

Efficacy of PD-1/PD-L1 pathway disruptors in syngeneic models

A. Lagrange¹, R. Boidot², M. Hillairet de Boisferon³, O. Duchamp³, J.-F. Mirjolet³, F. Ghiringhelli^{1,2}

¹INSERM 866, Université de Bourgogne, Dijon, ²Center Georges Francois Leclerc, Dijon, ³Oncodesign, Dijon (France)

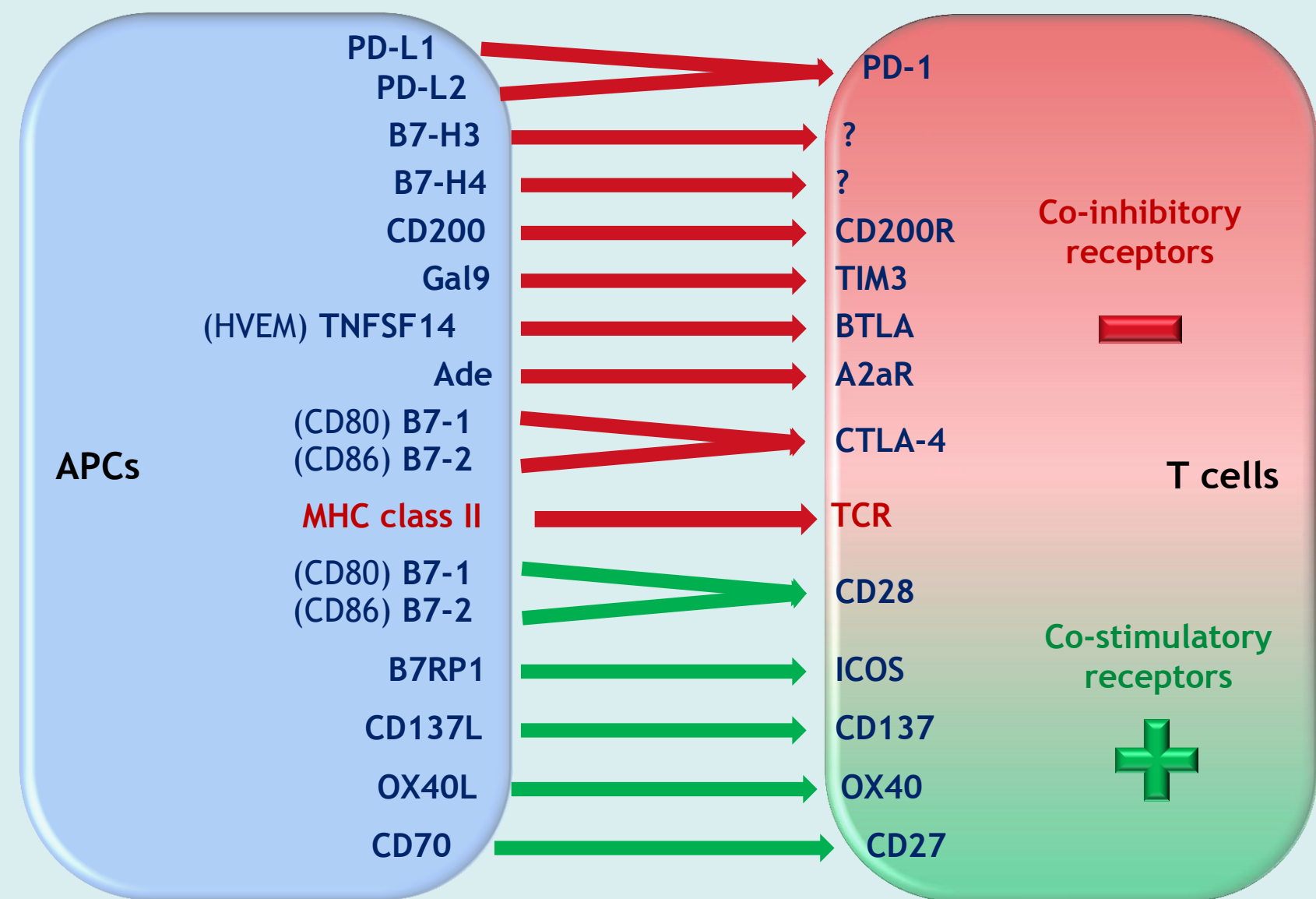


For more information: contact@oncodesign.com

Immune-checkpoints: efficacy but still a lot of challenges

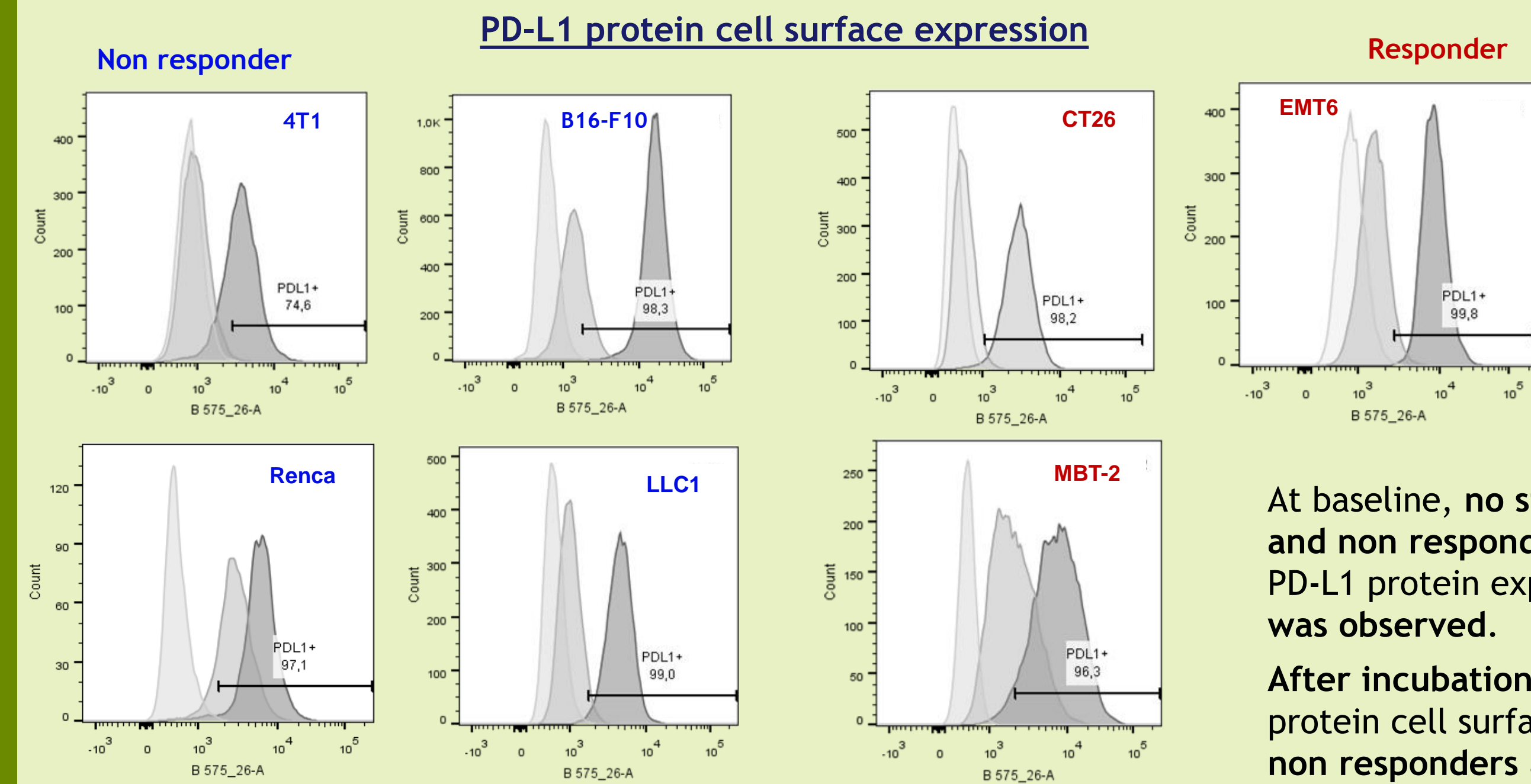
- How to choose the best target, the best compound?
- Antibody format:
 - IgG1, IgG2, IgG4,...
 - Humanized, fully human,...
- Prognostic biomarker (genetic basis only?):
 - mutation loads (which cut off?),
 - MMR-D,
 - PD-L1,...
- Early biomarker of response
- Right way to analyse efficacy:
 - RECIST, irRC, irRECIST
- Durable response in absence of treatment (duration of treatment?)

Are syngeneic mouse models relevant?



INTRODUCTION

In-vitro modulation of PD-L1 and IRF expression after IFNγ exposure

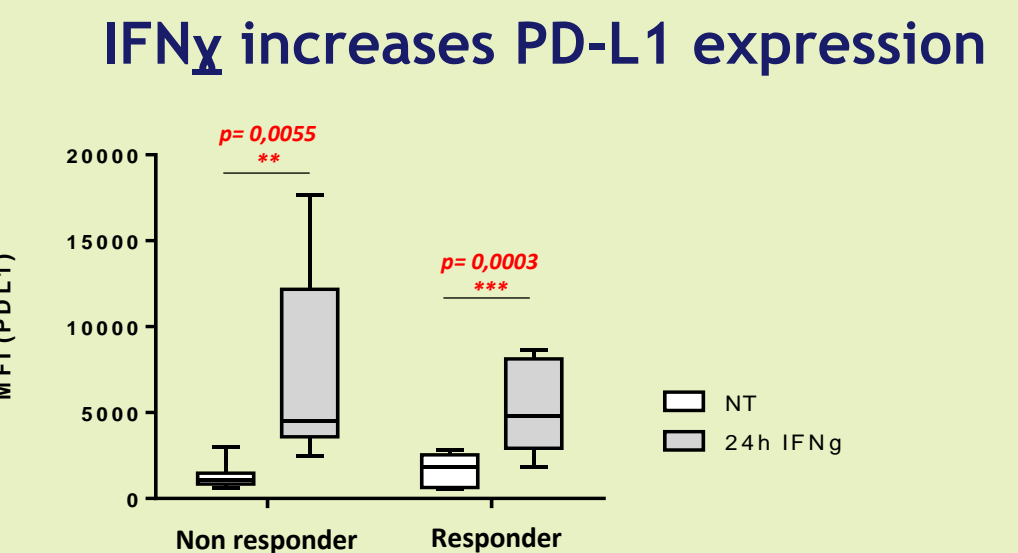


PD-L1 expression (using RT-qPCR, WB and flow cytometry) was analyzed on cell lines before and after IFNγ.

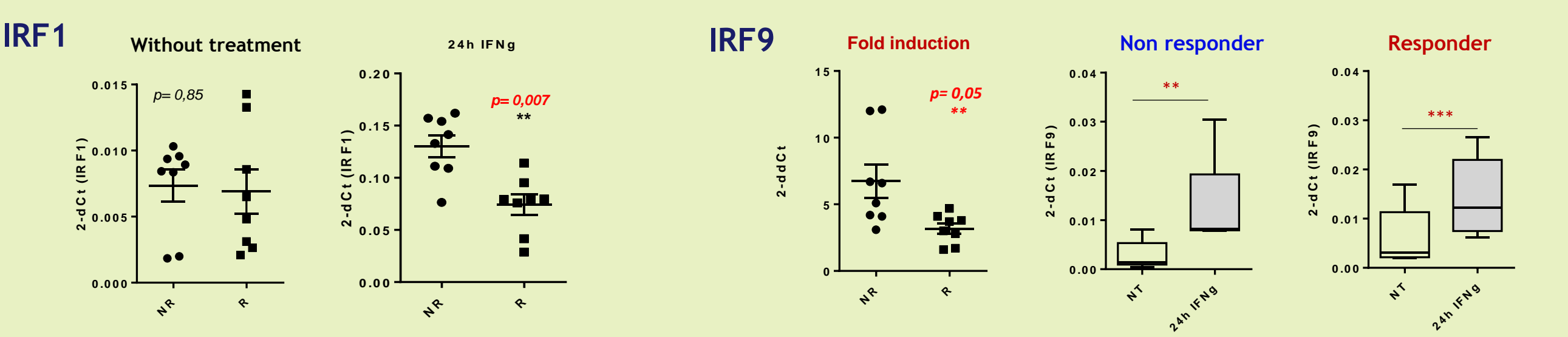
At baseline, no significant difference between responders and non responders whatever the analysis (mRNA, total PD-L1 protein expression or cell surface PD-L1 expression) was observed.

After incubation with IFNγ, the level of PD-L1 (mRNA protein cell surface expression) was highly increased for non responders as compared to responders.

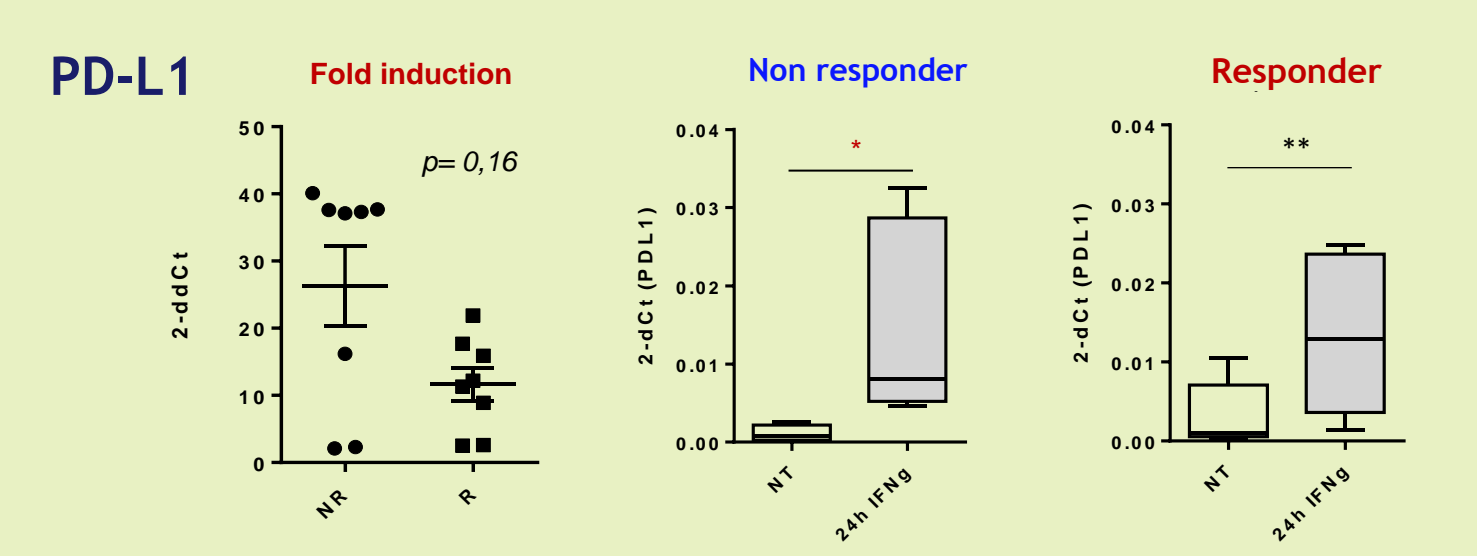
RESULTS



Changes in IRF mRNA expression in tumor cells after IFNγ exposure

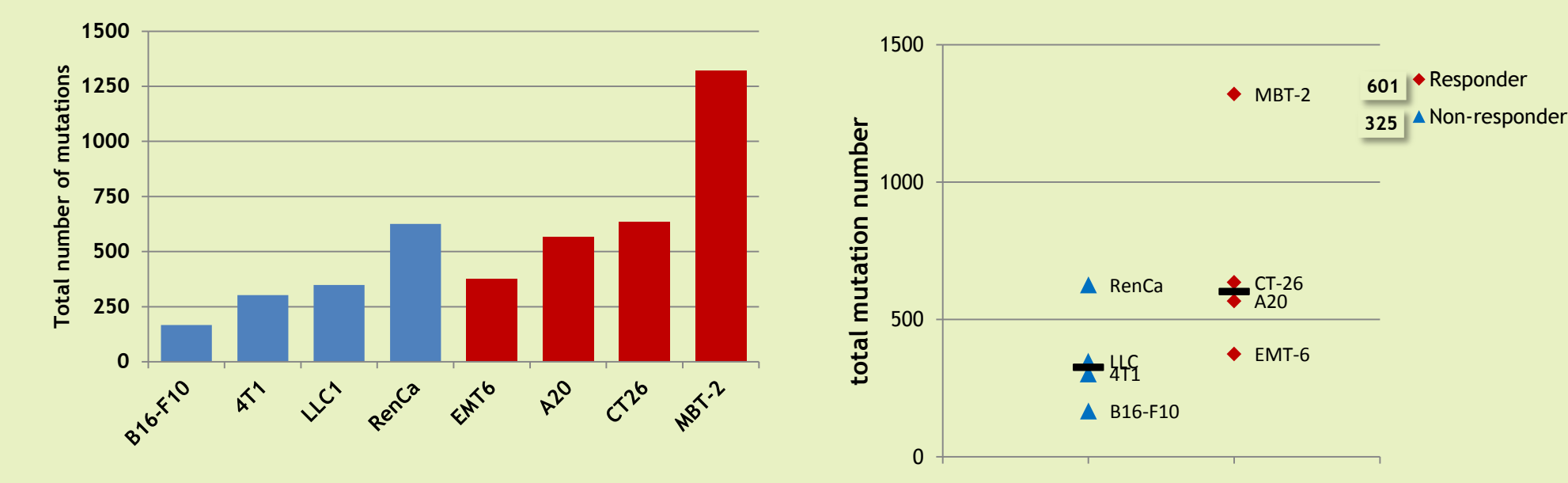


Changes in PD-L1 mRNA expression in tumor cells after IFNγ exposure



- Expression of IRF1, IRF3, IRF7 and IRF9 mRNA was analyzed before and after IFNγ exposure,
- At baseline or after IFNγ stimulation, no significant difference for IRF3, and IRF7 mRNA expression was observed between responders and non-responders (data not shown),
- In contrast, IRF1 and IRF9 mRNA are less expressed at baseline in responders as compared to non-responders,
- After IFNγ stimulation, a highest increase in IRF1, IRF9 and PD-L1 expression was observed in non-responders compared to responders population.

Number of gene mutations and sensitivity to ICI



T/C (%) < 80 is used as cut-off criteria for responder and non-responder populations (SC models)

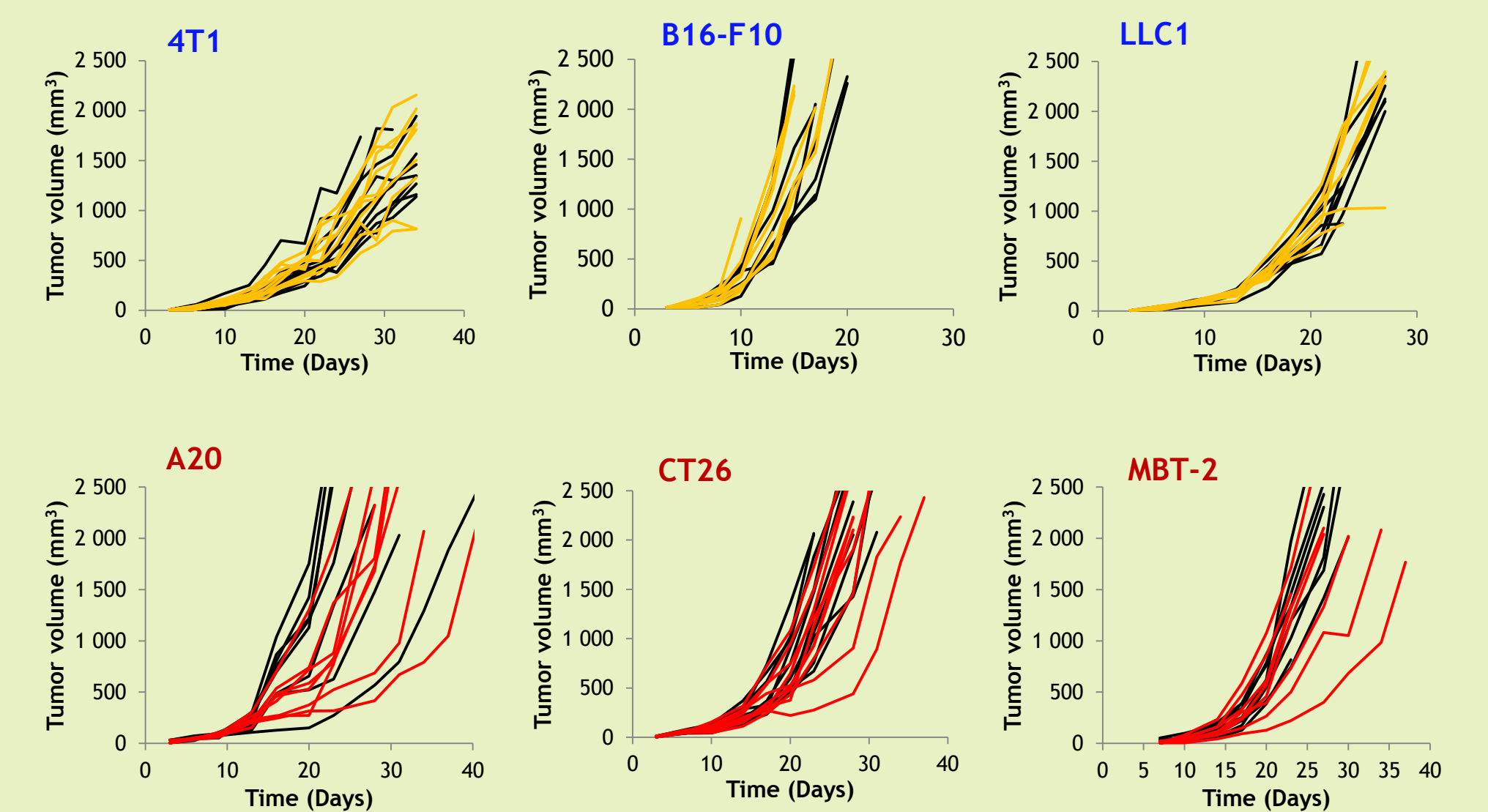
- The genomic mutations were analyzed using whole exome sequencing,
- Responder have highest number of mutations in comparison to non responder cell lines.

RESULTS

In-vivo Efficacy

Model				PD-1		PD-L1	
Name	Site	Type	Strain	n	T/C (median)	n	T/C (median)
4T1	OT	Breast	Balb/C	13	102	2	116
A20	SC	BCL	Balb/C	1	37	0	NA
B16-F10	SC	Melanoma	C57Bl/6	5	80	2	121
C38	SC	Colon	C57Bl/6	1	11	0	NA
CT26	SC	Colon	Balb/C	15	70	7	68
EMT6	SC	Breast	Balb/C	15	63	2	77
EMT6	OT	Breast	Balb/C	1	68	0	NA
HEPA1-6	OT	Liver	C57Bl/6	0	NA	0	NA
LLC1	SC	Lung	C57Bl/6	2	97	1	88
MBT2*	OT	Bladder	C3H	2	149	0	NA
MBT2	SC	Bladder	C3H	2	79	2	66
Renca*	OT	Kidney	Balb/C	1	100	0	NA

T/C < 42%
42% < T/C < 80%
T/C > 80%



Mice were SC injected with murine tumor cells at D0. Mice were randomized based on tumor volume (50-100 mm³) and treated IP with mAb against PD-1 (clone RMP1-14) at 10 mg/kg/inj (TWx2).

- 10 mouse models were tested for response to PD-1/PD-L1 targeting antibodies:
- 4T1, B16-F10, LLC1 and Renca models were characterized as non-responder,
 - A20, C38, CT26, EMT6, MBT-2 showed sensitivity to PD-1/PD-L1 inhibitors,
 - Efficacy study on HEPA1-6 OT model is on-going.

Conclusions and perspectives

- PD-L1 expression and genomic variation could be used for predicting tumor response to anti PD-L1/PD-1 therapy after IFNγ exposure,
- 10 well characterized syngeneic models are effective approach for immune oncology research and drug development,
- Cytometry, NGS and IHC technologies are available for drug efficacy monitoring and biomarker identifications,
- New humanized mouse models are under development to circumvent limitations of syngeneic models.