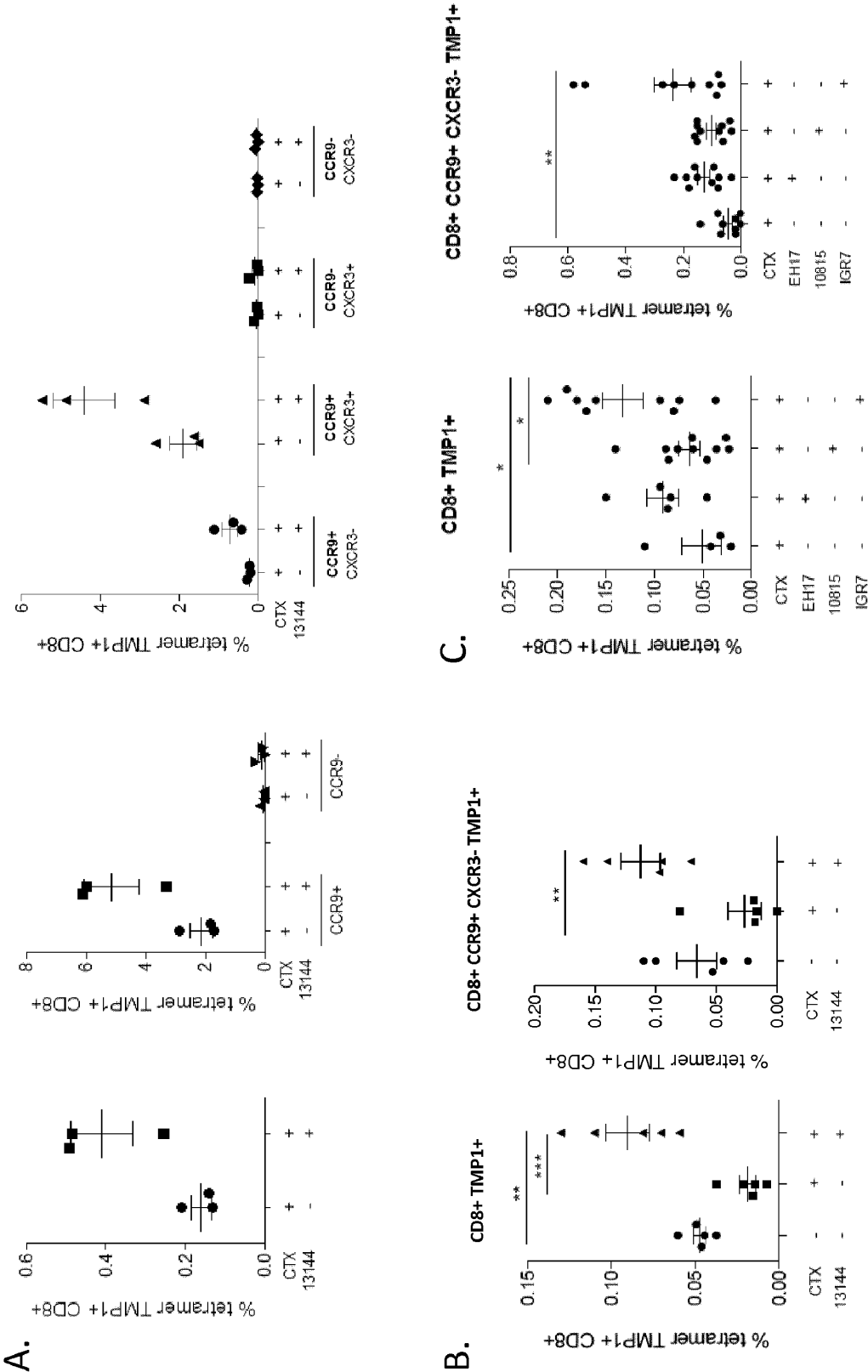
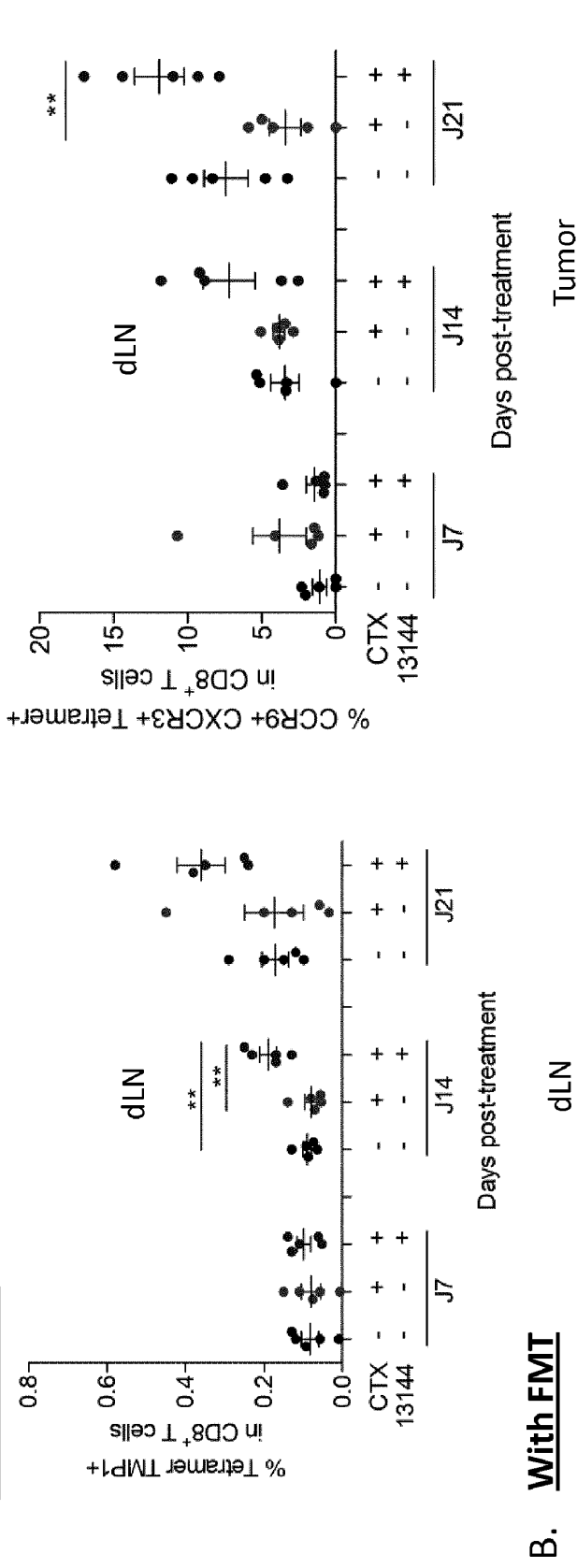


Figure 13E



A. Without FMT



B. With FMT

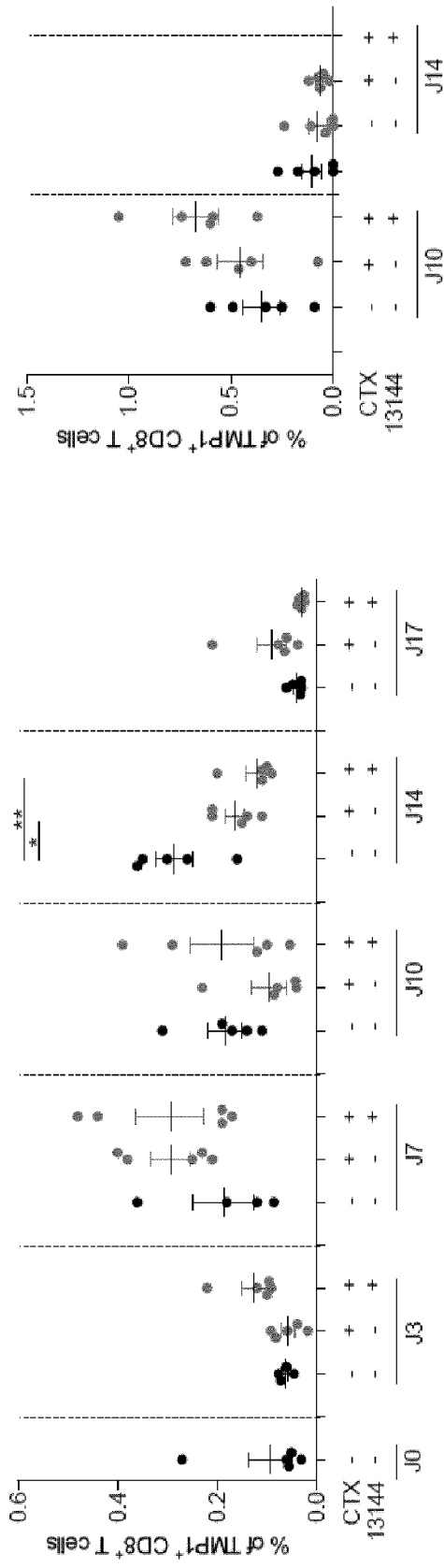


Figure 15

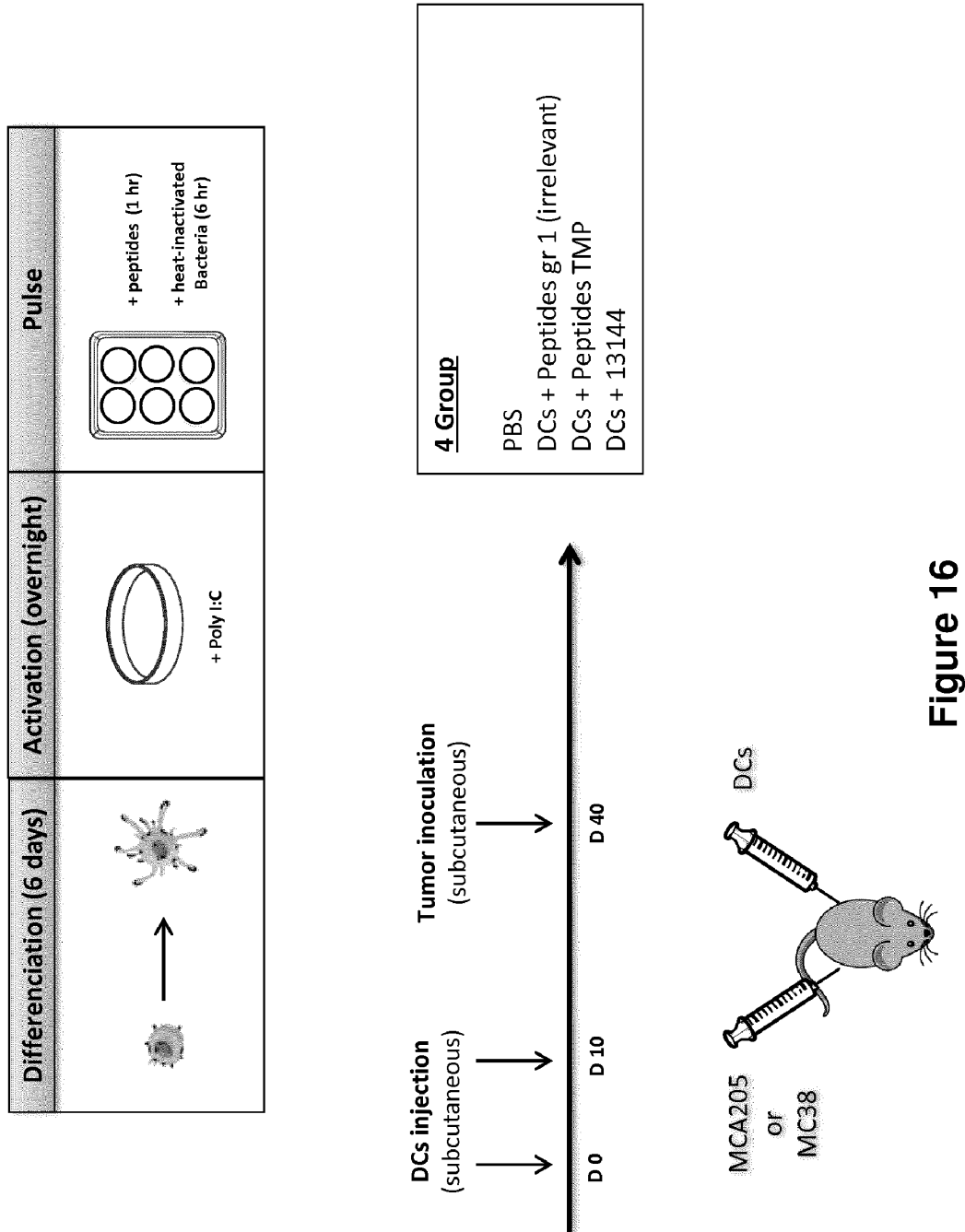


Figure 16

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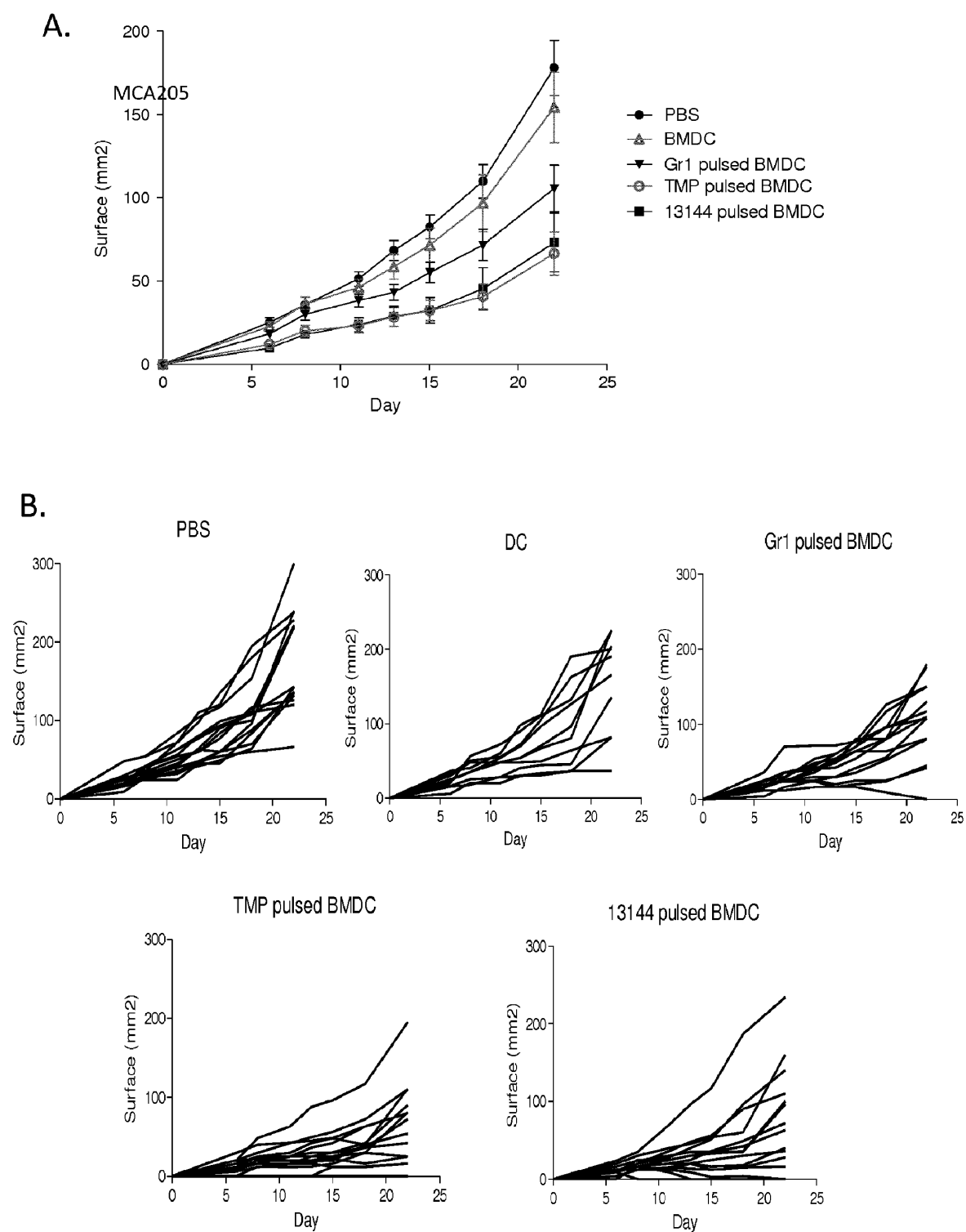
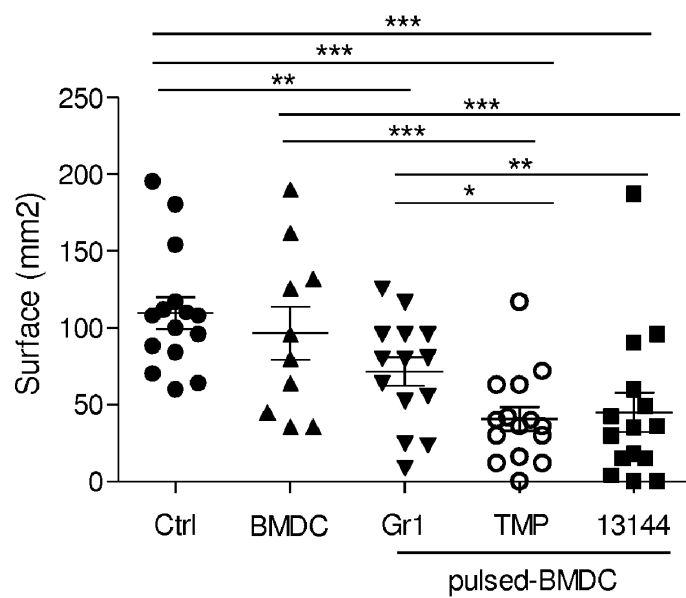


Figure 17A-B

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C.

Day 18



Day 22

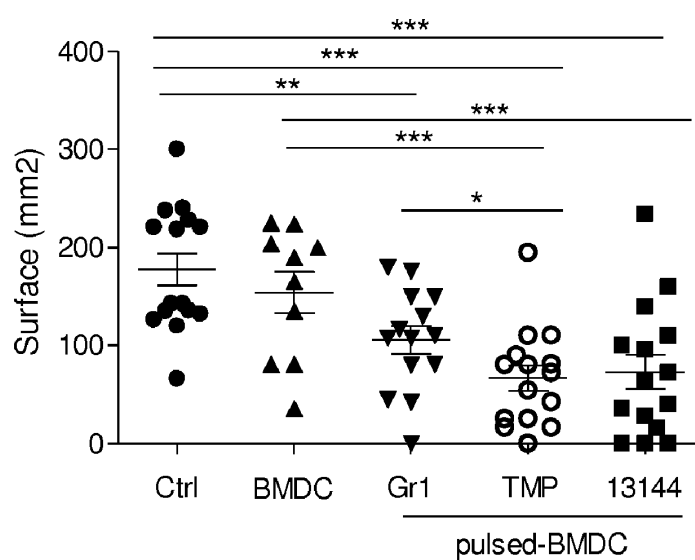


Figure 17C

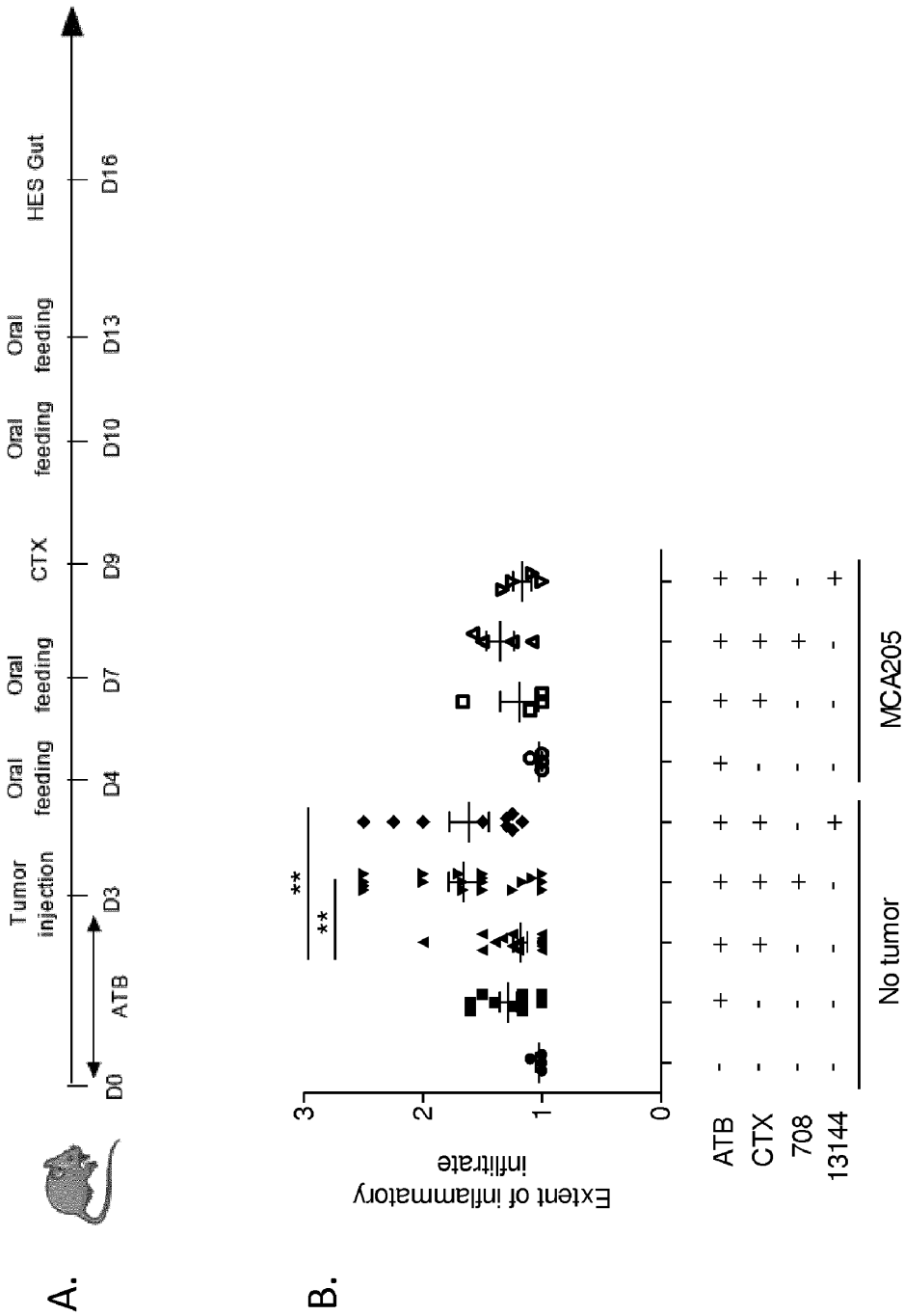
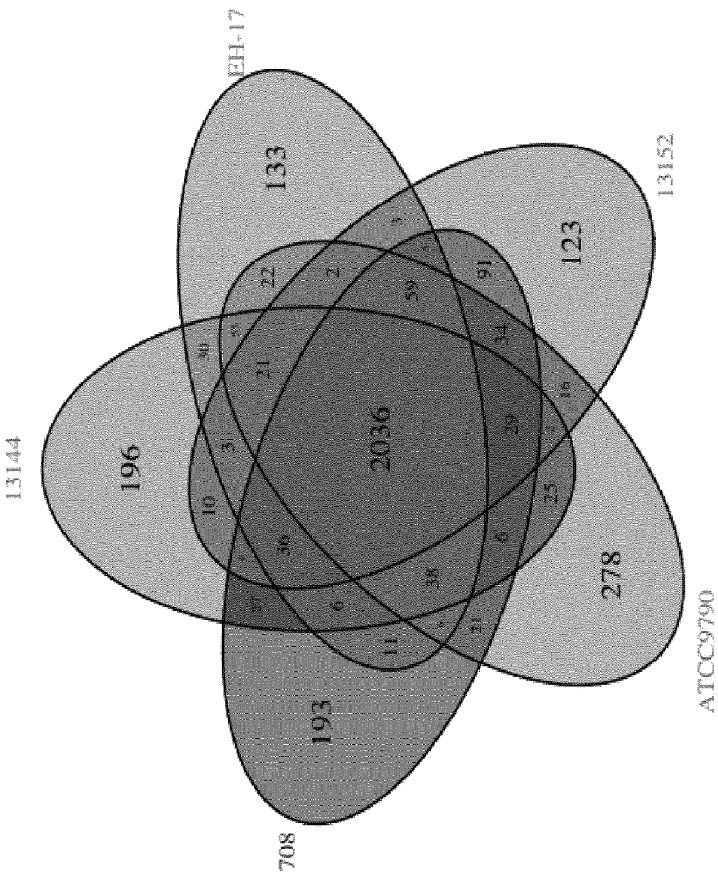


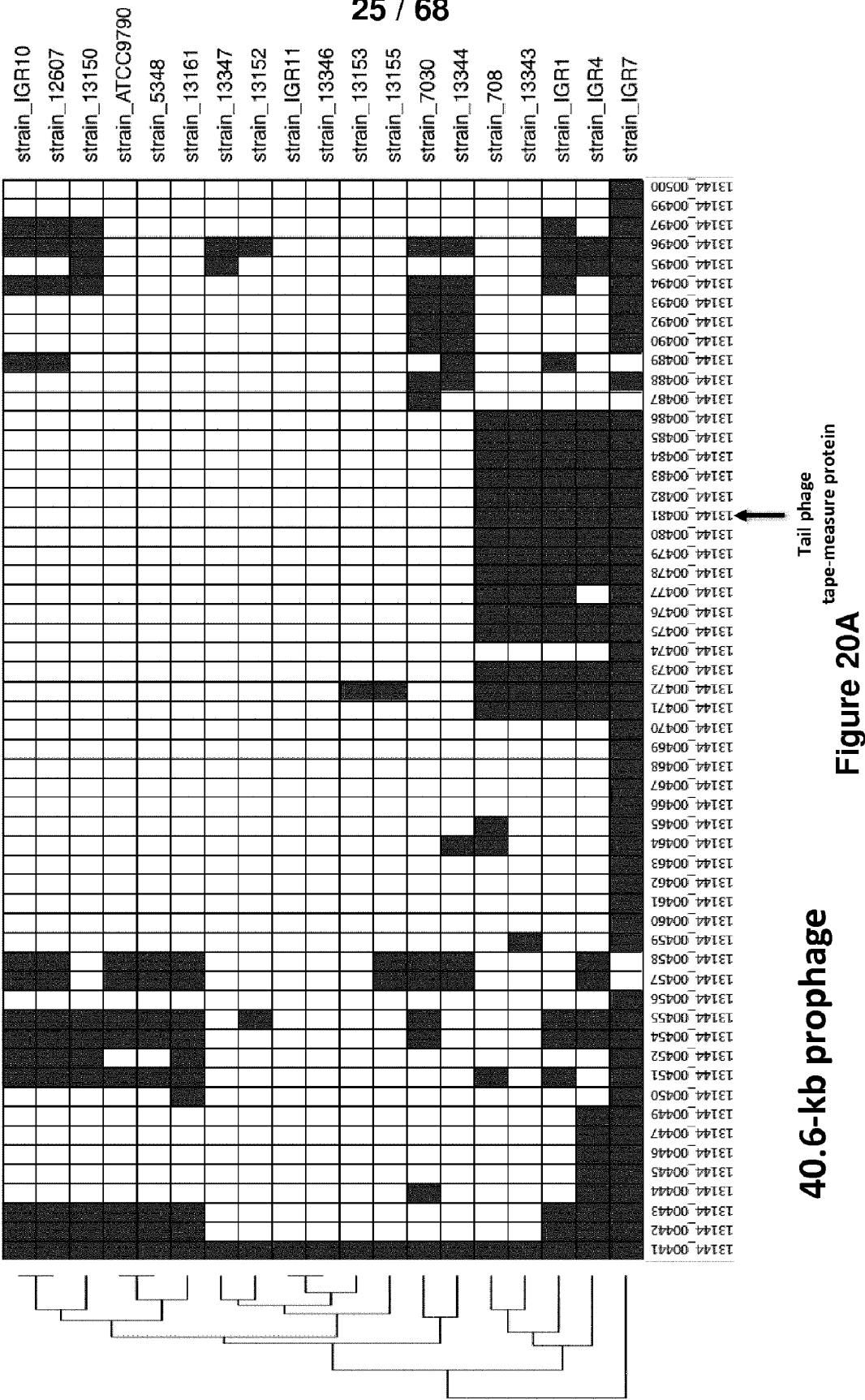
Figure 18

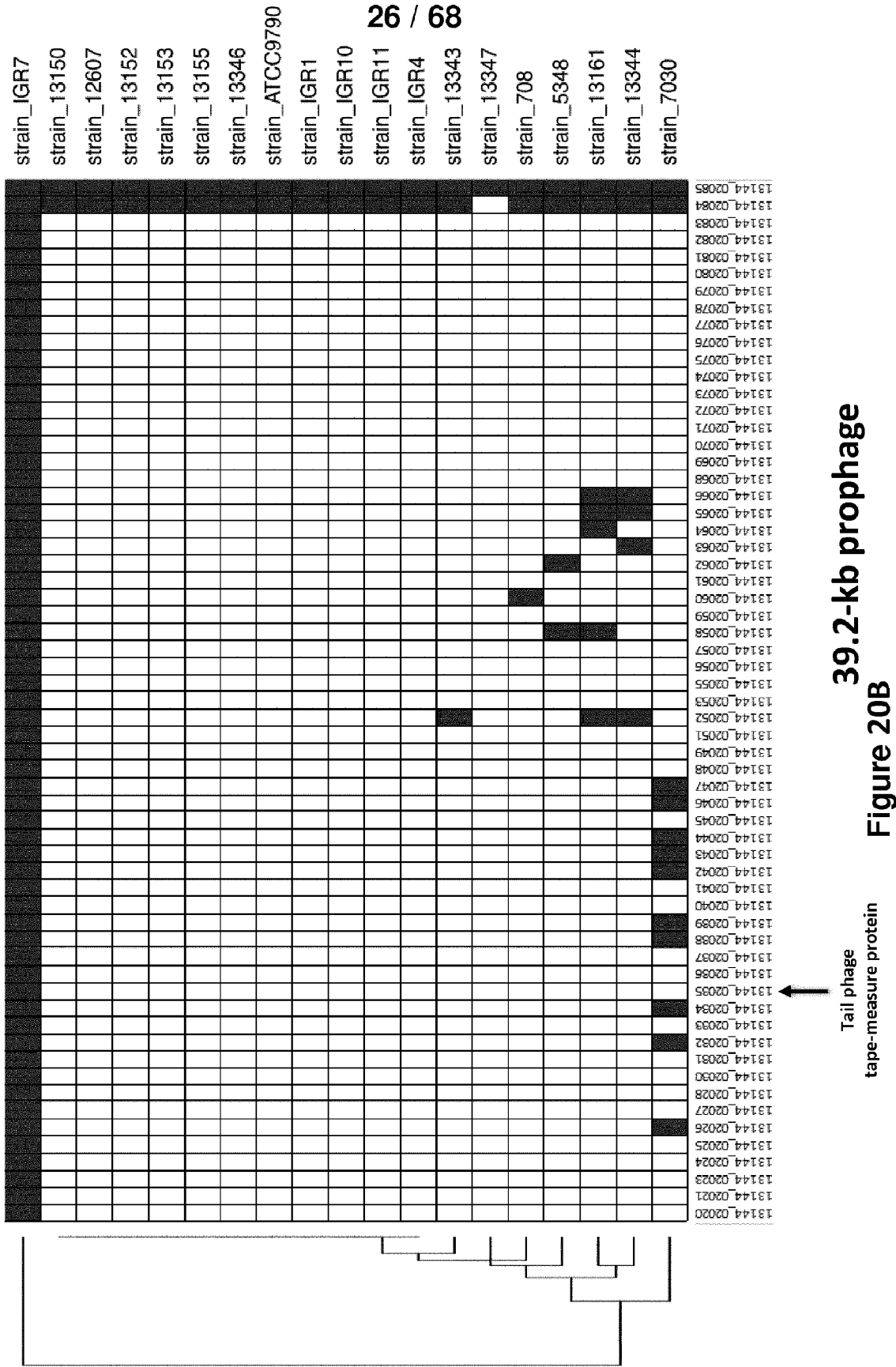


B.

Region	Region Length	Completeness	Score	# Total Proteins	Region Position	Most Common Phage	GC %
1	40.6Kb	intact	150	58	<u>481066-521729</u>	PHAGE_Entero_phiEf11_NC_013696(9)	33.79%
2	39.9Kb	questionable	70	26	<u>1748419-1788354</u>	PHAGE_Entero_phiFL2A_NC_013643(7)	34.24%
3	39.2Kb	intact	150	59	<u>2123983-2163272</u>	PHAGE_Staphy_CNPx_NC_031241(8)	34.95%

Figure 19





13144 Tape Measure protein

Figure 21

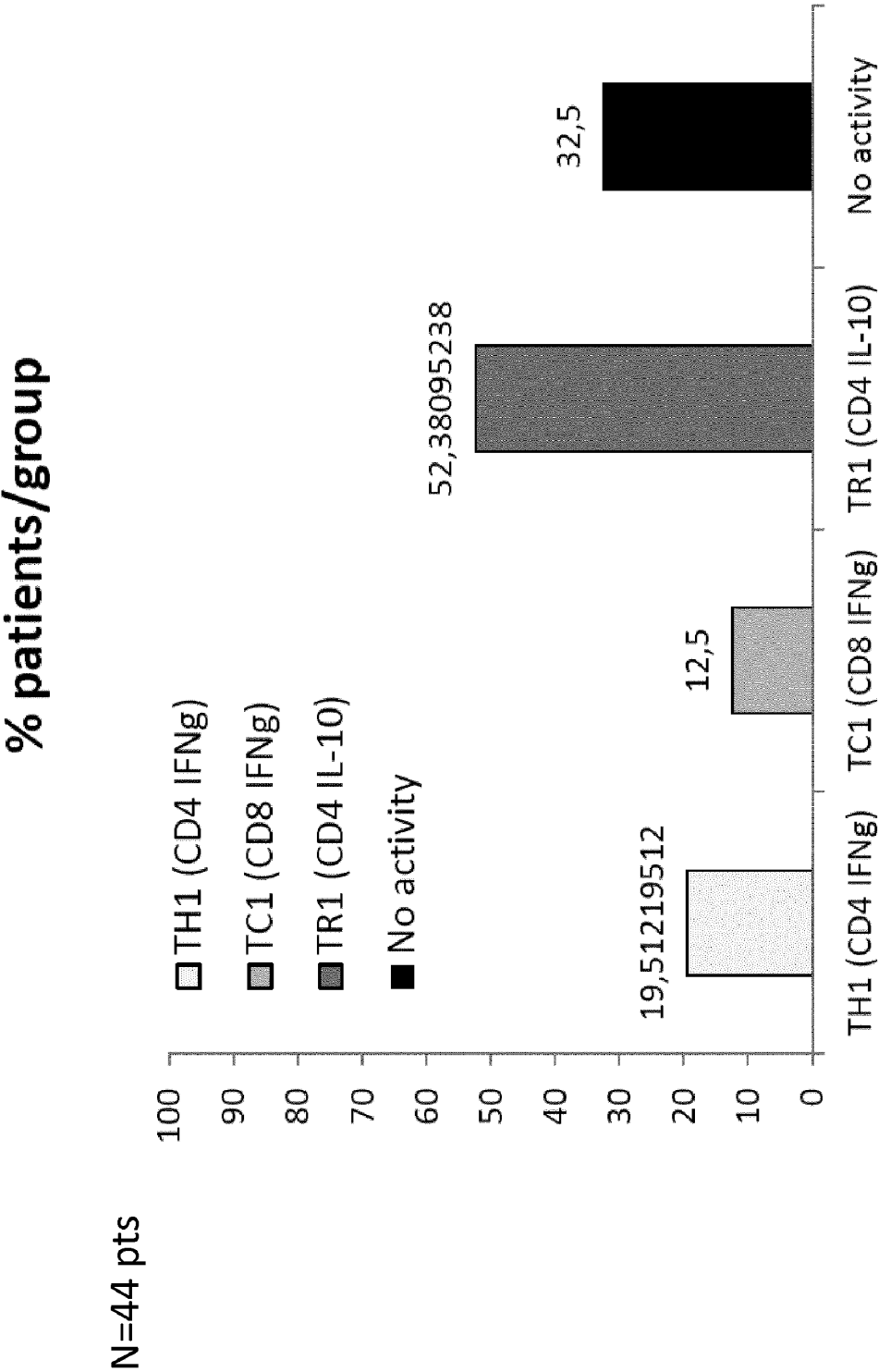
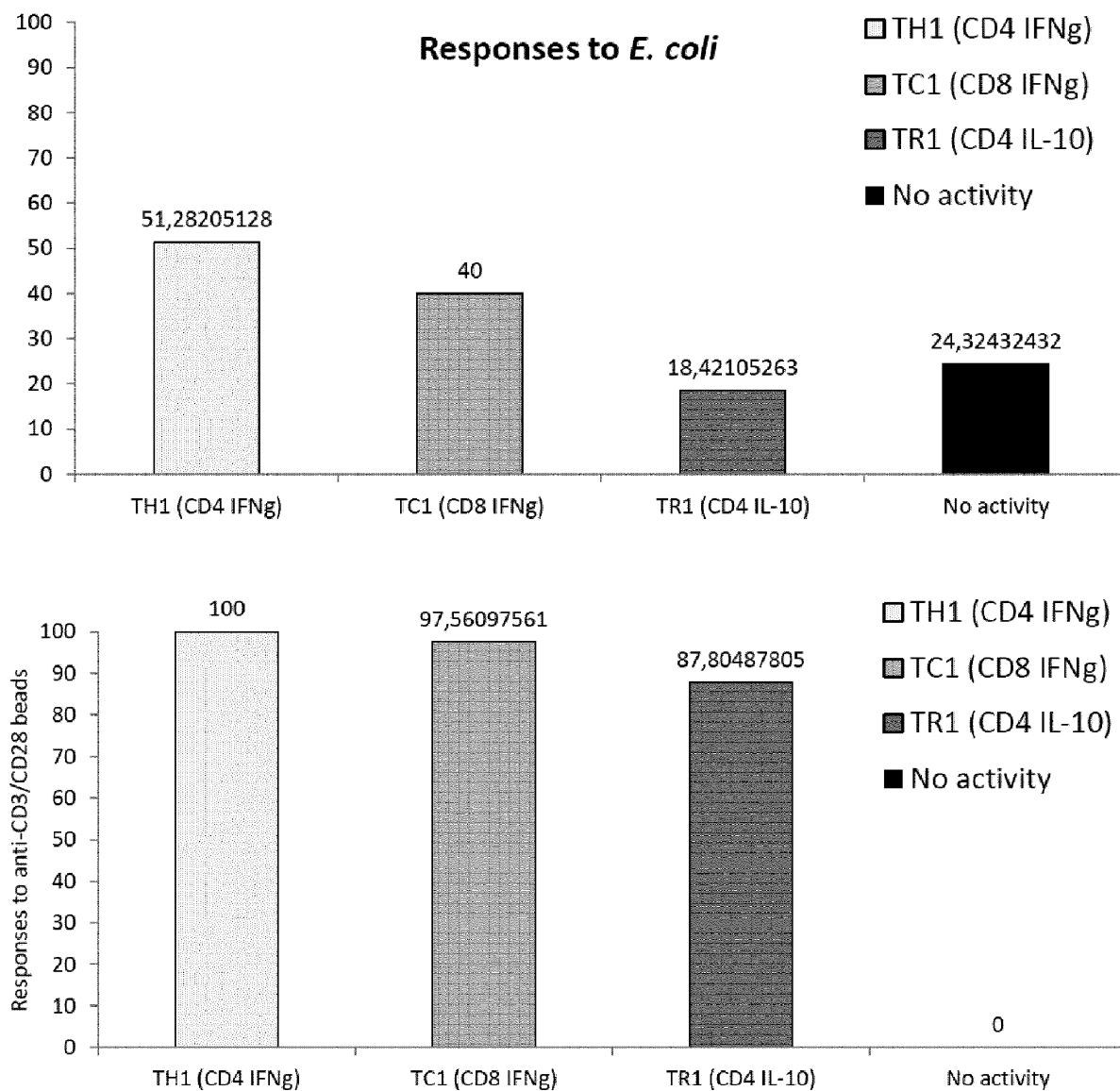


Figure 22A

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**Figure 22B**

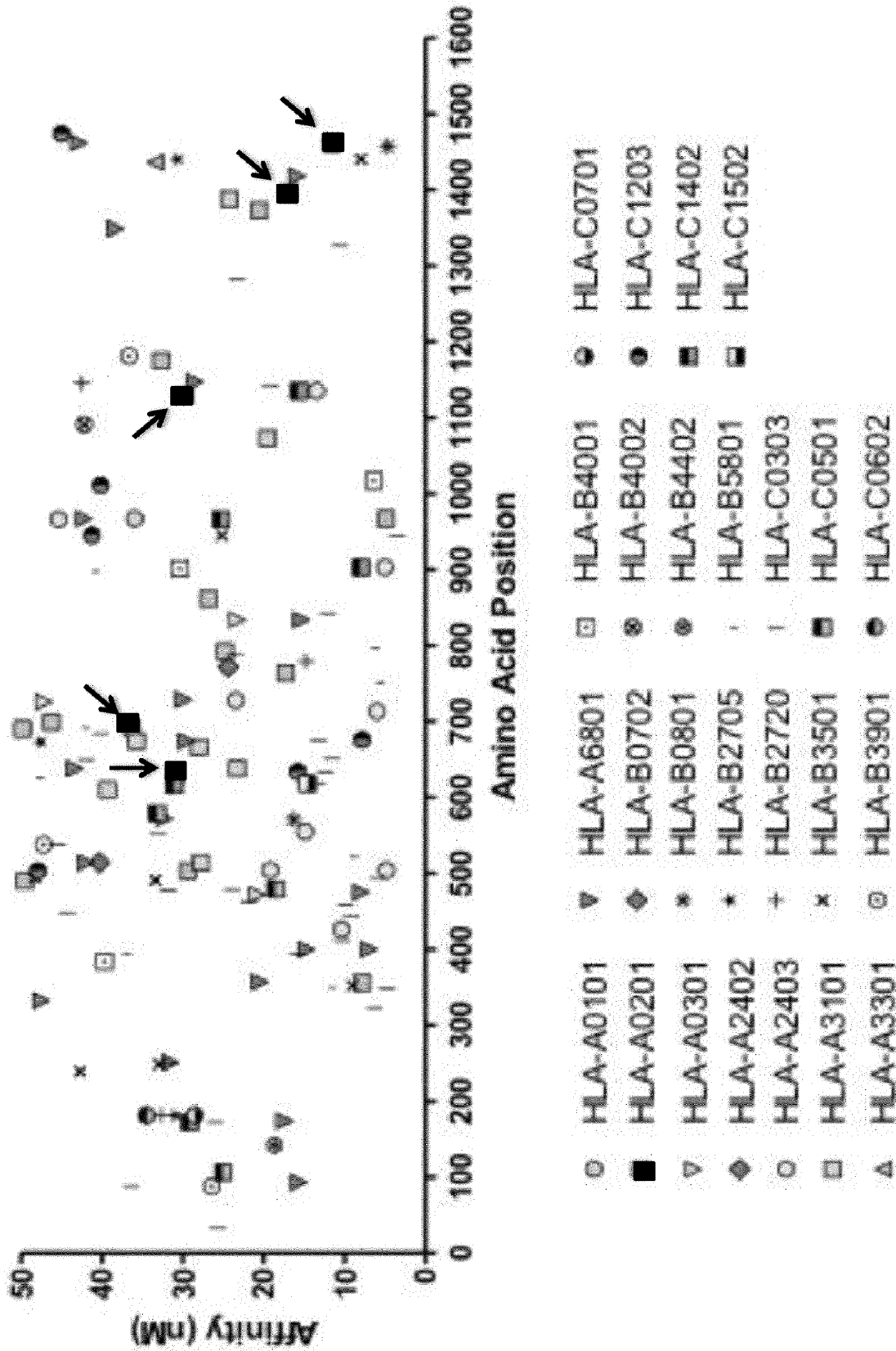
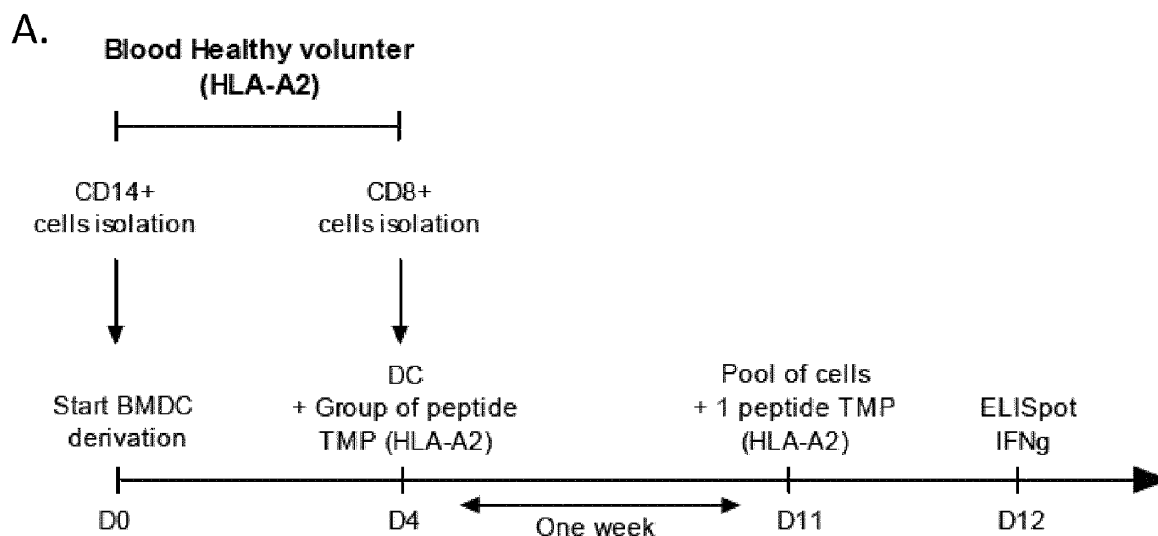


Figure 23

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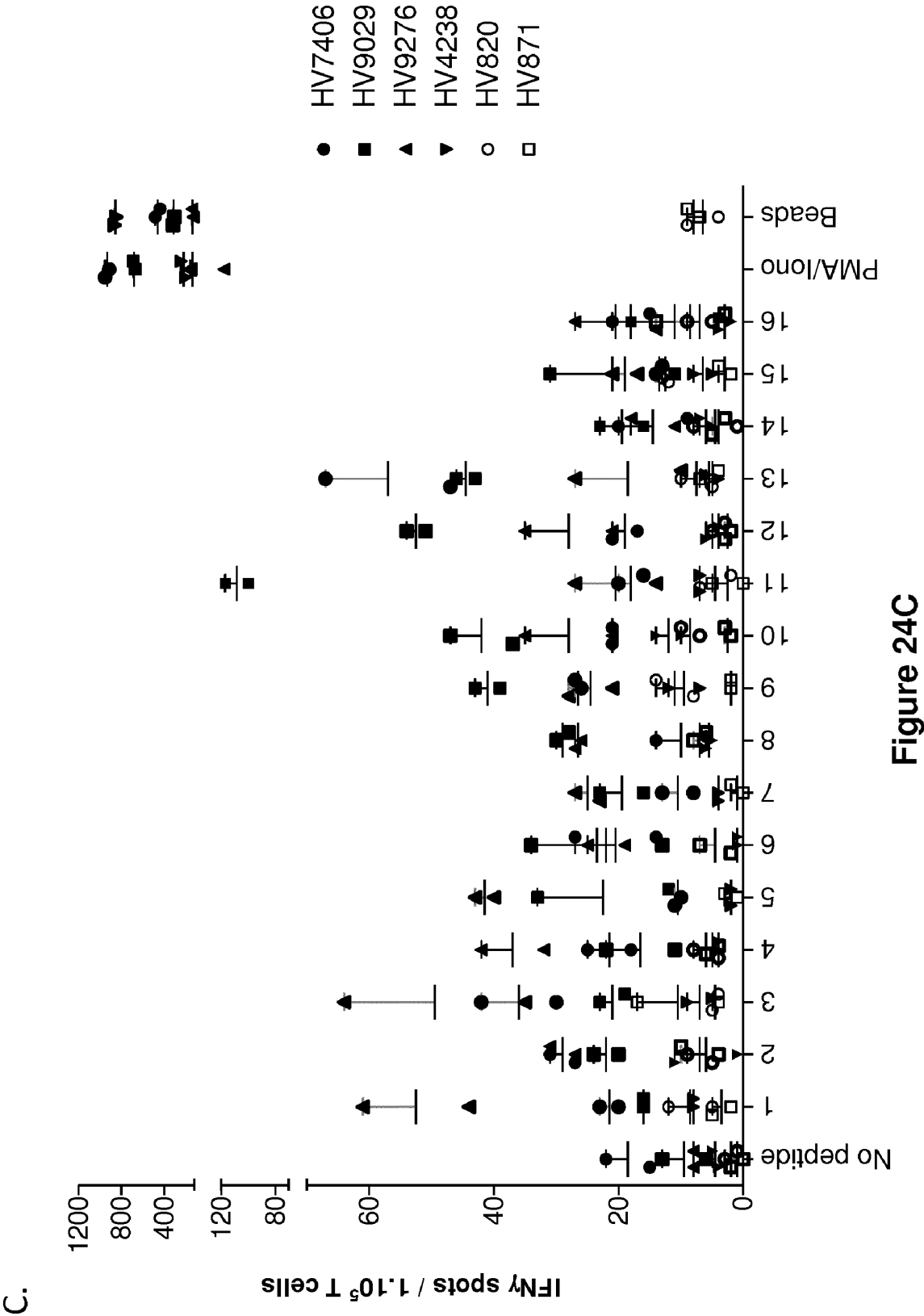


B.

n°peptide	Start	Stop	HLA	Peptide	Affinity(nM)
1	357	365	HLA-A0201	AMIEFIQGL	4,88
2	1462	1470	HLA-A0201	KMVEILEEI	7,8
3	1397	1405	HLA-A0201	RLLKYDVGCV	11,55
4	765	773	HLA-A0201	TLVGVTFAI	16,94
5	1374	1382	HLA-A0201	AMQNLVAAV	17,32
6	793	801	HLA-A0201	AIMAIANGV	20,56
7	862	870	HLA-A0201	AMSMNMEEV	24,83
8	504	512	HLA-A0201	KVFGKMTSV	26,84
9	1130	1138	HLA-A0201	LLGIYQSYV	29,4
10	631	639	HLA-A0201	KLAKFASVV	29,89
11	1176	1184	HLA-A0201	KLWANMSKA	30,99
12	692	700	HLA-A0201	MLSNPITAI	32,68
13	700	708	HLA-A0201	ILVAITTTI	36,32
14	491	499	HLA-A0201	KMAALAASA	46,27
15	691	699	HLA-A0201	AMLSNPITA	49,58
16	473	481	HLA-A0201	NMAEAFASA	49,85

Figure 24A-B

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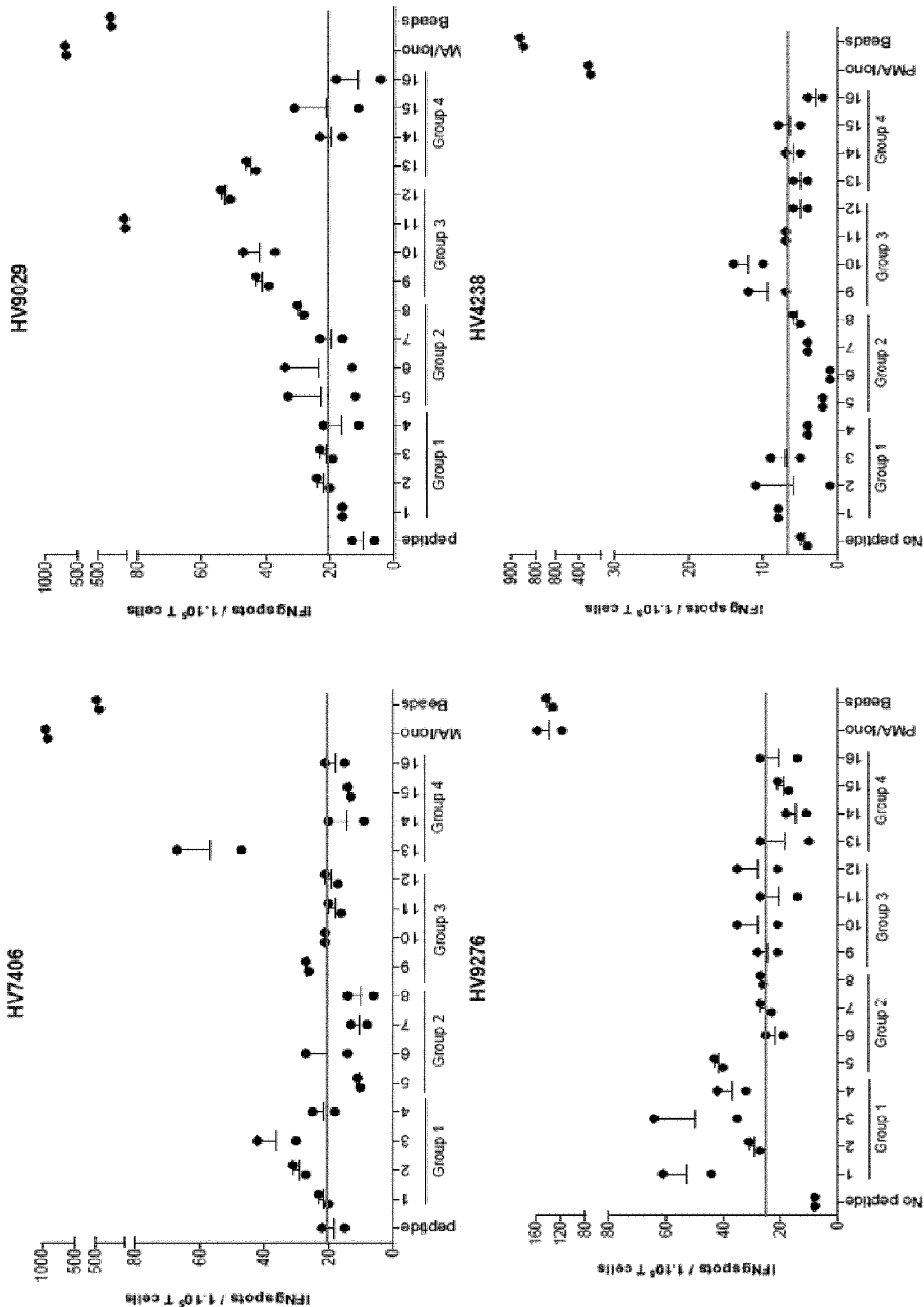


Figure 24D

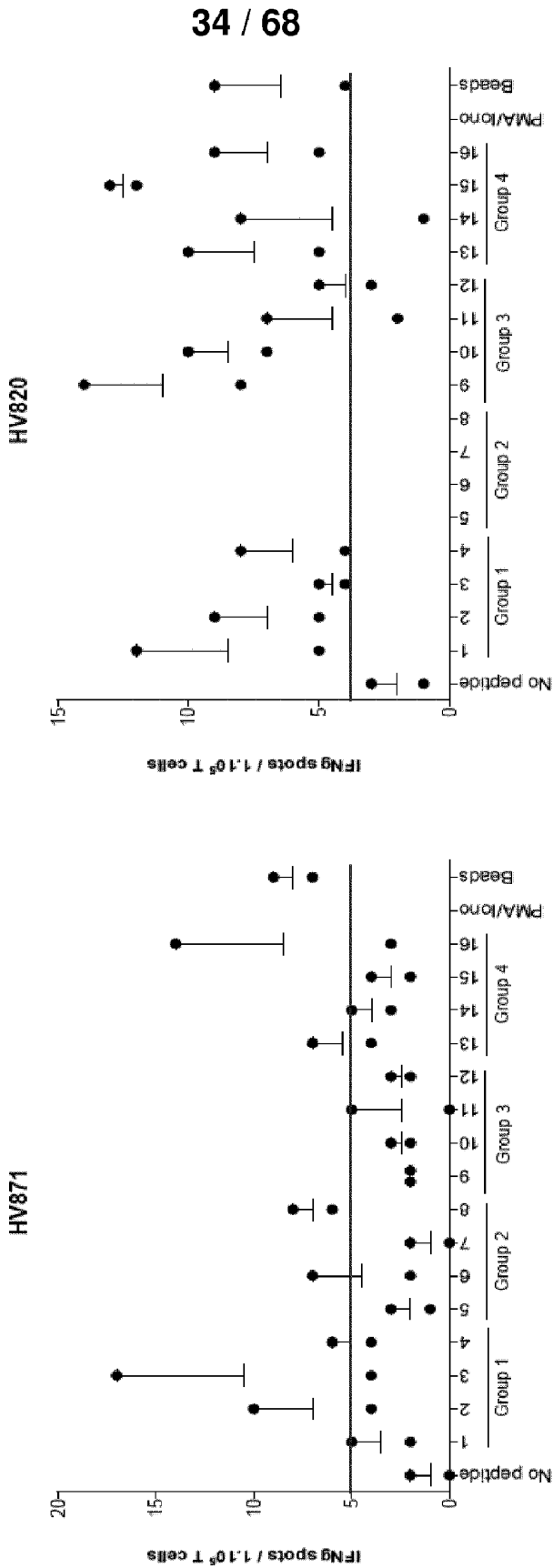


Figure 24D (Following)

E.

		Number of positive well							% responders
		HV4238	HV7406	HV9029	HV9276	HV871	HV820	TOTAL	
Peptides TMP (HLA-A2)	1	2	0	0	2	0	1	5	50
	2	1	2	0	2	1	1	7	83,33
	3	1	2	0	2	1	0	6	66,66
	4	0	0	0	2	1	1	4	50
	5	0	0	1	2	0	0	3	33,33
	6	0	1	1	0	1	0	3	50
	7	0	0	0	0	0	0	0	16,66
	8	0	0	2	0	2	0	4	33,33
	9	2	2	2	0	0	2	8	66,66
	10	2	0	2	1	0	2	7	66,66
	11	0	0	2	0	0	1	3	33,33
	12	0	0	2	1	0	0	3	33,33
	13	0	2	2	0	1	1	6	66,66
	14	0	0	0	0	0	1	1	16,66
	15	0	0	1	0	0	2	3	33,33
	16	0	0	0	0	1	1	2	33,33

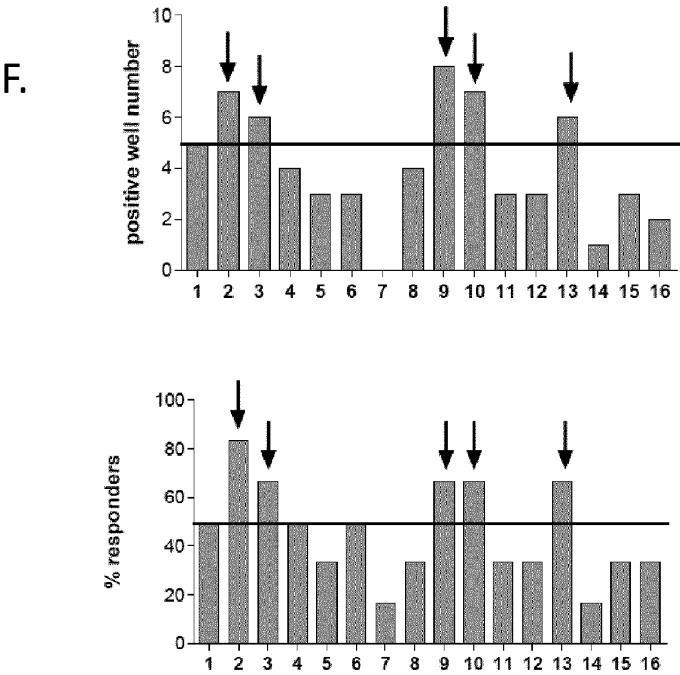


Figure 24E-F

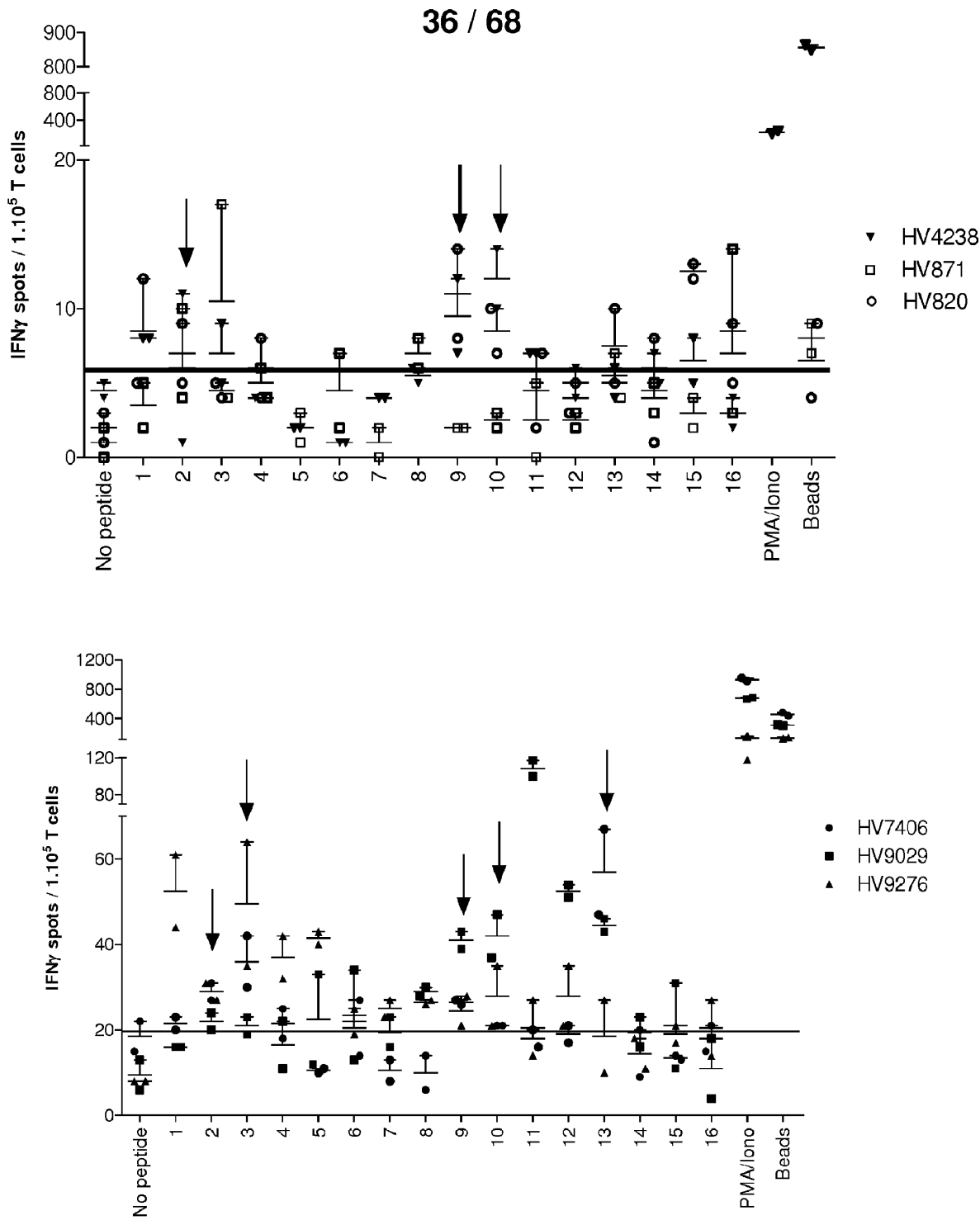


Figure 24G

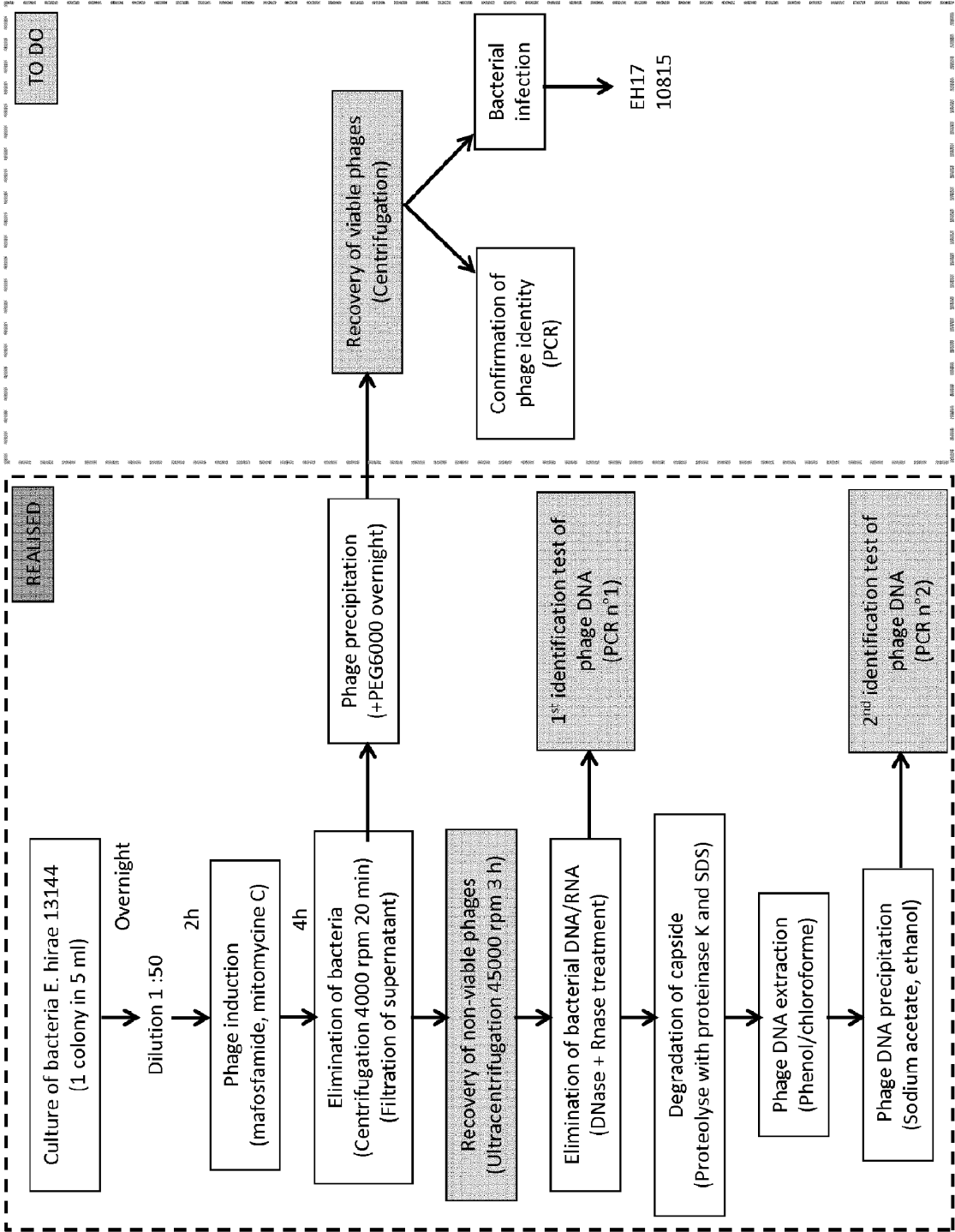


Figure 25

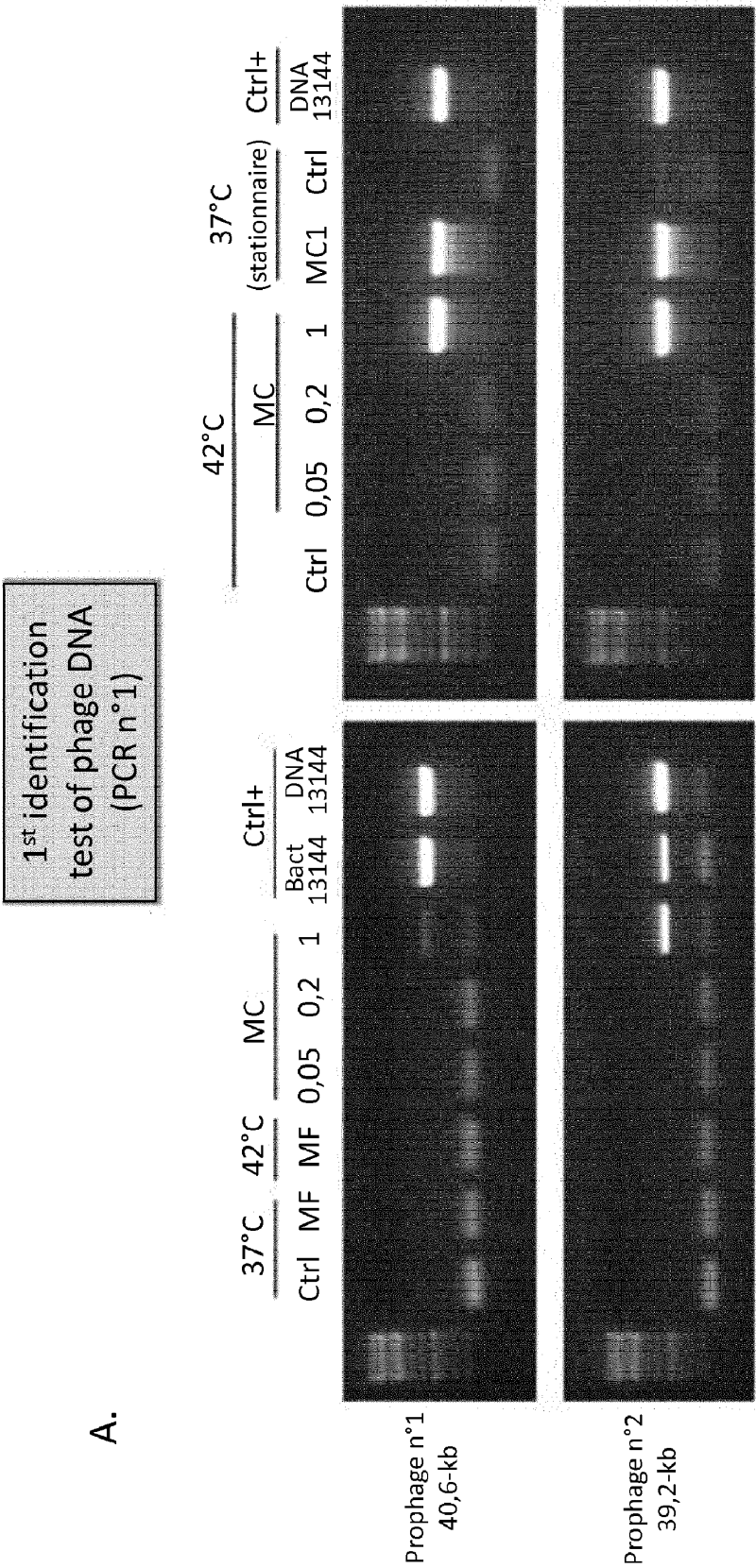


Figure 26A

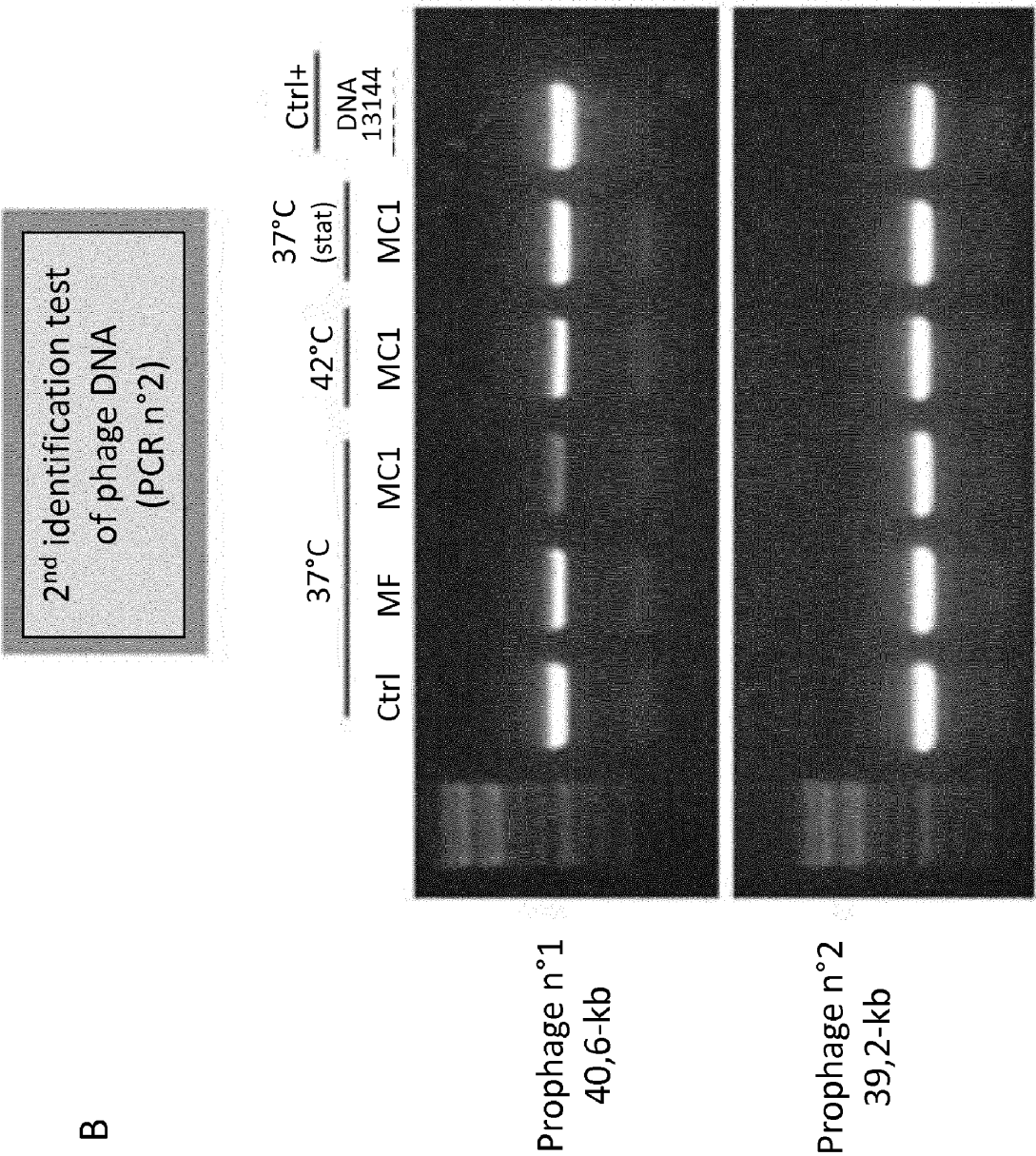


Figure 26B

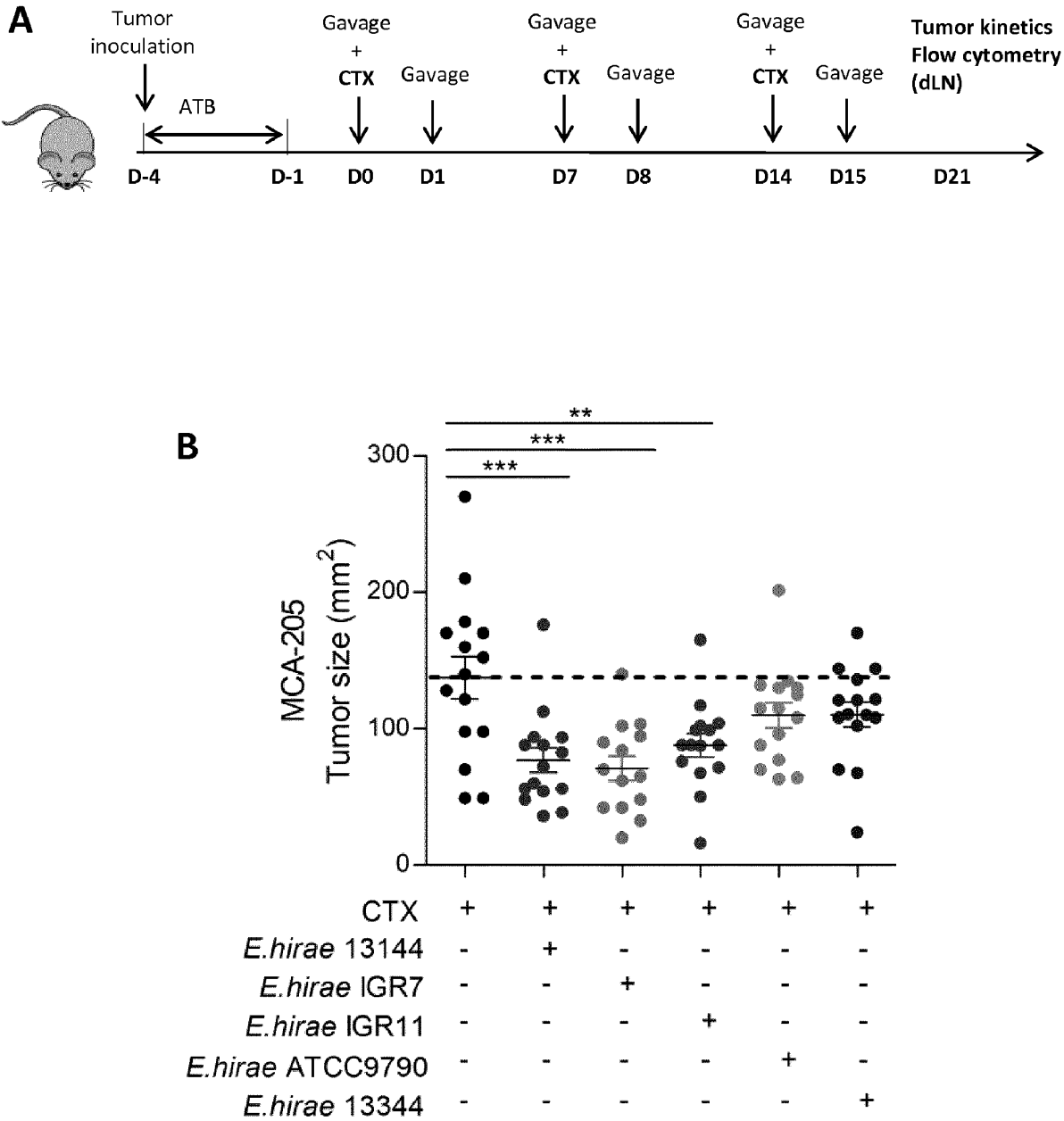


Figure 27A-B

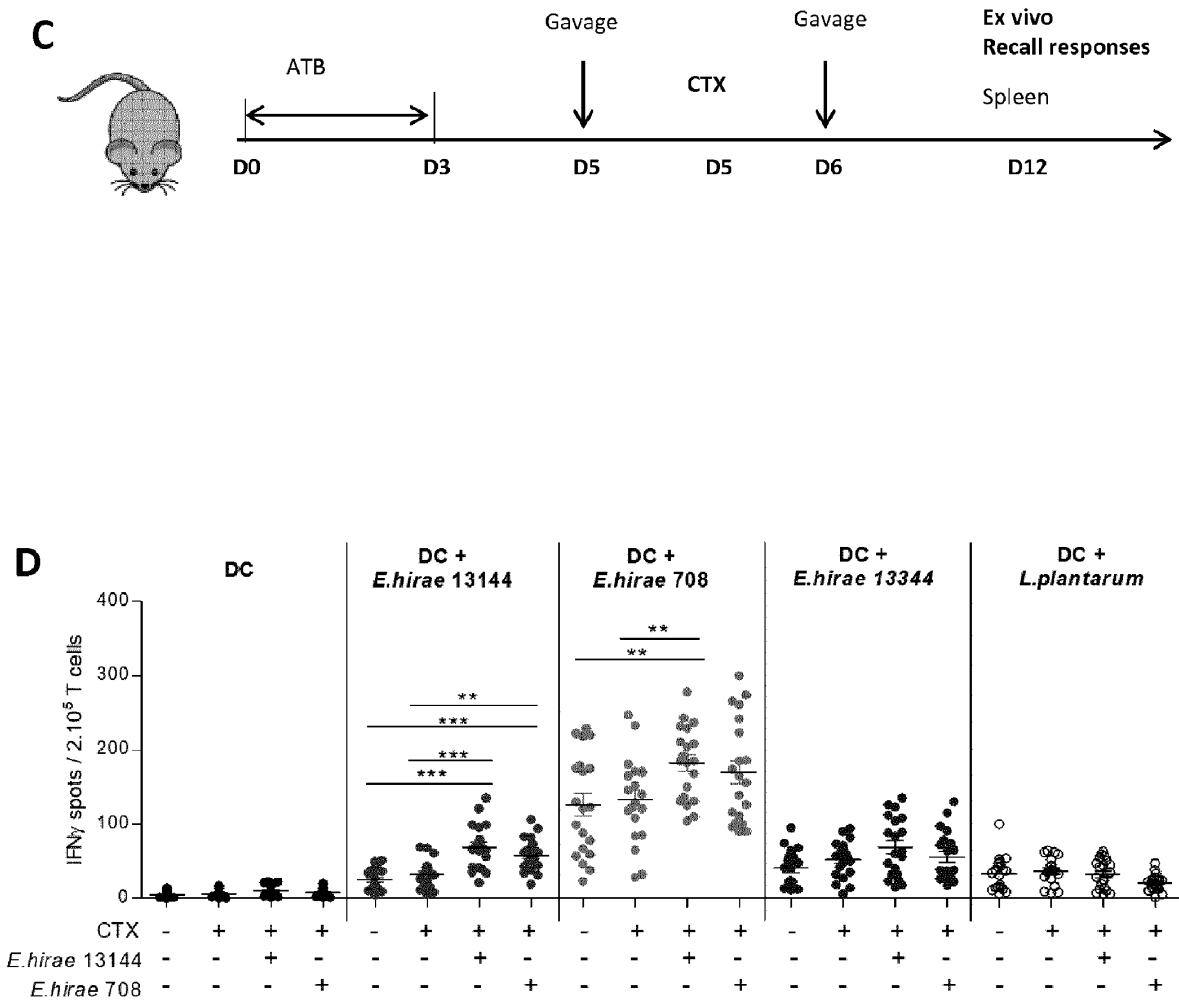


Figure 27C-D

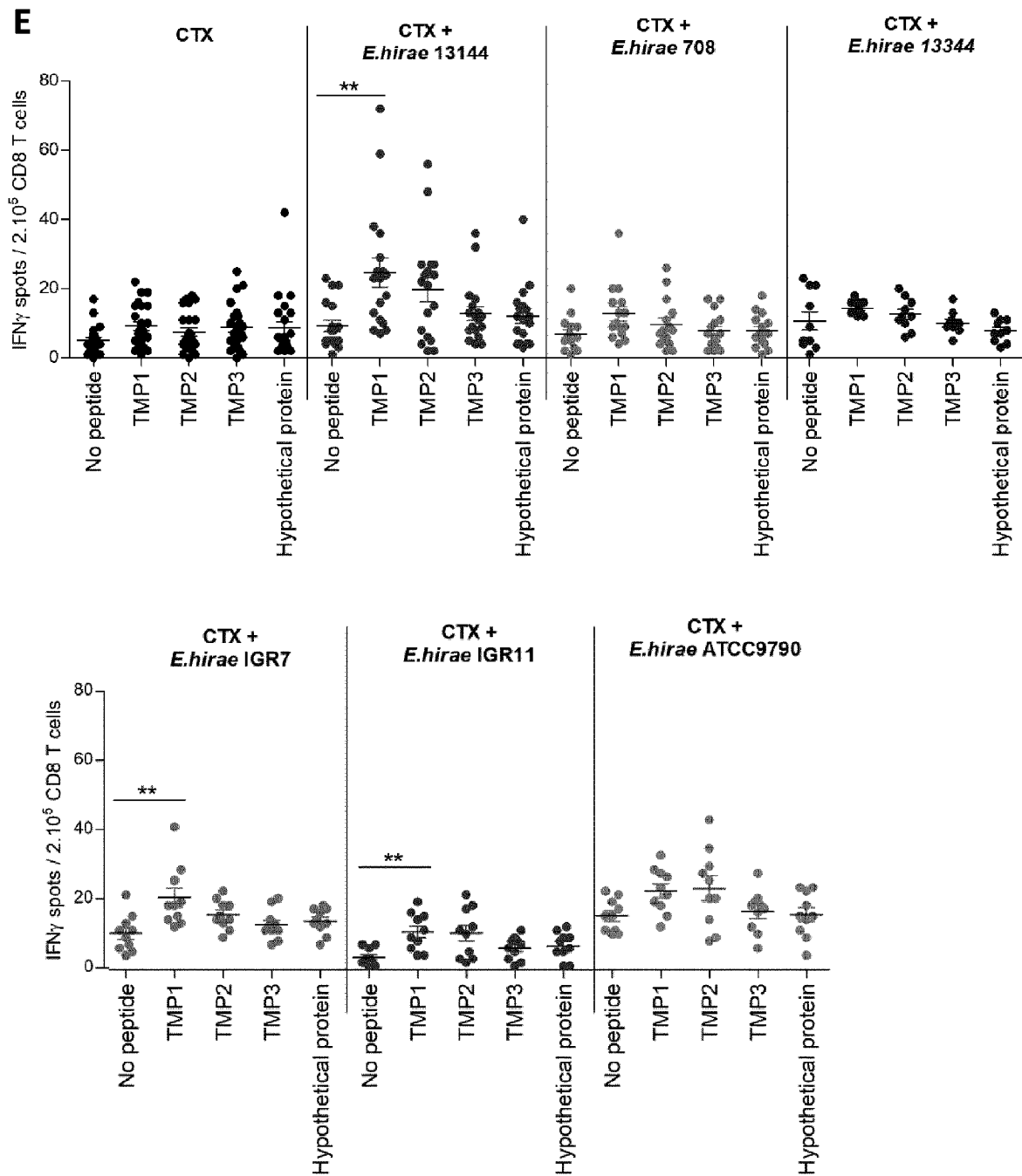


Figure 27E

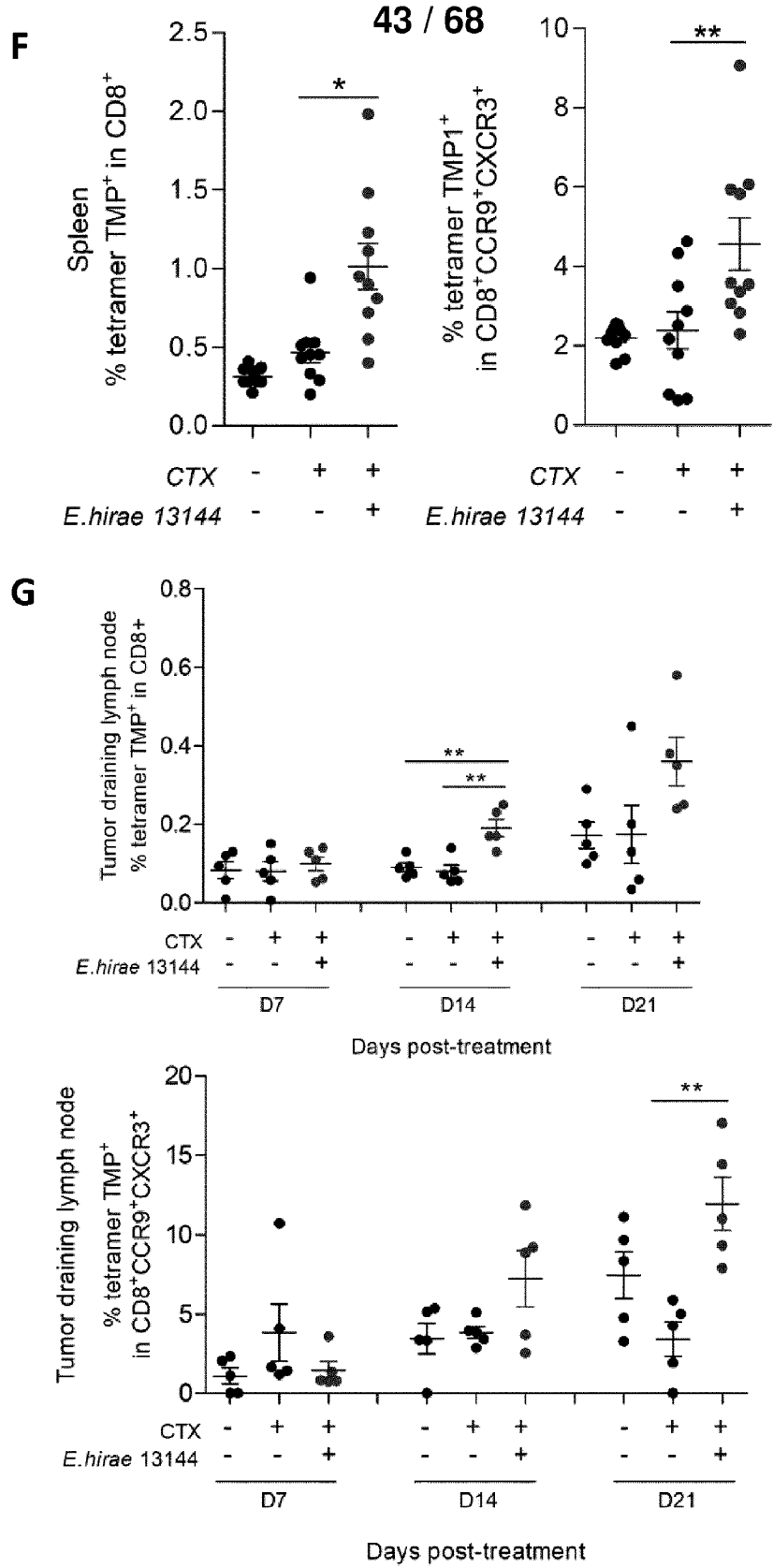


Figure 27F-G

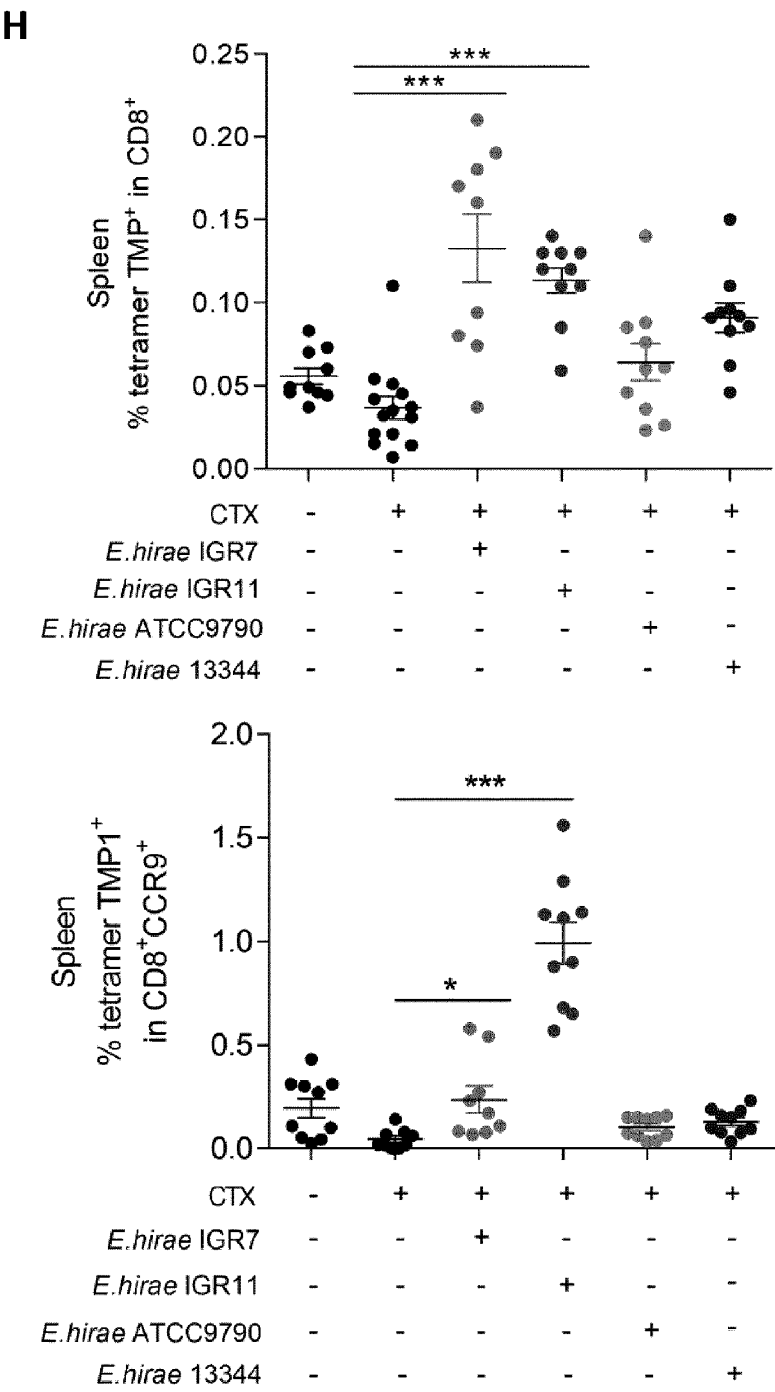
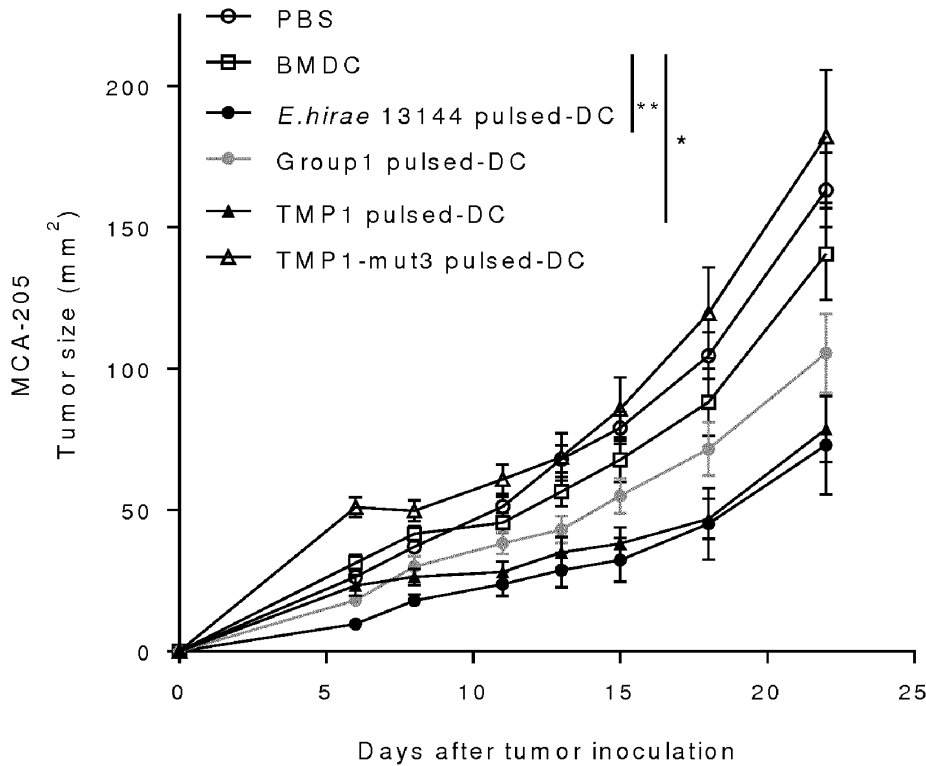


Figure 27H

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TMP1-mut2 (mutation in position 2)
=> TSLARFANI to TALARFANI
TMP1-mut3 (mutation in position 3)
=> TSLARFANI to TSFARFANI

A



B

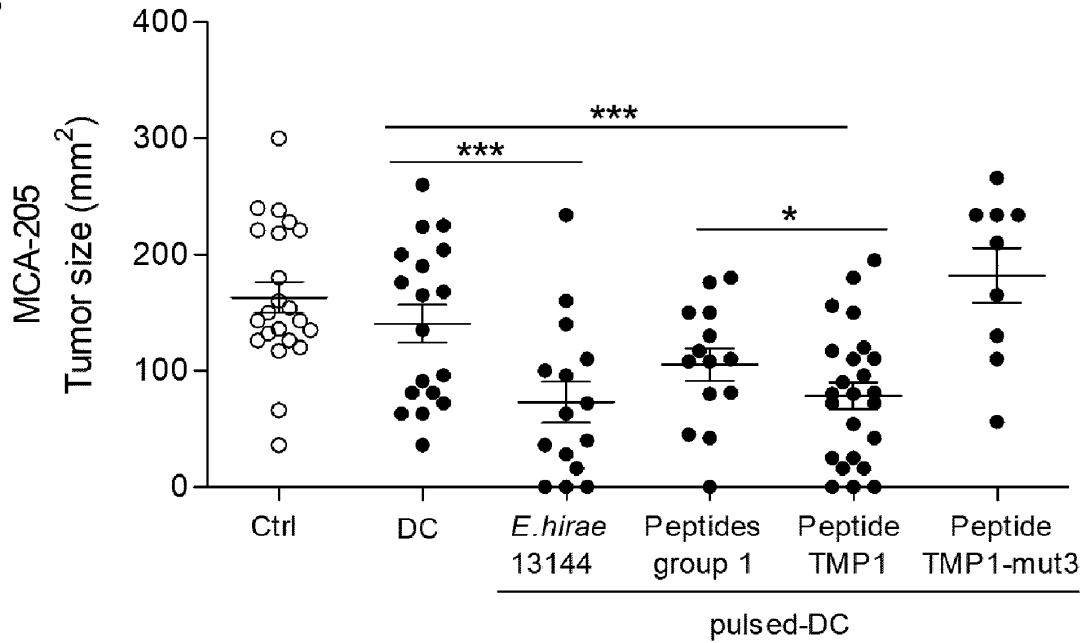
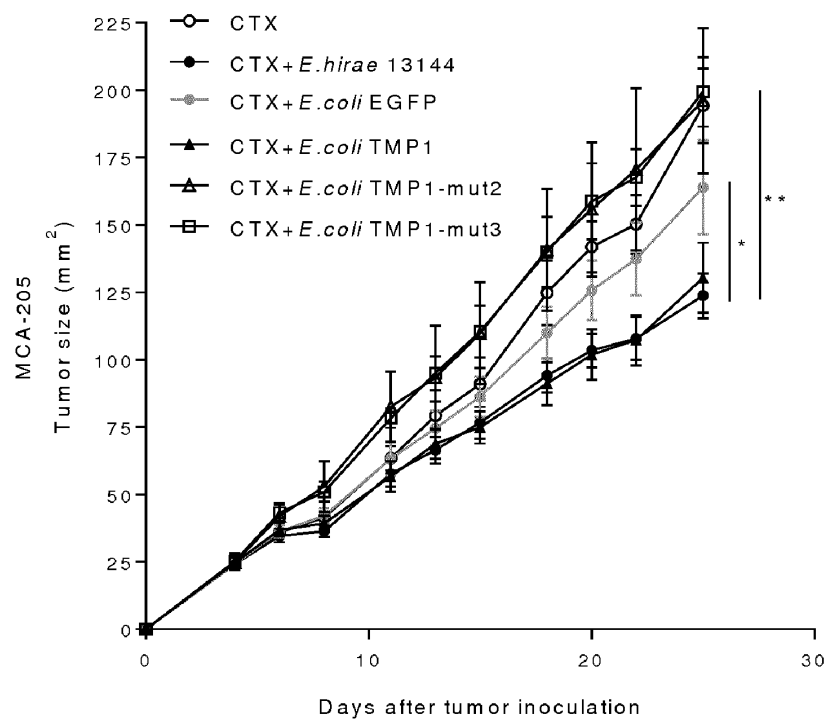


Figure 28A-B

C



Day 25

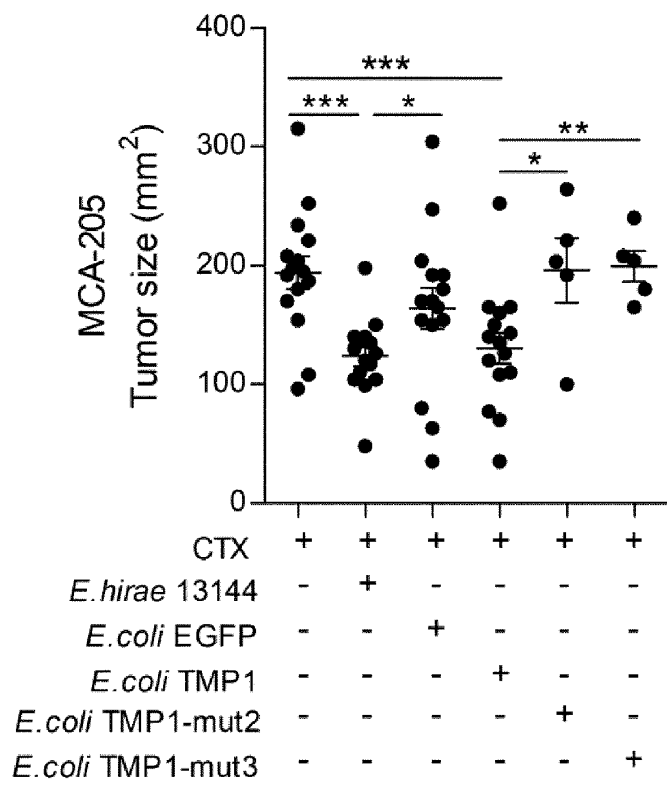


Figure 28C

D

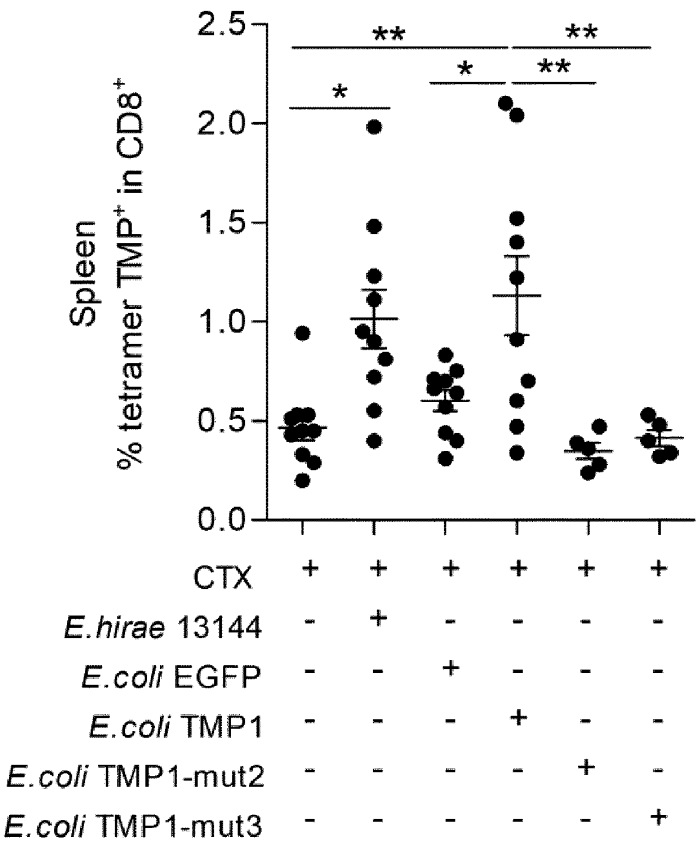


Figure 28D

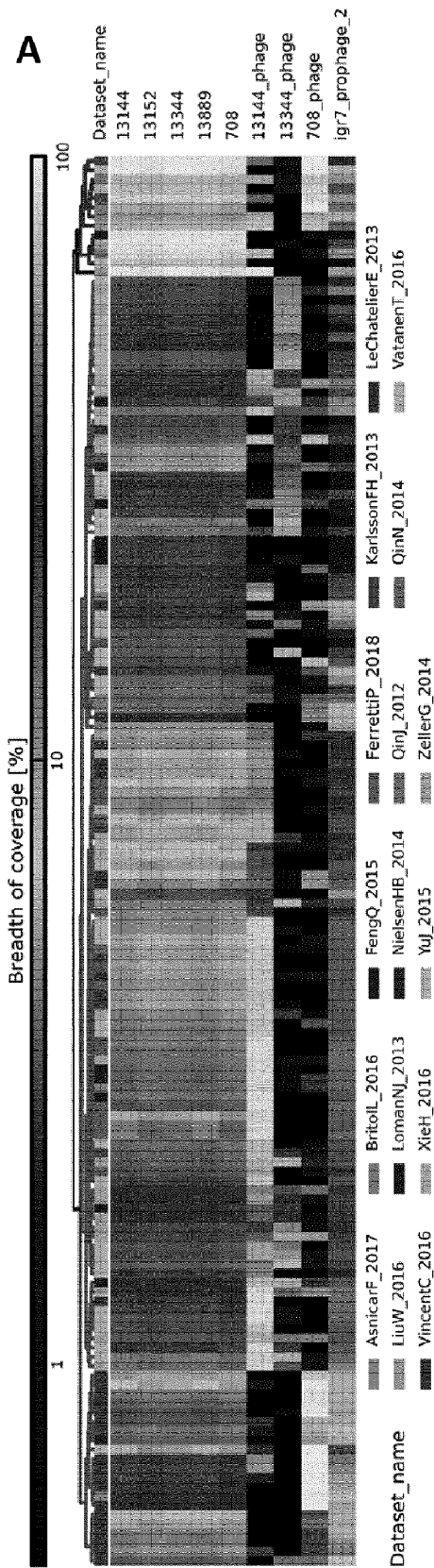


Figure 29A

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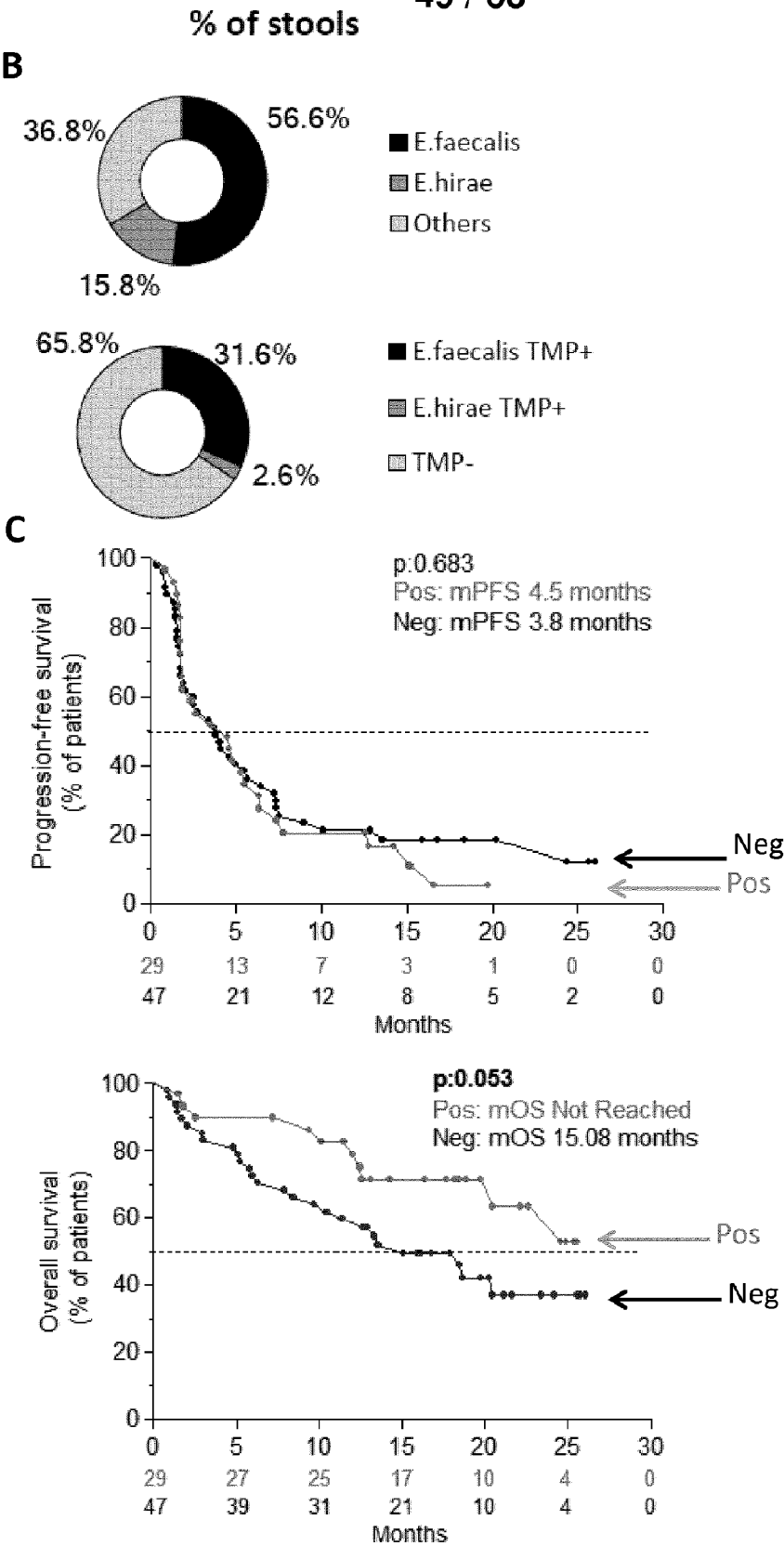


Figure 29B-C

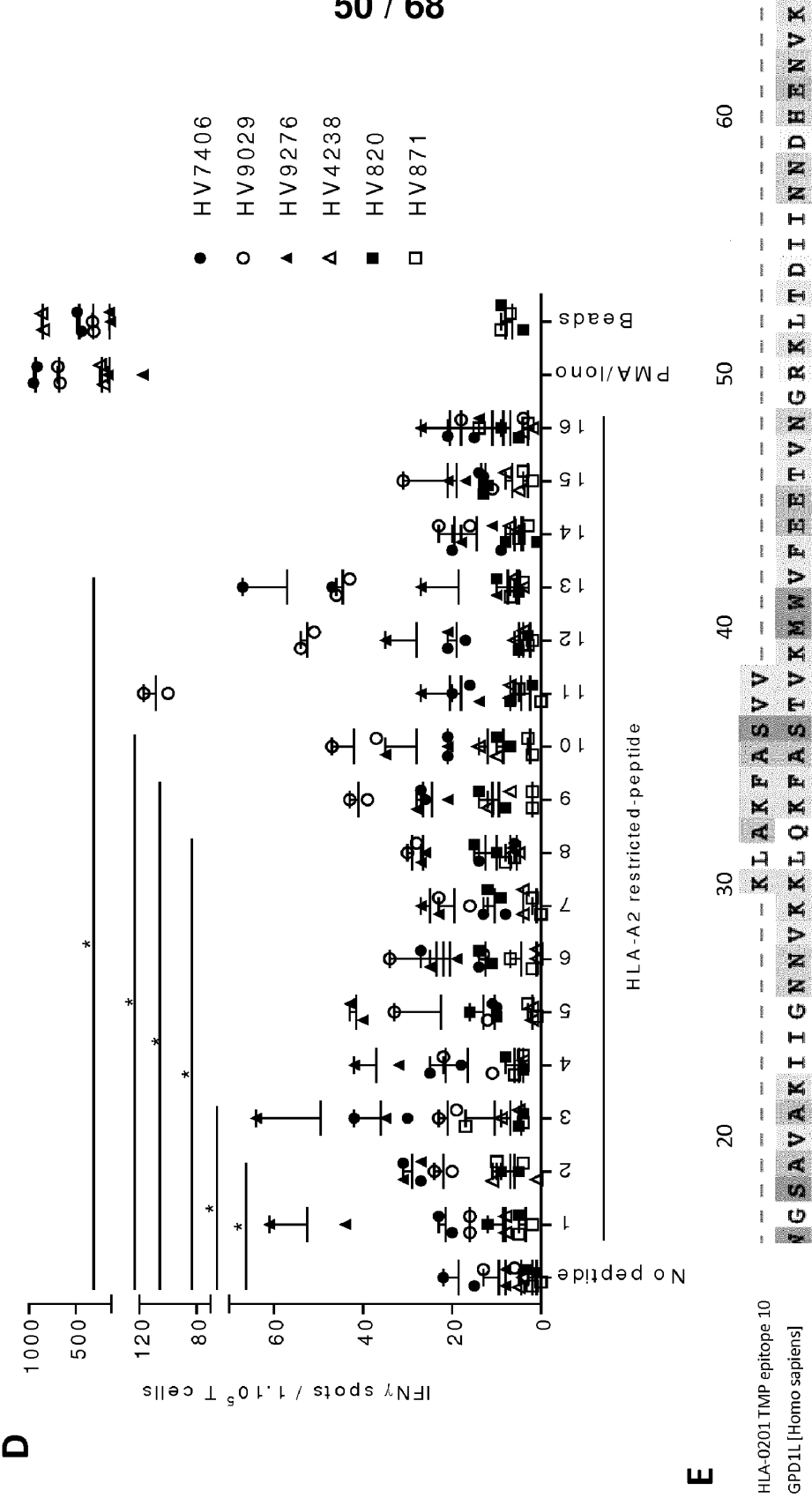


Figure 29D-E

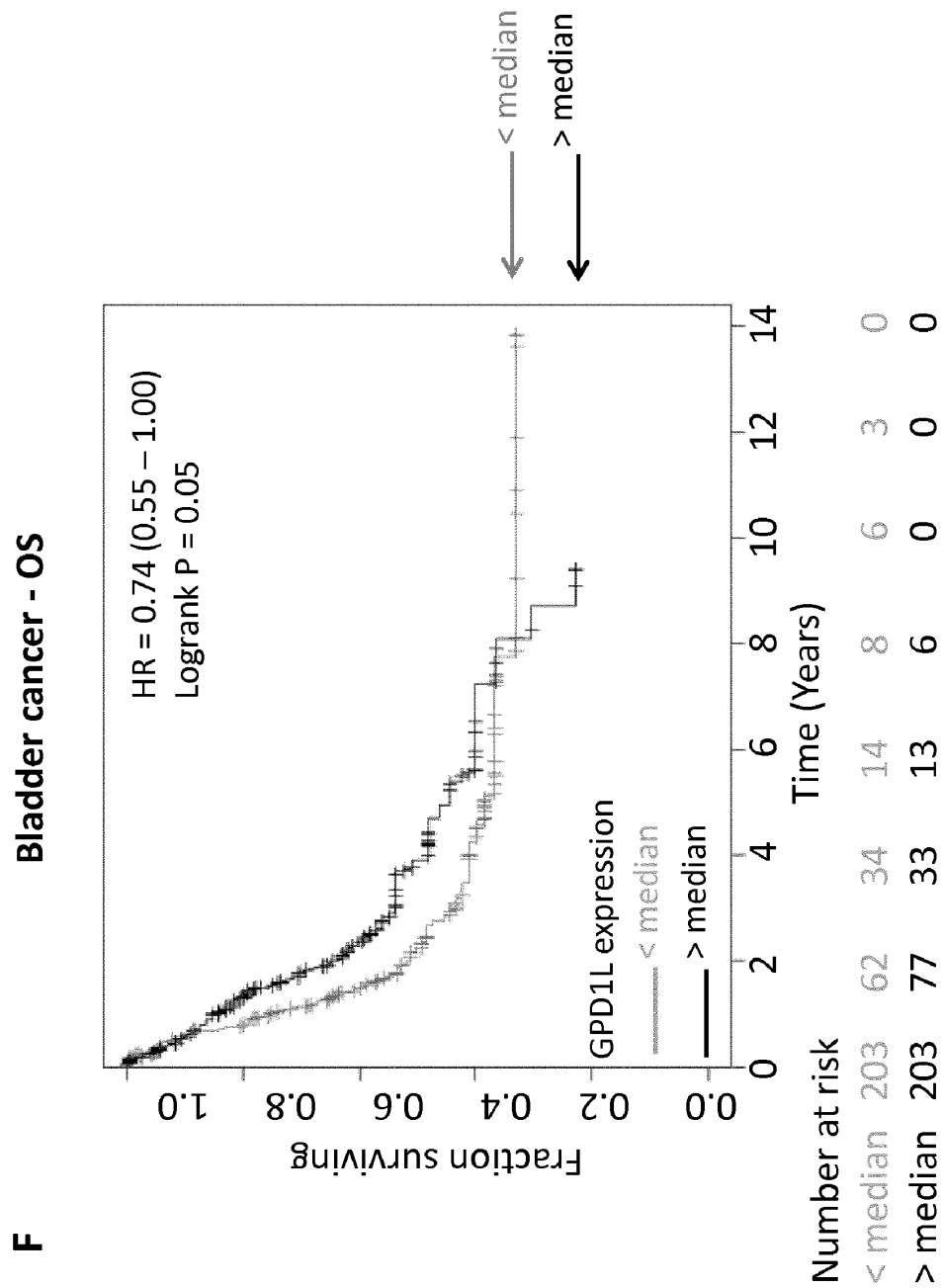


Figure 29F

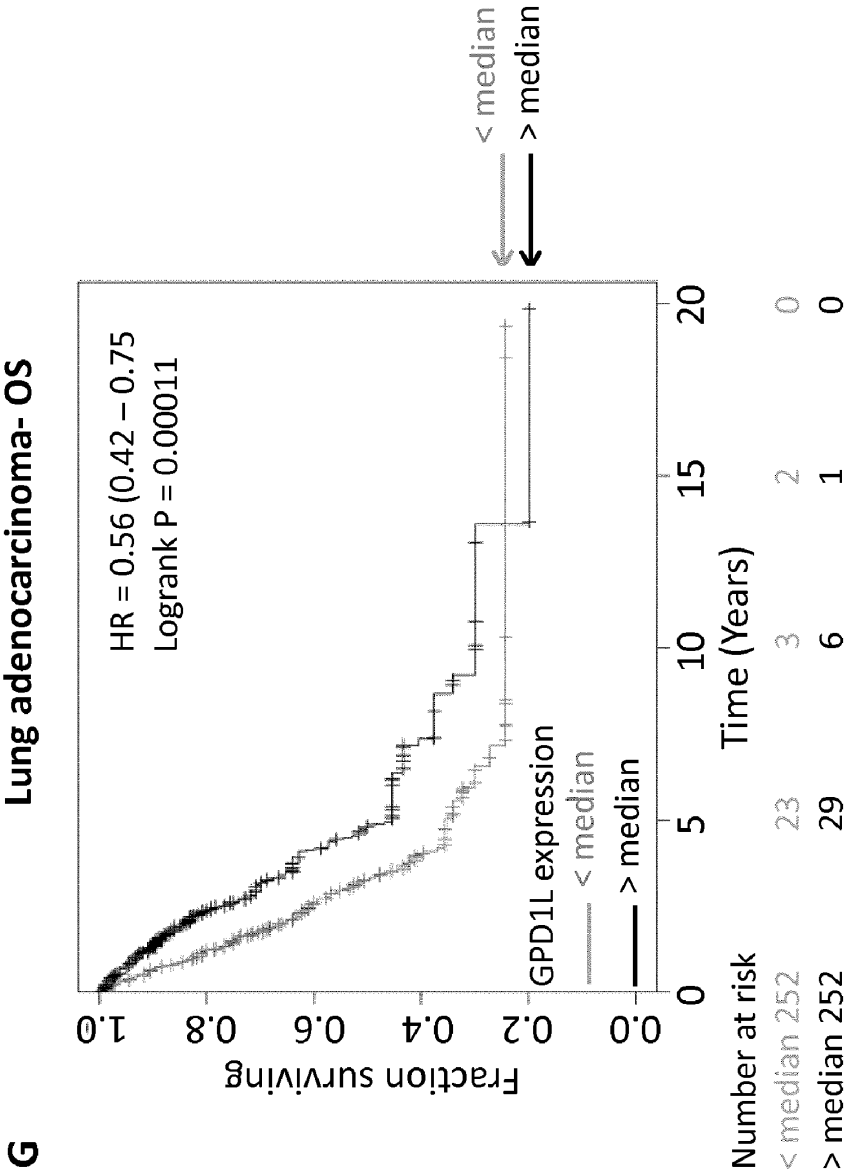


Figure 29G

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Clear cell renal cancer - OS

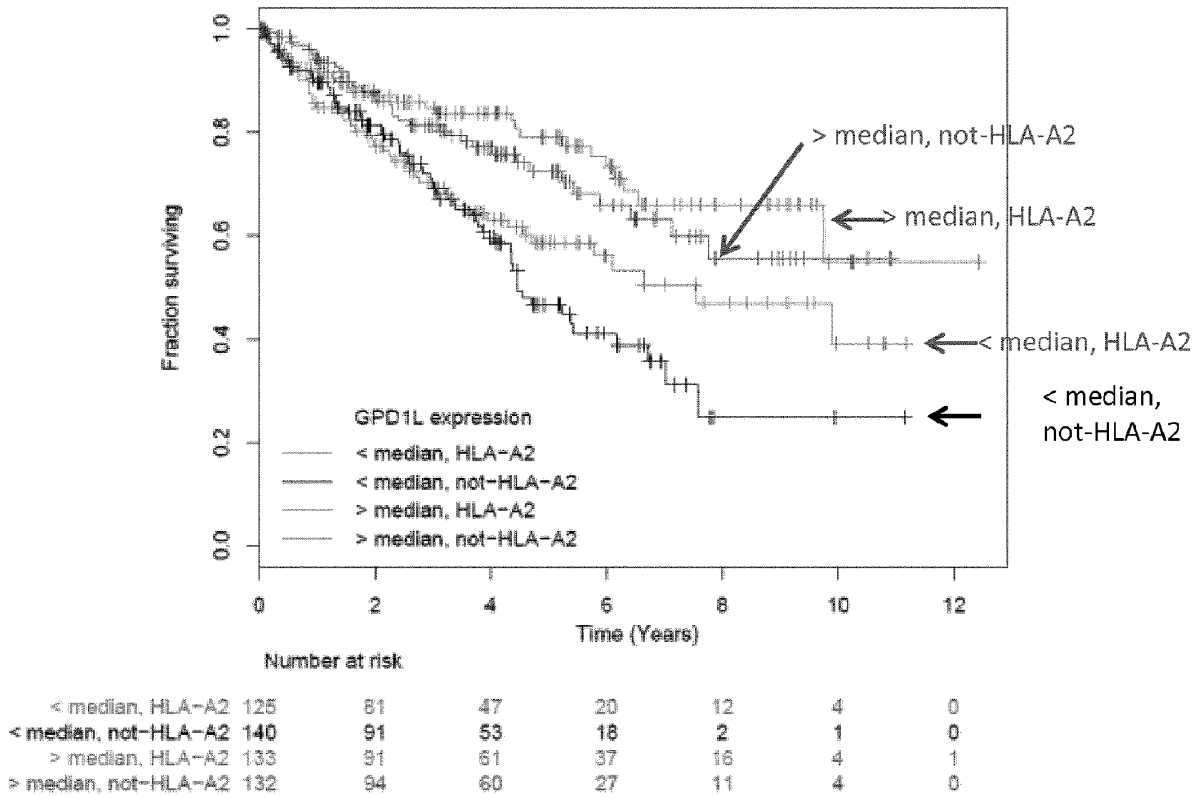
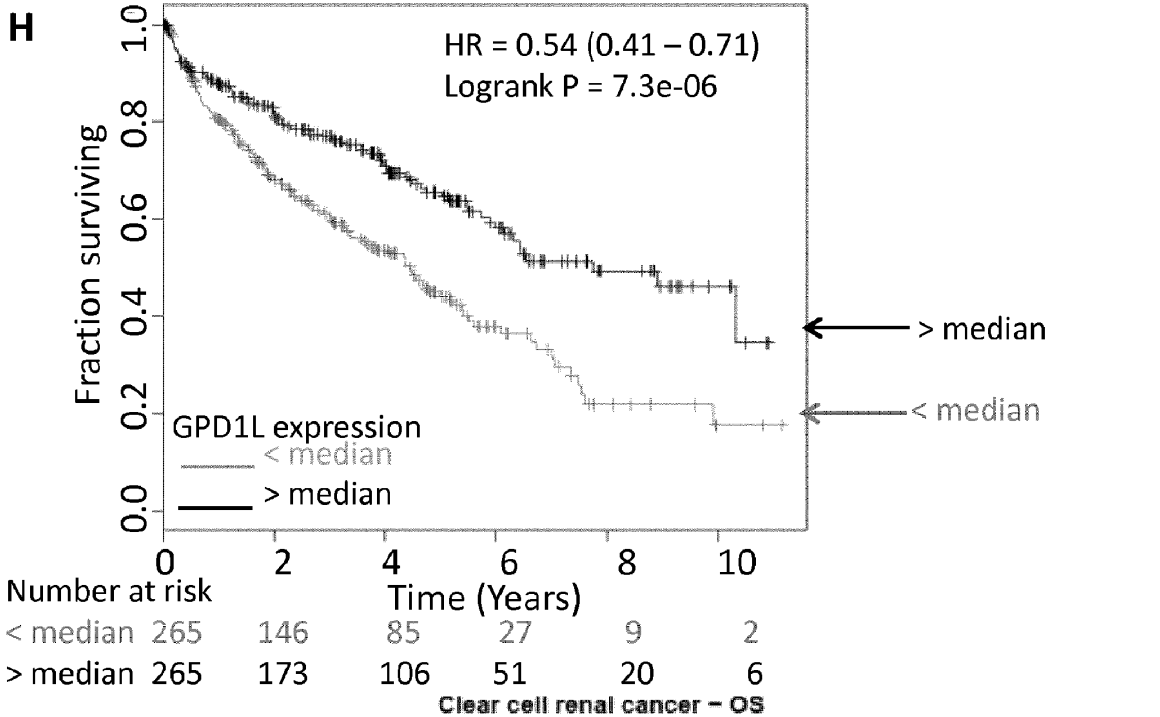


Figure 29H

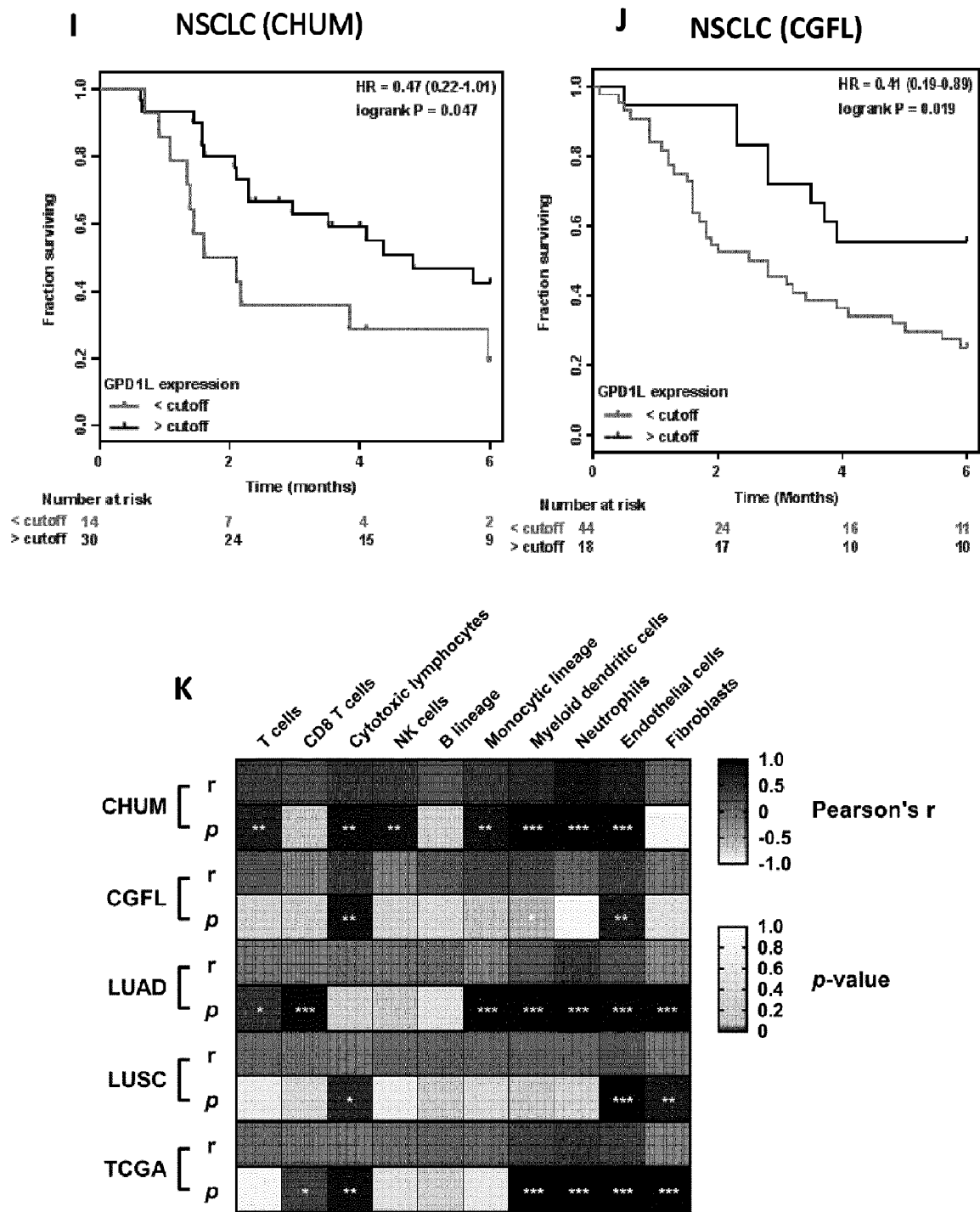


Figure 29I-K

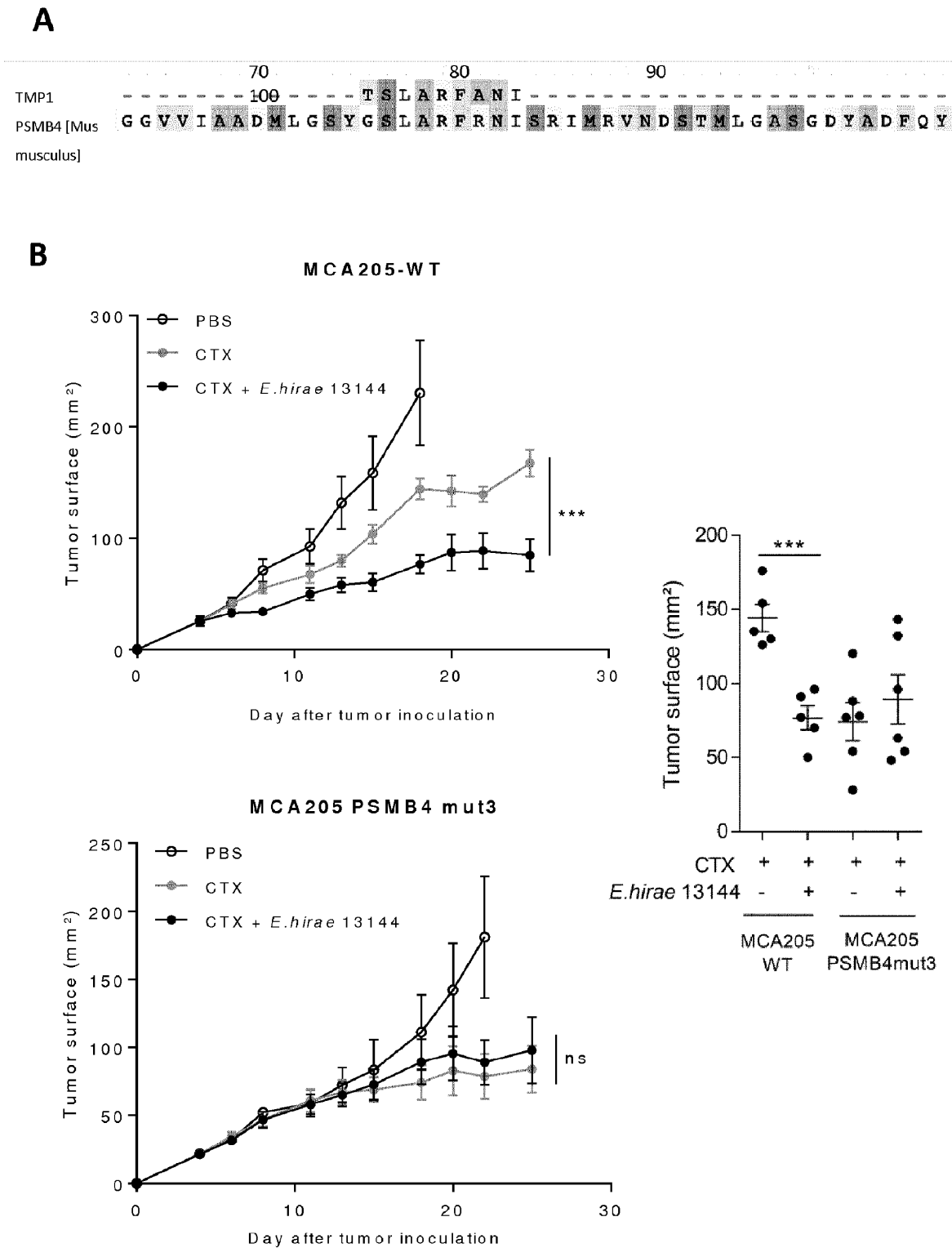


Figure 30A-B

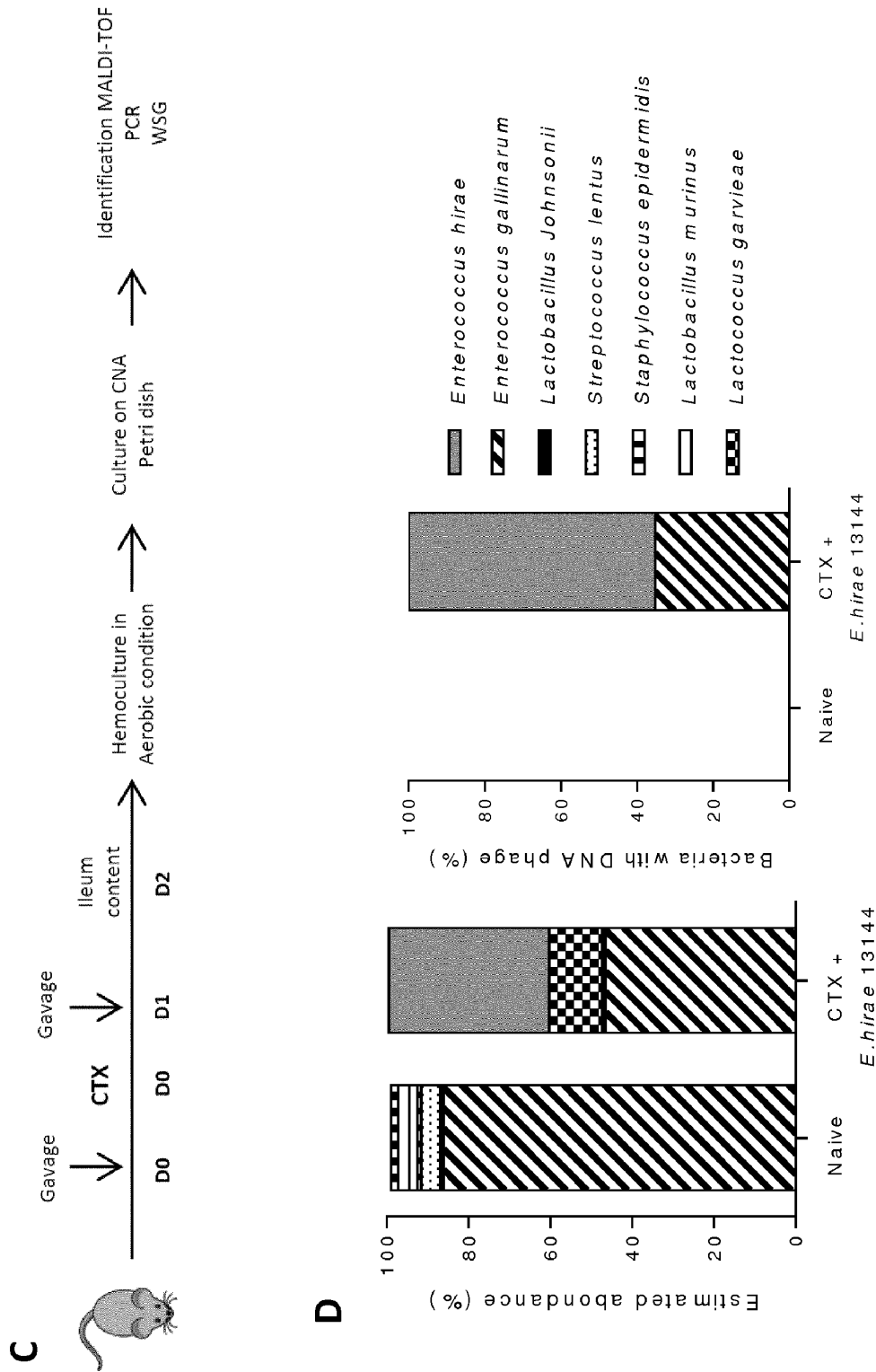


Figure 30C-D

E

Mapping

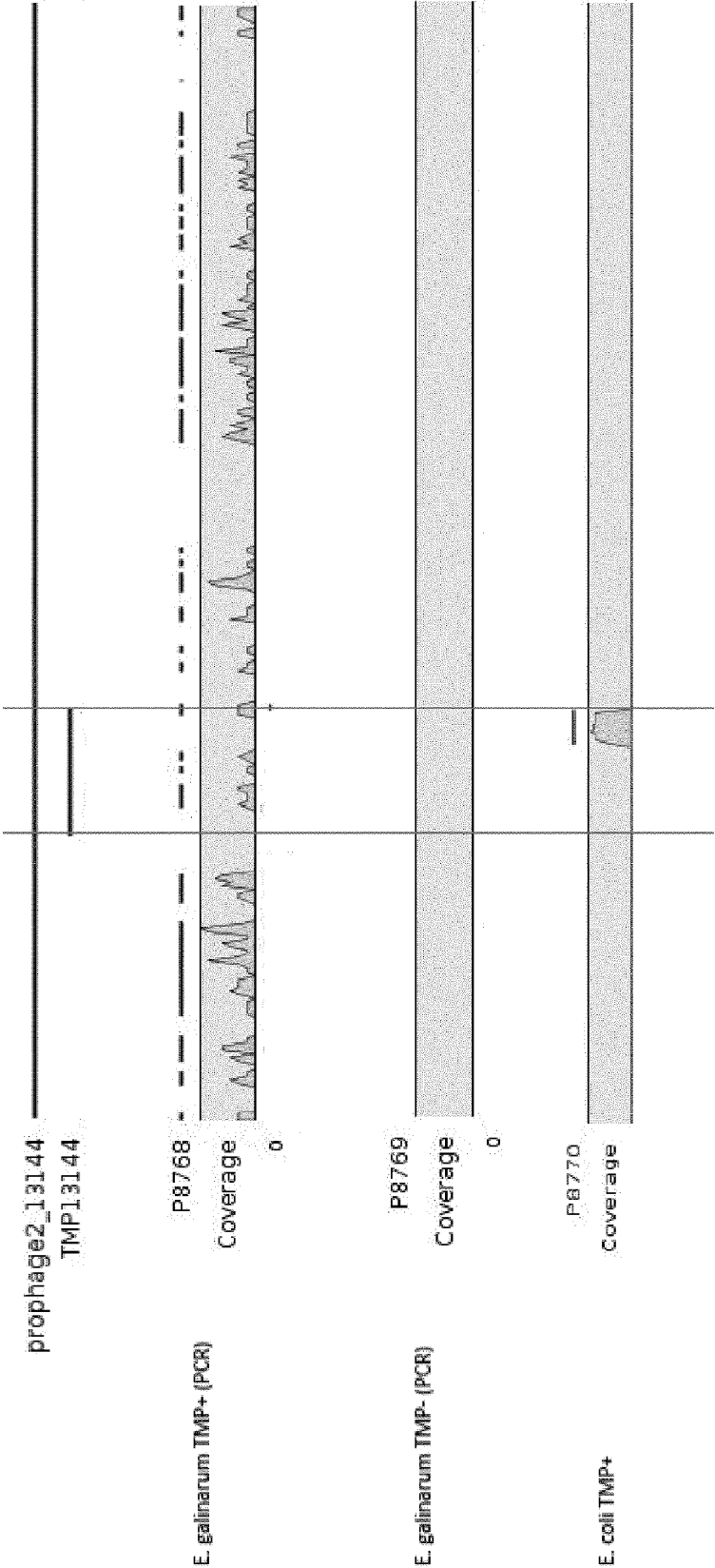


Figure 30E

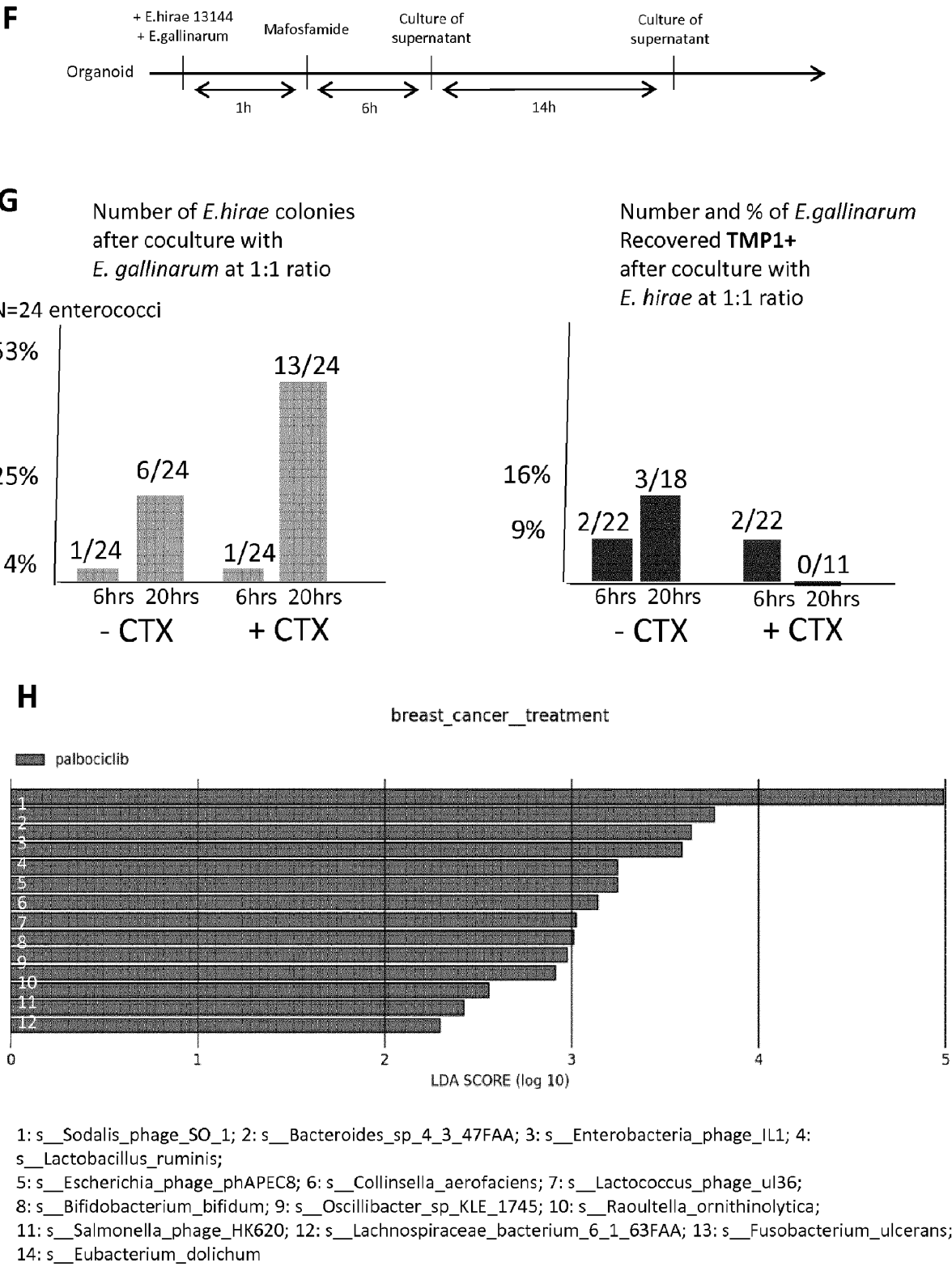


Figure 30F-H

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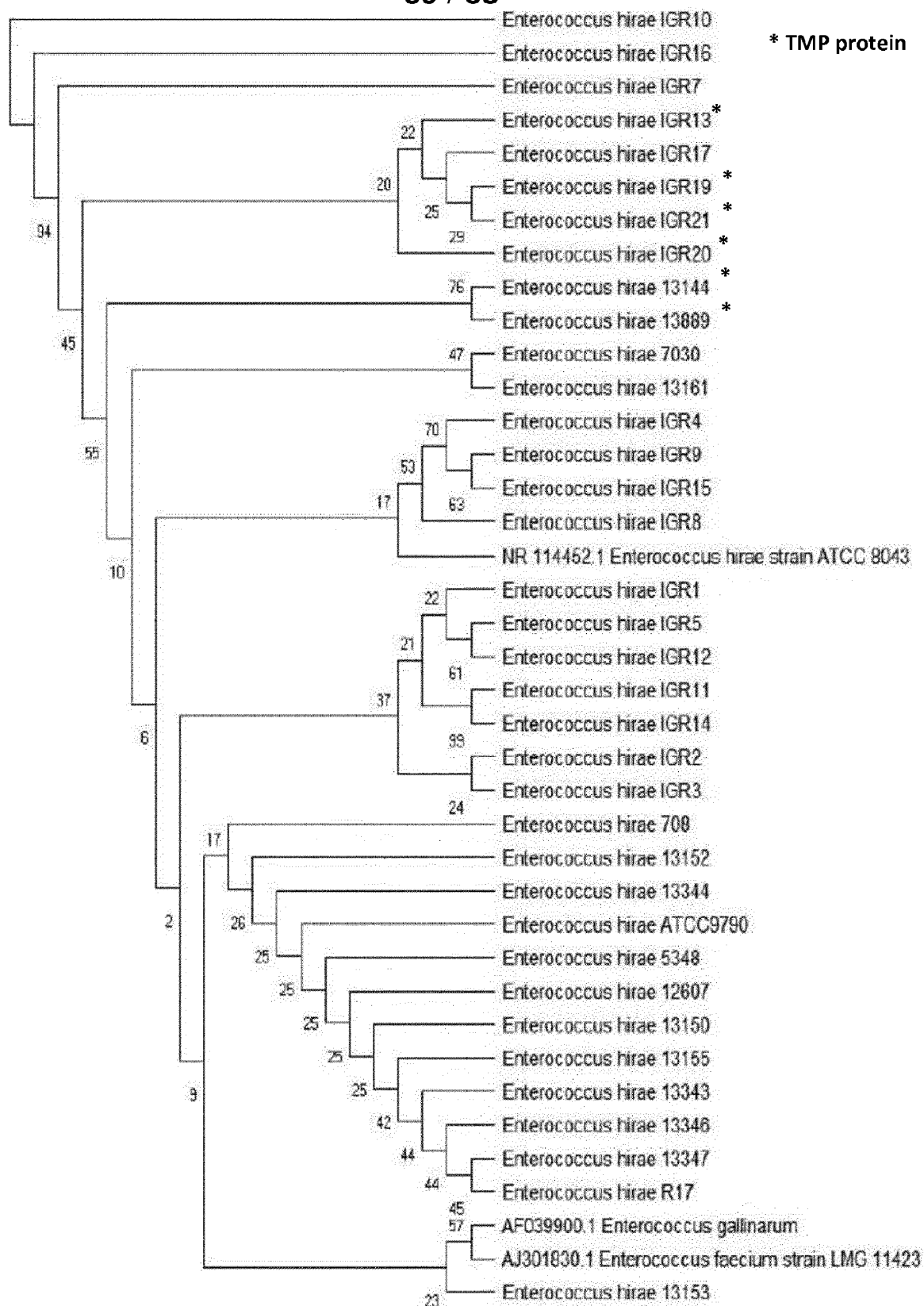
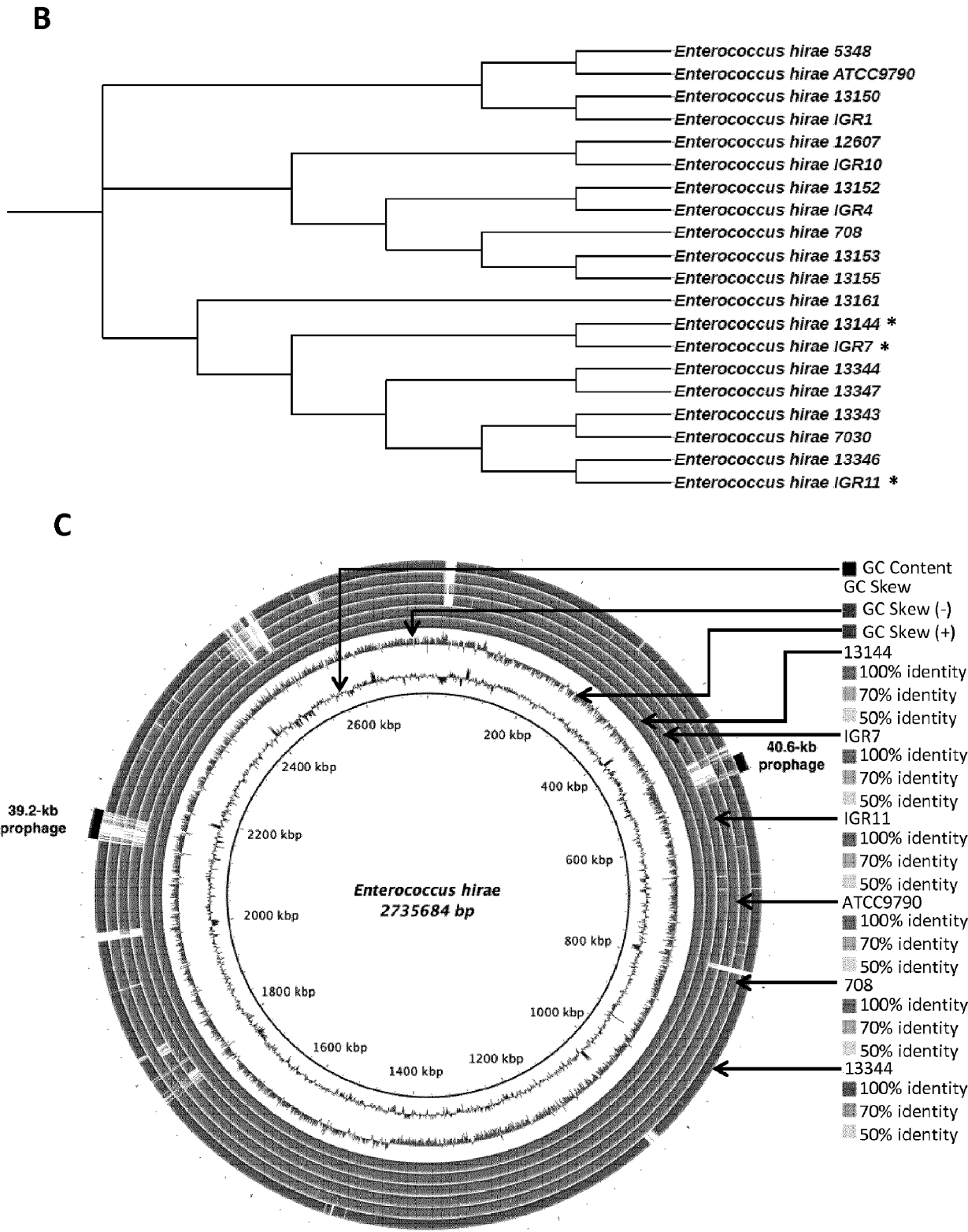


Figure 31A

* TMP1 epitope



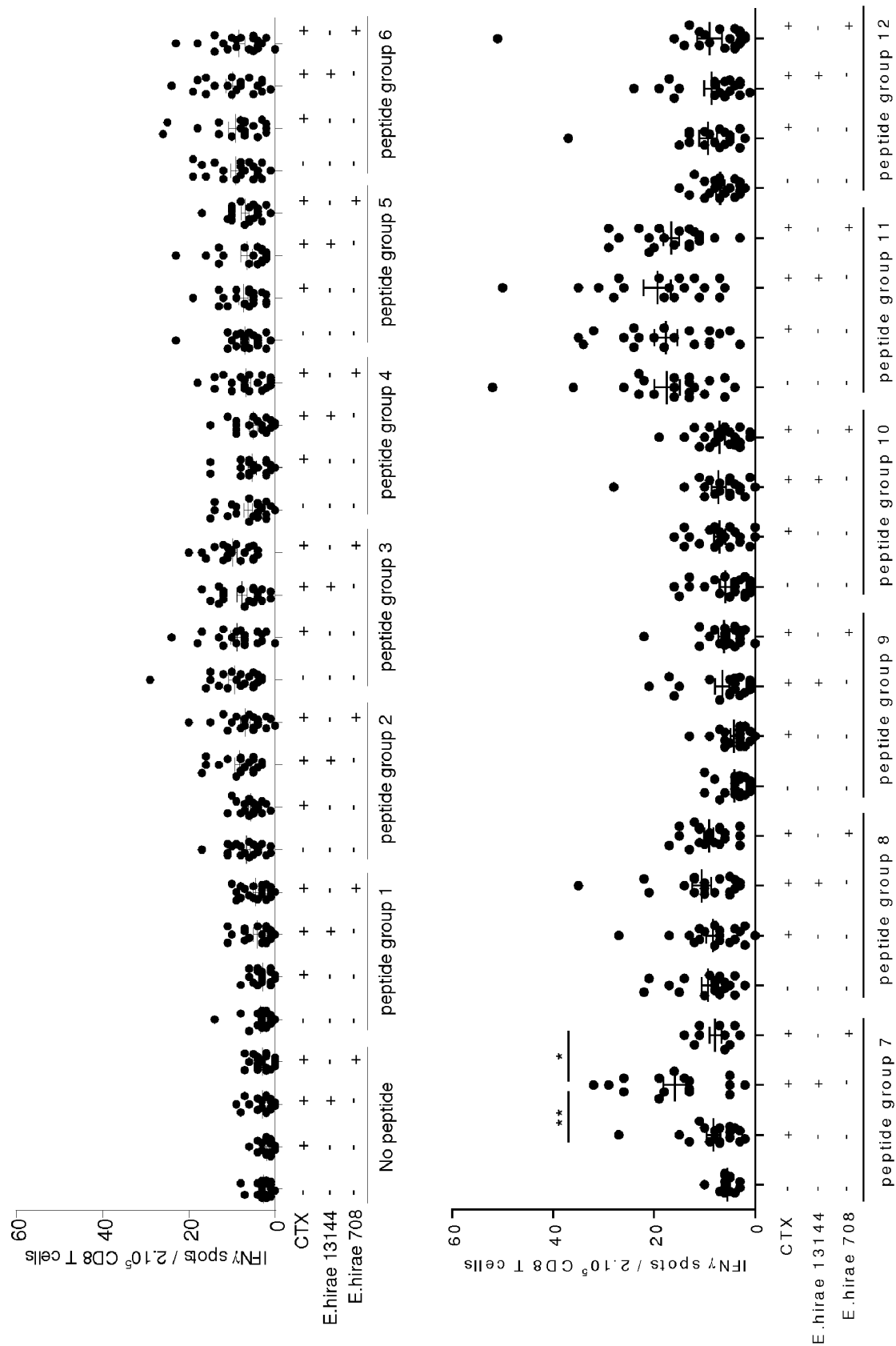


Figure 32

A TMP 39.2-kb prophage (1506 aa)

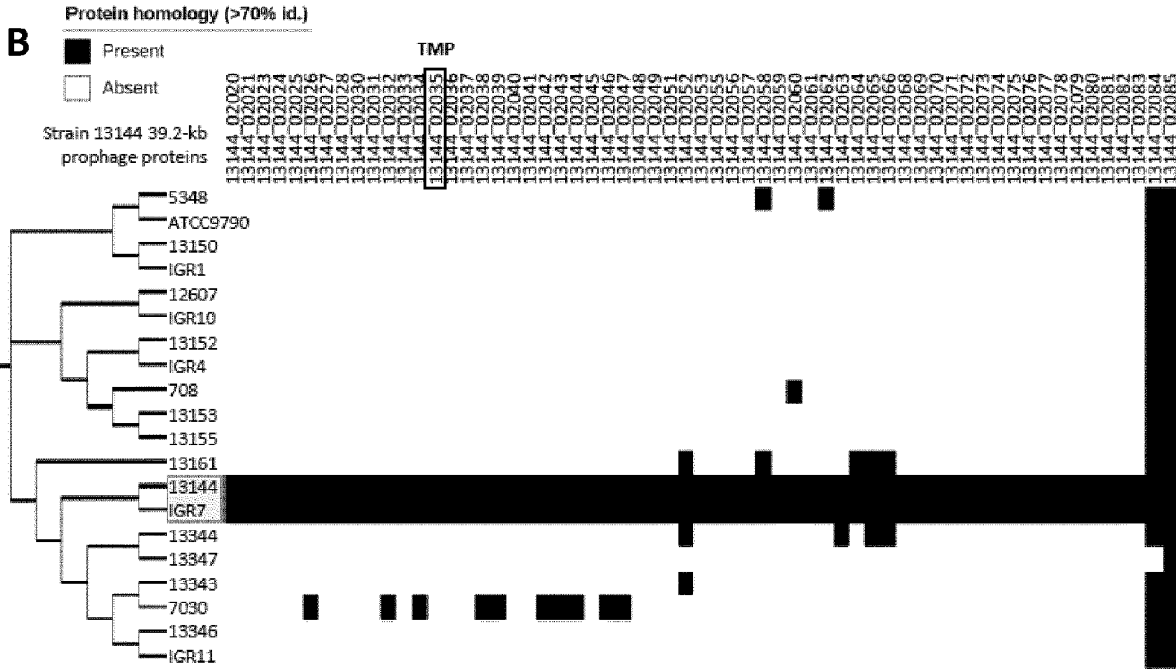


Figure 33A-B

260 270 280 290 300 310
 TMPI
 13144
 IGR7
 IGR11
 ATCC9790
 13344
 708

Figure 34

A

TMP-FLAG => TSLARFANI

MAQSKTVKAVLTAIDKGFTQTMGSATSSLKKLSSNASDIPSNLNTVSGAMKSFSGDKTASIGQSIEKVGGSMGKGLPIAGAVGAVTTAA
VKWESAFTGVKKTNDEMVDNSNGKVIYSYDDLEKGLRDLAKELPTSHHEIAKVAEAGQLGIKTDKVVGFTKTMIDMGESTNMSADTAA
TSLARFANITQMSQDKFSNLGSAIVDLGNNLATTESEITEMGLRLAGAGKQIGMTEGDIVGFAAALSSVGIEAEAGGSFSLRMVQMQ
LATETGVKAPEPLKQAVAIQGVSWVEKFVHAVNWGGKELTAVSKQMGVPASELKKLYKEASKASGSLEDVANVTGRTGEEFAELFKSNP
SQAMIEFIQGLKDSEKHGISAIVLDMGITEVRLRDSLLR**DYKDDDDK**

TMP-mut2-FLAG (mutation in position 2) => TSLARFANI to TALARFANI

MAQSKTVKAVLTAIDKGFTQTMGSATSSLKKLSSNASDIPSNLNTVSGAMKSFSGDKTASIGQSIEKVGGSMGKGLPIAGAVGAVTTAA
VKWESAFTGVKKTNDEMVDNSNGKVIYSYDDLEKGLRDLAKELPTSHHEIAKVAEAGQLGIKTDKVVGFTKTMIDMGESTNMSADTAA
TALARFANITQMSQDKFSNLGSAIVDLGNNLATTESEITEMGLRLAGAGKQIGMTEGDIVGFAAALSSVGIEAEAGGSFSLRMVQMQ
LATETGVKAPEPLKQAVAIQGVSWVEKFVHAVNWGGKELTAVSKQMGVPASELKKLYKEASKASGSLEDVANVTGRTGEEFAELFKSNP
SQAMIEFIQGLKDSEKHGISAIVLDMGITEVRLRDSLLR**DYKDDDDK**

TMP-mut3-FLAG (mutation in position 3) => TSLARFANI to TSFARFANI

MAQSKTVKAVLTAIDKGFTQTMGSATSSLKKLSSNASDIPSNLNTVSGAMKSFSGDKTASIGQSIEKVGGSMGKGLPIAGAVGAVTTAA
VKWESAFTGVKKTNDEMVDNSNGKVIYSYDDLEKGLRDLAKELPTSHHEIAKVAEAGQLGIKTDKVVGFTKTMIDMGESTNMSADTAA
TSFARFANITQMSQDKFSNLGSAIVDLGNNLATTESEITEMGLRLAGAGKQIGMTEGDIVGFAAALSSVGIEAEAGGSFSLRMVQMQ
LATETGVKAPEPLKQAVAIQGVSWVEKFVHAVNWGGKELTAVSKQMGVPASELKKLYKEASKASGSLEDVANVTGRTGEEFAELFKSNP
SQAMIEFIQGLKDSEKHGISAIVLDMGITEVRLRDSLLR**DYKDDDDK**

B

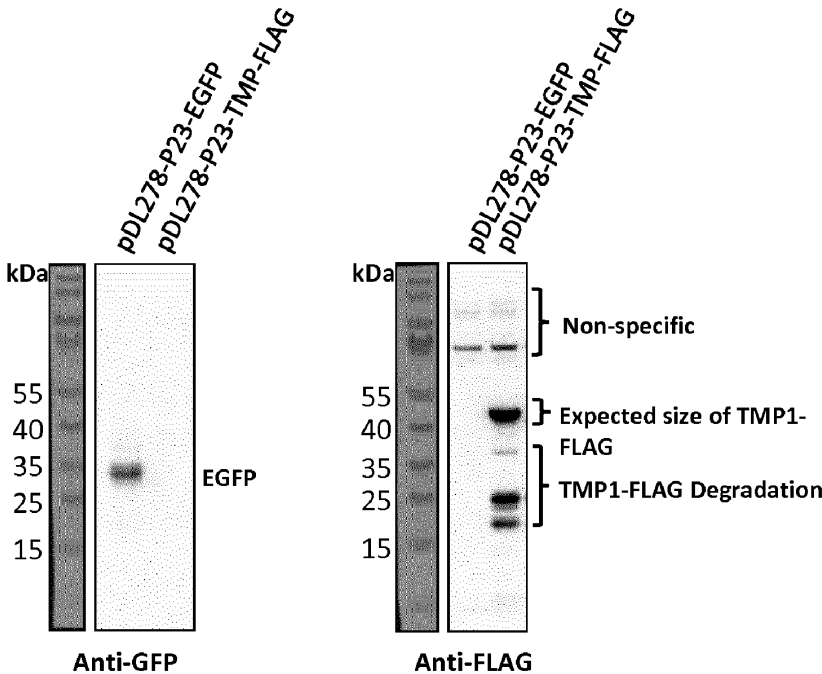


Figure 35A-B

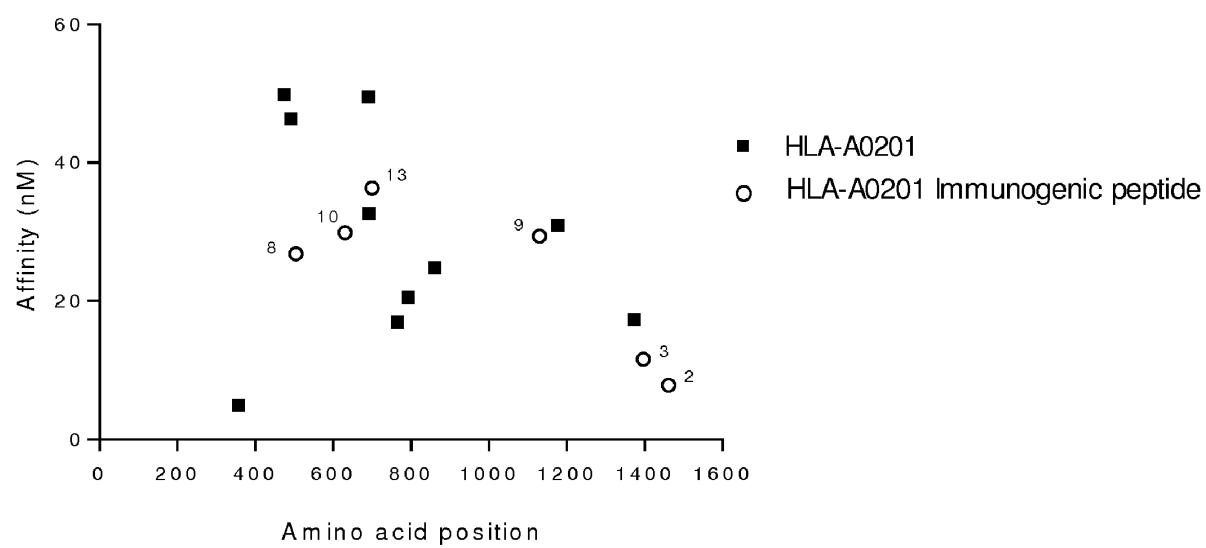
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Primers

Sequence of TMP1

Figure 36

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**Figure 37**

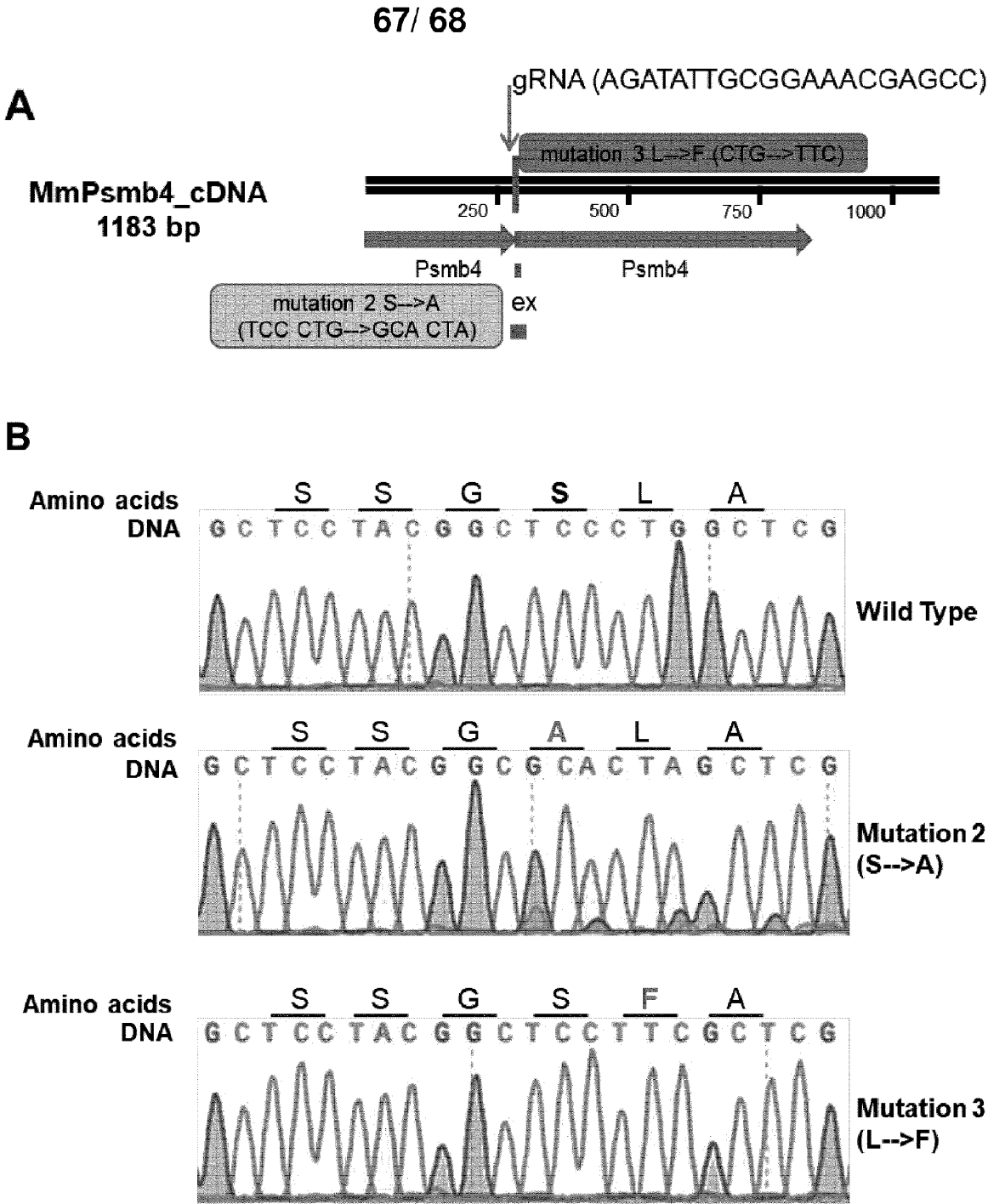
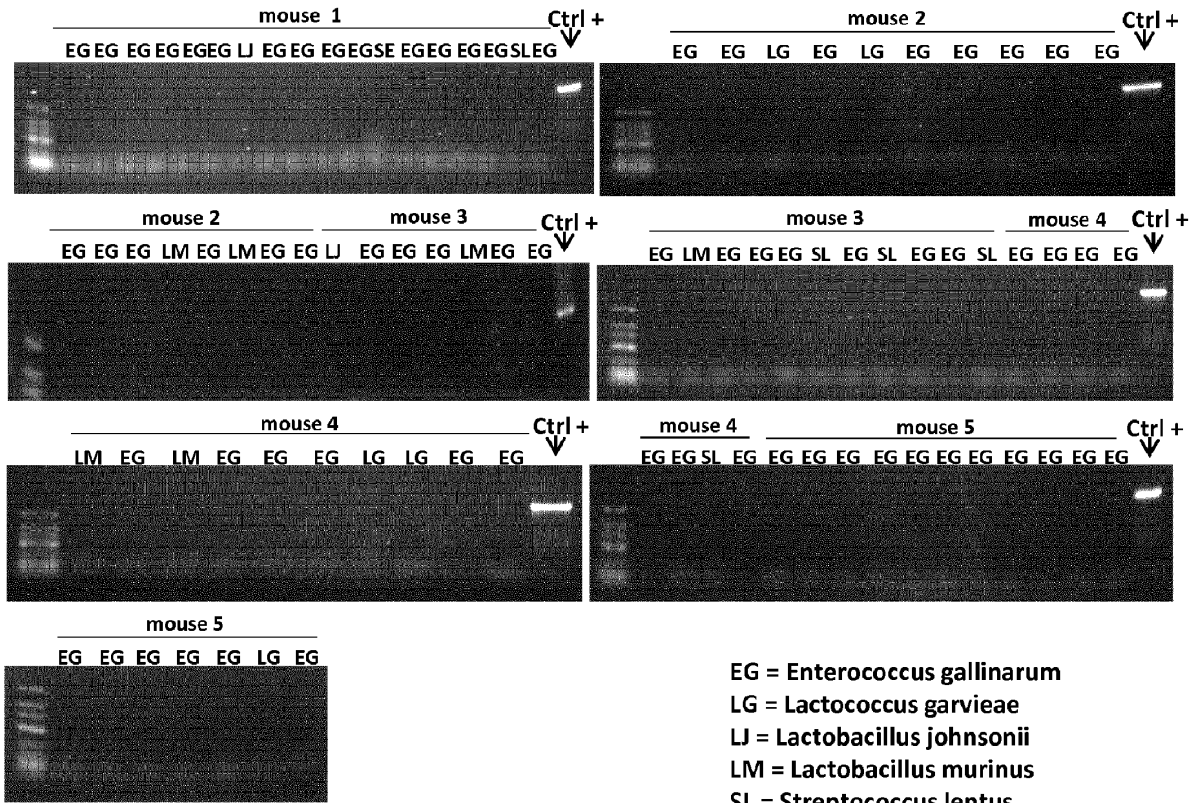


Figure 38A-B

A Naïve mice

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B CTX + *E.hirae* 13144 mice

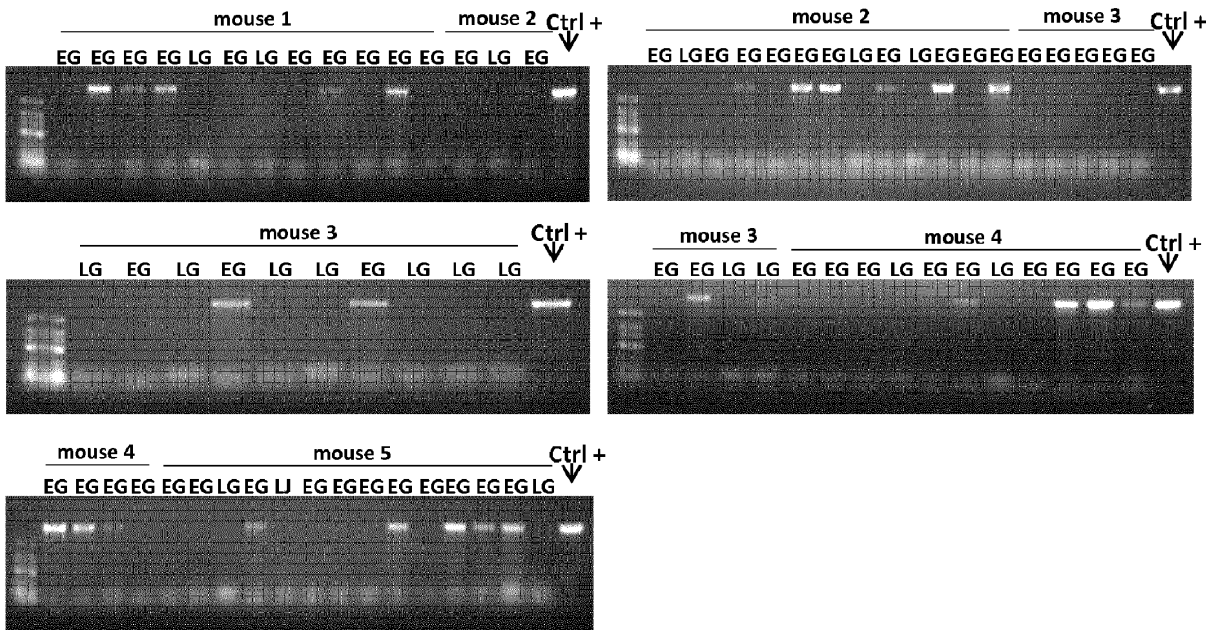


Figure 39A-B