

## **Multipeptide immune response to cancer vaccine IMA901 after single-dose cyclophosphamide associates with longer patient survival**

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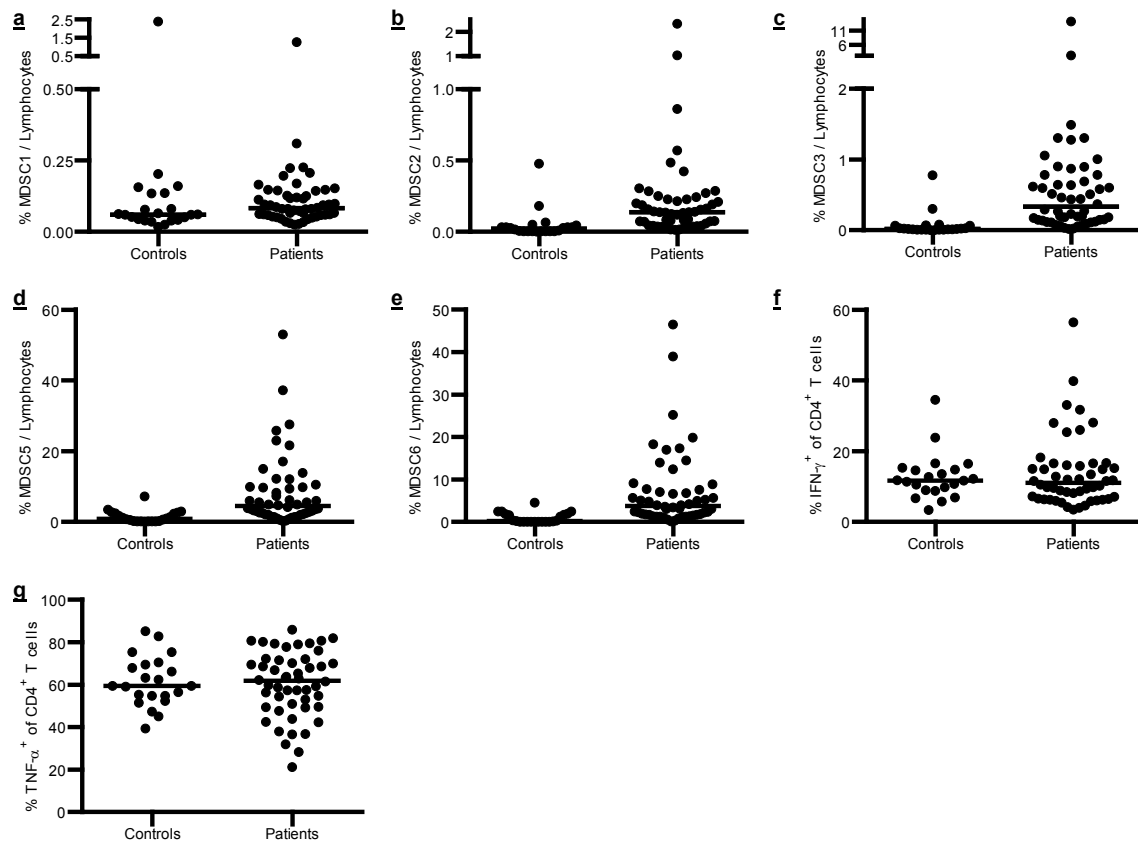
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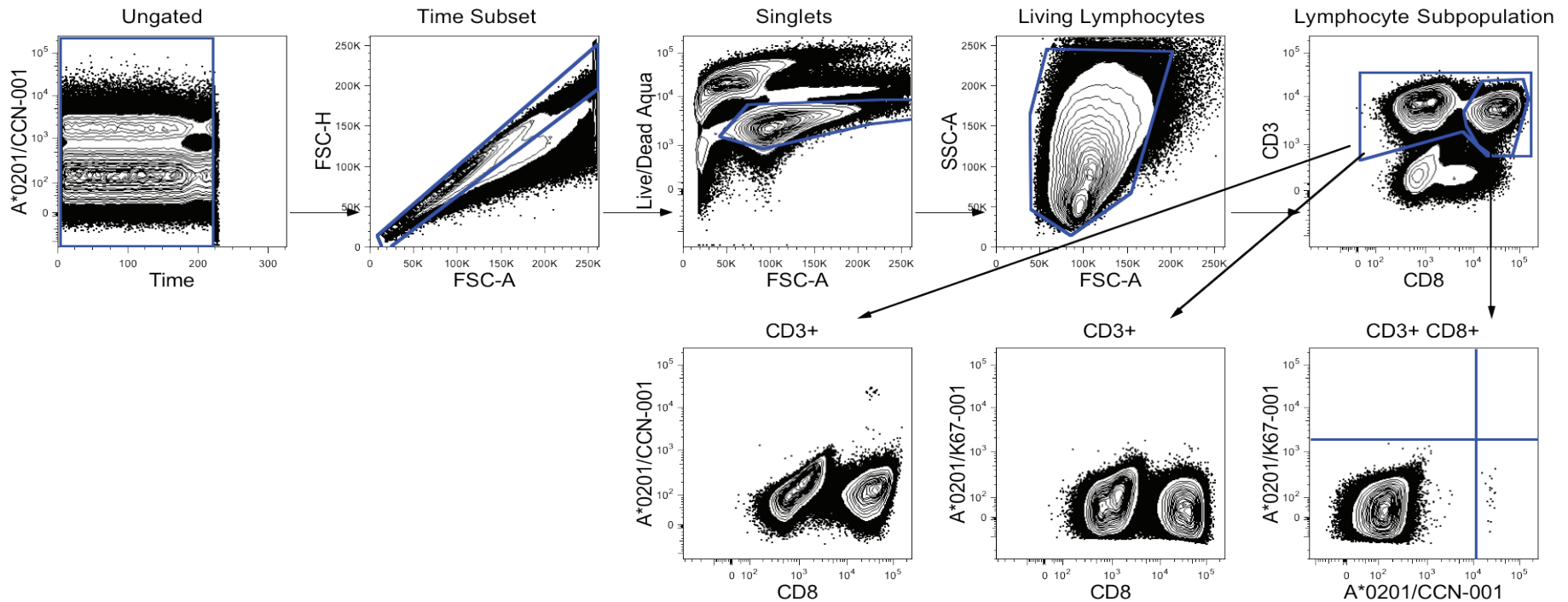
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**Supplementary Figure 1: Analysis of pre-treatment biomarkers.**

Comparison of pre-treatment cellular biomarkers of evaluable ITT patients aged < 70 years (N=50-52) and age/gender-matched healthy controls (N=22). (●) represent individuals and (—) represent medians. (a) MDSC1 p=0.091, (b) MDSC2 p<0.0001, (c) MDSC3 p<0.0001, (d) MDSC5 p<0.0001, (e) MDSC6 p<0.0001, (f) IFN- $\gamma$ <sup>+</sup> p=0.73 and (g) TNF- $\alpha$ <sup>+</sup> T<sub>H</sub> subset p=0.99.

Walter et al., Supplementary Figure 2



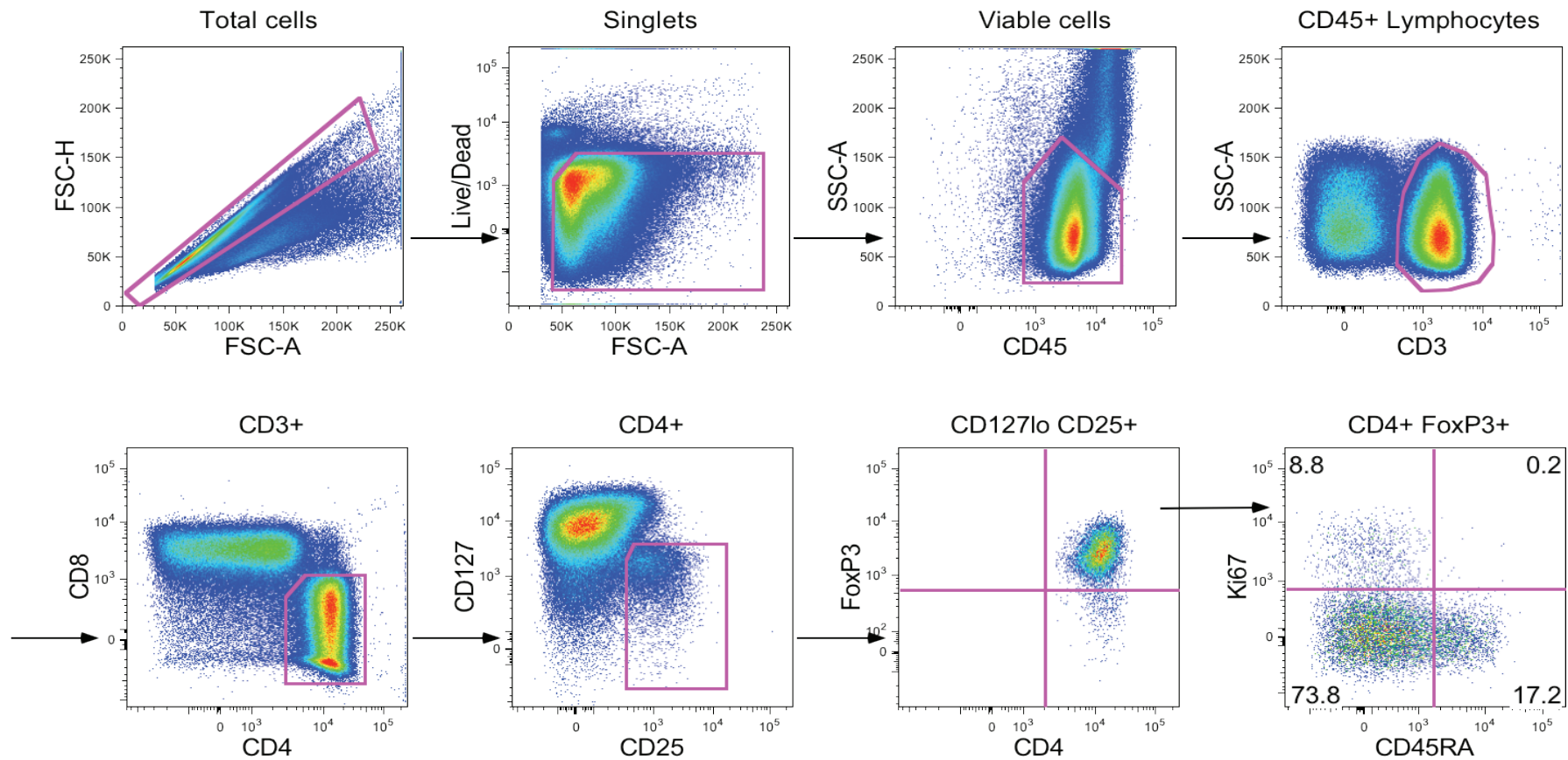
**Supplementary Figure 2: Flow cytometry analysis of one representative vaccine-induced response of the IMA901 phase II study with detailed gating strategy.**

Staining was performed using a live/dead marker, CD3- and CD8-antibodies and two different PE- and APC-labeled multimeric HLA/peptide complexes. Due to the high variability of the HLA multimer staining to individual patient T-cell populations, a uniform gating for the entire study was not feasible, however all gates were kept identical for each patient and antigen. First, singlets were identified by setting a time gate followed by exclusion of doublets using an FSC-A vs. FSC-H plot. Within the singlets living lymphocytes were identified by gating dead cell marker negative cells and subsequently a lymphocyte subpopulation was defined by gating FSC-A vs. SSC-A. Next, gates were set around CD3<sup>+</sup> and CD3<sup>+</sup>CD8<sup>+</sup> cells respectively. Stainings for PE-labeled or APC-labeled multimers were then visualized first within the CD3<sup>+</sup> subset by plotting each multimer staining vs. CD8 and finally in a multimer vs. multimer plot showing CD3<sup>+</sup>CD8<sup>+</sup> cells to identify single multimer binding T cells.



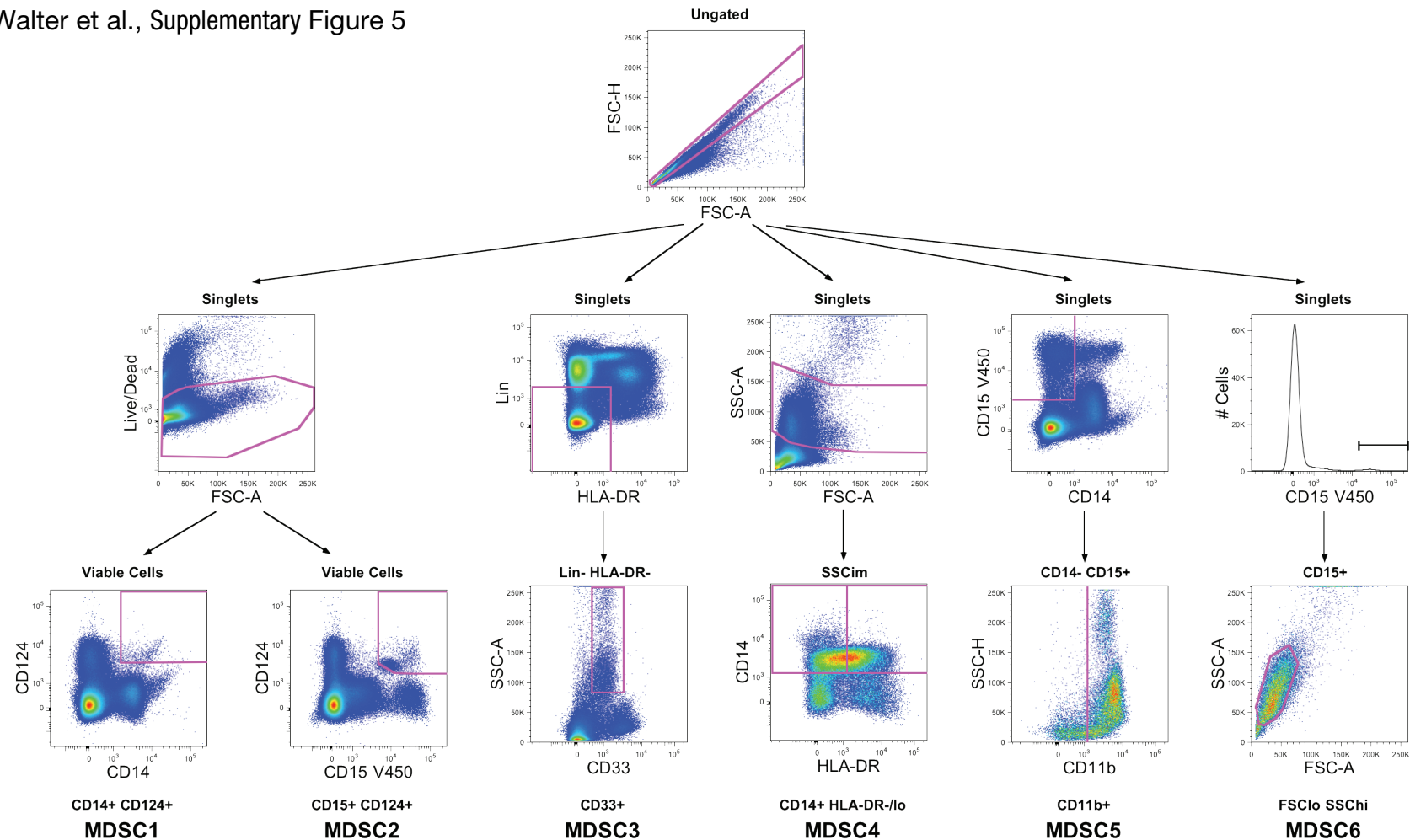
**Supplementary Figure 3**

**Flow cytometry plots of 20 vaccine-induced responses of the IMA901 phase II study.** Staining and gating analysis was performed as detailed in legend to Supplementary Figure 2. For each patient two plots of the pre-vaccination time-point and a post-vaccination time-point are shown: (1.) CD8 vs. multimer-1 showing CD3<sup>+</sup> cells and (2.) multimer-1 vs. multimer-2 showing CD3<sup>+</sup>CD8<sup>+</sup> cells, the latter allowing demonstration of peptide specific multimer binding. A response was determined as vaccine-induced if the frequency of multimer-positive cells in the respective post-vaccination time-point was at least 4x the frequency compared to the pre-vaccination time-point, and the population of multimer-positive cells was classified as clustered and discrete by a jury consisting of five members. Jury members individually inspected each plot which was blinded for patient data and multimer specificity. Each multimer plot received a score of 0 (clearly negative), 1 (possibly positive) or 2 (clearly positive) by each jury member. Each staining could therefore receive a maximum of 2x5 = 10 points. A multimer staining was considered as clustered and discrete if its total score was at least 9. Vaccine-induced responses from 10 patients treated with and from 10 patients treated without low-dose cyclophosphamide are shown.



**Supplementary Figure 4**

**Representative flow cytometry plots showing the detailed gating strategy for quantification of regulatory T cells (Tregs).** Identical gates were used for analyses of all study samples. Samples were set as evaluable if at least 75,000 live CD45<sup>+</sup> lymphocytes were counted. To quantify Tregs, first total cells were identified by excluding debris using an FSC-A histogram. Singlets were selected as defined by having a similar height (FSC-H) and area (FSC-A) measurement in the forward scatter. Next, a gate was set to identify viable cells. Then CD45<sup>+</sup> lymphocytes and CD3<sup>+</sup> cells were selected. The CD4<sup>+</sup> CD8<sup>-</sup> subset among CD3<sup>+</sup> cells was identified and plotted for CD25 and CD127 expression. FoxP3<sup>+</sup> cells within CD127<sup>lo</sup> CD25<sup>+</sup> cells were identified as Tregs. Last, Tregs were characterized in terms of Ki67 and CD45RA expression which allows quantification of Treg subpopulations such as dividing vs. non-dividing (Ki67<sup>+</sup> vs. Ki67<sup>-</sup>).



**Supplementary Figure 5**

**Representative flow cytometry plots showing the detailed gating strategy for quantification of myeloid-derived suppressor cells (MDSCs).** Identical gates were used for analyses of all study samples. Samples were set as evaluable if at least 75,000 live CD45<sup>+</sup> lymphocytes were counted. To quantify MDSCs, doublets corresponding to cell aggregates were excluded by the FSC-A/FSC-H profile and single cells were further analyzed. Progressive gating was next performed on singlet cells for all MDSC populations. For MDSC populations 1 and 2 a live/dead gating was included to avoid non-specific binding of anti-CD124 to dead cells.

MDSC1: gated on viable cells and identified as CD14<sup>+</sup> CD124<sup>+</sup>

MDSC2: gated on viable cells and identified as CD15<sup>+</sup> CD124<sup>+</sup>

MDSC3: gated on Lin<sup>-</sup> HLA-DR<sup>-</sup> CD33<sup>+</sup> (whereby Lin is CD3/14/19/56)

MDSC4: gated on CD14<sup>+</sup> HLA-DR<sup>-/lo</sup>

MDSC5: gated on CD14<sup>-</sup> CD15<sup>+</sup> CD11b<sup>+</sup>

MDSC6: gated CD15<sup>+</sup> FSC<sup>lo</sup> SSC<sup>hi</sup>



**Supplementary Table 1: Baseline characteristics and survival of IMA901-202 patients (PP).**

		<b>All</b>	<b>+CY</b>	<b>-CY</b>
<b>Sample size (n)</b>		64	31	33
<b>Overall survival</b>	<b>Median months</b>	19.8	23.5	14.8
	<b>≥ 1 year</b>	67%	76%	59%
	<b>≥ 2 years</b>	41%	48%	34%
<b>Age</b>	<b>Median years</b>	57	57	56
<b>Sex</b>	<b>% Male</b>	78%	84%	73%
<b>Karnofsky status ≥ 80</b>		100%	100%	100%
<b>Time since initial tumor diagnosis</b>	<b>Mean years</b>	3.4	2.4	4.3
	<b>Median years</b>	2.3	1.7	2.8
	<b>&lt; 1 year</b>	25%	29%	21%
<b>Nephrectomy</b>		91%	84%	97%
<b>Prior cytokine therapy</b>		69%	68%	70%
<b>Other prior anti-tumor therapies</b>	<b>Chemotherapy</b>	27%	26%	27%
	<b>Hormones</b>	2%	0%	3%
	<b>Vaccines</b>	3%	3%	3%
	<b>Investigational</b>	2%	0%	3%
<b>MSKCC prognostic score</b>	<b>Favorable</b>	41%	39%	42%
	<b>Intermediate</b>	59%	61%	58%
<b>Metastatic sites</b>	<b>Lung</b>	83%	84%	82%
	<b>Regional lymph nodes</b>	25%	23%	27%
	<b>Distant lymph nodes</b>	67%	71%	64%
	<b>Liver</b>	34%	36%	33%
<b>No. of tumor lesions</b>	<b>1</b>	8%	10%	6%
	<b>2</b>	9%	13%	6%
	<b>≥ 3</b>	83%	77%	88%

**Supplementary Table 2: Baseline characteristics of patients stratified by immune responses (PP).**

		Immune responders (n=39)	Non-immune responders (n=22)	Multi-TUMAP responders (n=16)	Non-multi-TUMAP responders (n=45)
<b>Age – years</b>	mean	57.4	58.6	50.9	60.3
	median	56	58	52.5	59
	<i>P</i>	0.693		0.008	
<b>Gender – males</b>	<i>n</i> (%)	29 (74.4%)	18 (81.8%)	15 (93.8%)	32 (71.1%)
	<i>P</i>	0.508		0.095	
<b>Karnofsky status – ≥80%</b>	<i>n</i> (%)	39 (100%)	22 (100%)	16 (100%)	45 (100%)
<b>MSKCC risk group</b>					
Favorable	<i>n</i> (%)	16 (41%)	8 (36%)	7 (44%)	17 (38%)
Intermediate	<i>n</i> (%)	23 (59%)	14 (64%)	9 (56%)	28 (62%)
	<i>P</i>	0.721		0.675	
<b>Time since initial tumor Diagnosis – years</b>	mean	3.5	2.7	2.3	3.5
	median	1.9	2.0	1.5	2.5
	<i>P</i>	0.375		0.208	
<b>Time from prior therapy to Visit C – months</b>	mean	6.0	4.4	3.9	5.9
	median	2.0	2.2	2.2	1.9
	<i>P</i>	0.492		0.417	
<b>Nephrectomy – yes</b>	<i>n</i> (%)	36 (92.3%)	19 (86.4%)	16 (100%)	39 (86.7%)
<b>Prior therapy</b>					
Cytokines	<i>n</i> (%)	29 (74.4%)	13 (59.1%)	11 (68.8%)	31 (68.9%)
	<i>P</i>	0.220		0.992	
TKIs	<i>n</i> (%)	13 (33.4%)	10 (45.5%)	7 (43.8%)	16 (35.6%)
	<i>P</i>	0.350		0.562	
TKI: sorafenib	<i>n</i> (%)	7 (17.9%)	1 (4.5%)	2 (12.5%)	6 (13.3%)
TKI: sunitinib <sup>a</sup>	<i>n</i> (%)	7 (17.9%)	9 (40.9%)	5 (31.3%)	11 (24.4%)
	<i>P</i>	0.056		0.596	
<b>Prior radiotherapy – yes</b>	<i>n</i> (%)	6 (15.4%)	4 (18.2%)	1 (6.3%)	9 (20%)



		<b>Immune responders (n=39)</b>	<b>Non-immune responders (n=22)</b>	<b>Multi-TUMAP responders (n=16)</b>	<b>Non-multi-TUMAP responders (n=45)</b>
<b>Other prior antitumor therapies</b>					
Chemotherapy	<i>n</i> (%)	10 (25.6%)	6 (27.3%)	4 (25%)	12 (26.7%)
Monoclonal antibodies	<i>n</i> (%)	1 (2.6%)	1 (4.5%)	0 (0%)	2 (4.4%)
Hormones	<i>n</i> (%)	1 (2.6%)	0 (0%)	0 (0%)	1 (2.2%)
Vaccines (BCG)	<i>n</i> (%)	0 (0%)	2 (9.1%)	0 (0%)	2 (4.4%)
<b>Metastatic sites (radiologist)</b>					
Liver	<i>n</i> (%)	7 (17.9%)	10 (45.5%)	1 (6.3%)	16 (35.6%)
Lung	<i>n</i> (%)	28 (71.8%)	14 (63.6%)	13 (81.3%)	29 (64.4%)
Lymph nodes	<i>n</i> (%)	30 (76.9%)	15 (68.2%)	14 (87.5%)	31 (68.9%)
<b>Total sum of target lesion diameters – mm</b>					
	mean	112.0	138.2	101.8	128.8
	median	112.8	89.8	102.0	102.0
	<i>P</i>	0.288		0.332	
<b>Total number of lesions – <i>n</i></b>					
	mean	4.9	5.0	4.8	5.0
	median	5.0	4.5	5.5	5.0
	<i>P</i>	0.871		0.810	
<b>No. of locations of tumor lesions (central radiologist)</b>					
	1	6 (15.4%)	4 (18.2%)	4 (25.0%)	6 (13.3%)
	2	15 (38.5%)	6 (27.3%)	5 (31.3%)	16 (35.6%)
	>=3	18 (46.2%)	12 (54.5%)	7 (43.8%)	23 (51.1%)
	<i>P</i>	0.777		0.380	
<b>Baseline lymphocyte levels<sup>b</sup> – 10E9 l<sup>-1</sup></b>					
	mean	1.51	1.50	1.51	1.50
	median	1.31	1.34	1.30	1.31
	<i>P</i>	0.763		0.942	

Notes: <sup>a</sup> Patient 59-001 received both, sunitinib and sorafenib, as previous therapies.

<sup>b</sup> Values from VC for +CY patients and from V1 for –CY patients.

**Supplementary Table 3: Baseline characteristics and survival of IMA901-202 patients after prior cytokine therapy in comparison to historic controls.**

		IMA901-202 Prior Cytokine All	IMA901-202 Prior Cytokine -CY	IMA901-202 Prior Cytokine +CY	TARGET Placebo arm	TARGET Sorafenib arm	RTKCC-0511- 014 Sunitinib
<b>Sample size (n)</b>		40	20	20	452	451	63
<b>Overall survival</b>	<b>Median months</b>	19.8	15.8	not reached (max. follow-up 33.1)	15.2	17.8	16.4
	≥ 1 year	73.3%	66.8%	83.6%	~59%	~66%	~61%
	≥ 2 years	45.9%	38.2%	54.5%	~34%	~36%	<42%
<b>Age</b>	<b>Median years</b>	57	59	56	59	58	60
<b>Sex</b>	<b>% male</b>	78%	65%	90%	75%	70%	68%
<b>Karnofsky status ≥ 80</b>		100%	100%	100%	98%	98%	100%
<b>Time since initial tumor diagnosis</b>	<b>Mean years</b>	3.4	4.4	2.3	3.3 <sup>a</sup>	2.8 <sup>a</sup>	4.1
	<b>Median years</b>	1.7	2.6	1.3	1.9 <sup>a</sup>	1.6 <sup>a</sup>	1.7
<b>Nephrectomy</b>		93%	95%	90%	94%	93%	92%
<b>Prior cytokine therapy</b>		100%	100%	100%	81%	83%	100%
<b>Other prior anti-tumor therapies</b>	<b>Chemotherapy</b>	35%	40%	30%	31% <sup>ab</sup>	27% <sup>ac</sup>	NA
	<b>Hormones</b>	3%	5%	0%	7% <sup>a</sup>	7% <sup>a</sup>	NA
<b>MSKCC prognostic score</b>	<b>Favourable</b>	45%	45%	45%	50%	52%	54%
	<b>Intermediate</b>	55%	55%	55%	49%	48%	NA
<b>Metastatic sites</b>	<b>Lung</b>	90%	90%	90%	77%	77%	81%
	<b>Liver</b>	28%	20%	35%	26%	26%	16%
<b>No. of tumor lesions</b>	<b>1</b>	5%	10%	0%	14%	14%	18%
	<b>2</b>	8%	5%	10%	29%	29%	24%
	<b>≥ 3</b>	88%	85%	90%	57%	57%	59%

<sup>a</sup> Based on the Nexavar® EPAR with n=384 in the sorafenib and n=385 in the placebo arm

<sup>b</sup> Pyrimidine analogues 18.7%, Vinca alkaloids 12.7%

<sup>c</sup> Pyrimidine analogues 15.6%, Vinca alkaloids 11.5%

Shown are IMA901-202 patients of the per-protocol group that were first line treated with cytokines. Historic control parameters were derived from the Nexavar® EPAR (EMA/H/C/000690 -IA/00029/G

[http://www.ema.europa.eu/docs/en\\_GB/document\\_library/EPAR - Product Information/human/000690/WC500027704.pdf](http://www.ema.europa.eu/docs/en_GB/document_library/EPAR_-_Product_Information/human/000690/WC500027704.pdf),

September 2011), Sutent® EPAR (EMA/H/C/000687 -II/0028 [http://www.ema.europa.eu/docs/en\\_GB/document\\_library/EPAR - Product Information/human/000687/WC500057737.pdf](http://www.ema.europa.eu/docs/en_GB/document_library/EPAR_-_Product_Information/human/000687/WC500057737.pdf), September 2011) and references 1-3.

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