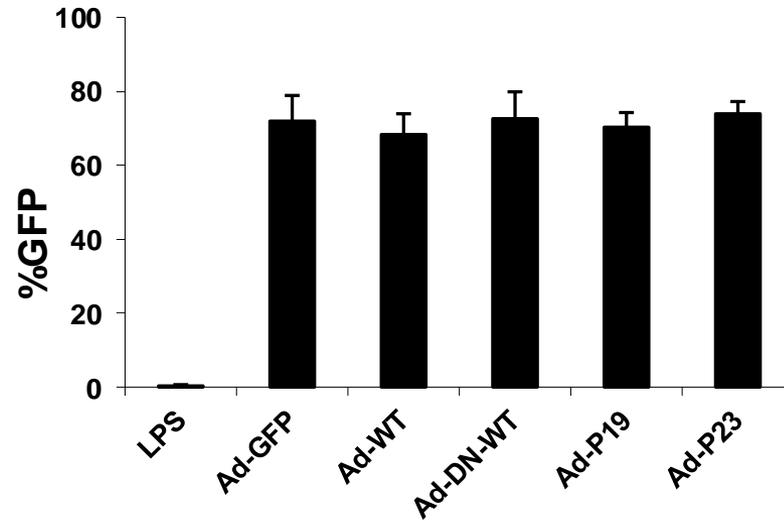


## Supplemental Figure S1



Flow cytometric analysis of GFP expression in transduced primary Mo-DC transduced with adenovirus as shown. LPS is the positive control for the experiment not transduced.

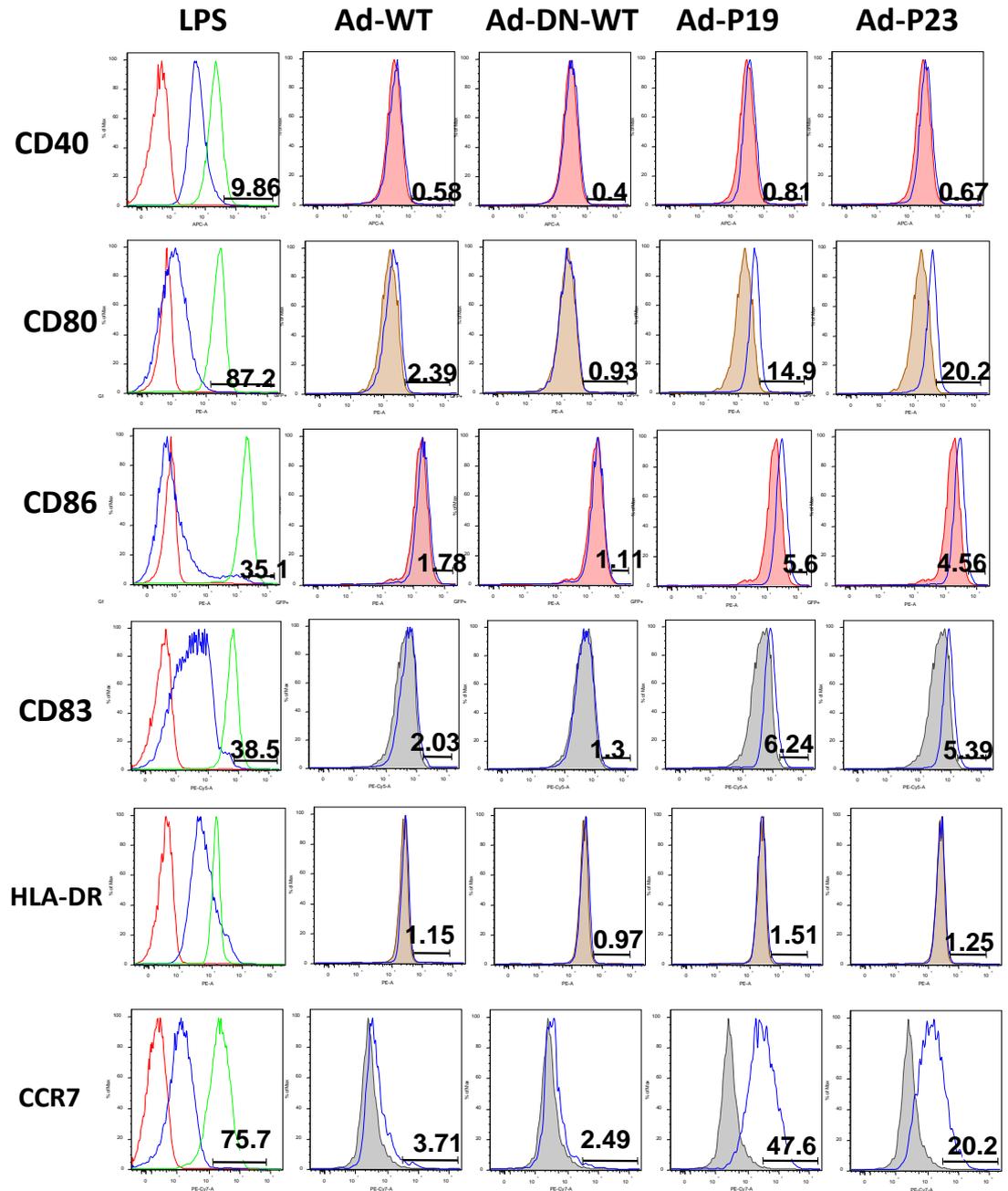
**Supplemental Table S1. The effects of Ad-P19 or Ad-P23 on Mo-DC surface marker expression**

	Percentage of GFP+ iDC coexpressing indicated markers					
	CD40	CD80	CD83	CD86	HLA-DR	CCR7
	%	%	%	%	%	%
Ad-LPS	6.7±4.8	75.8±15.2	16.9±9.3	24.1±15.0	0.4±0.5	50.2±5.0
Ad-WT	1.3±0.9	5.4±0.3	3.8±2.0	0.8±0.2	0.6±0.4	6.5±3.7
Ad-DN-WT	1.6±1.5	2.5±2.8	1.1±0.6	0.7±0.2	2.1±1.6	6.9±5.1
Ad-P19	2.5±1.2	<b>25.6±2.3</b>	<b>8.1±1.6</b>	1.5±0.9	1.4±1.2	<b>28.9±12.8</b>
Ad-P23	4.0±2.1	<b>23.1±0.6</b>	<b>8.0±2.0</b>	1.8±1.3	0.8±0.4	<b>26.4±8.1</b>

Comparative analysis +/- standard deviation of flow cytometric analysis of different markers in 5 separate experiments. Primary Mo-DC transduced with adenovirus as shown. LPS is the positive control for the experiment transduced with empty GFP+ vector.

## Supplemental Figure S2

Flow cytometric analysis of Mo-DCs treated with Ad-GFP, Ad-WT, Ad-DN-WT, Ad-P19, Ad-P23, or LPS (2  $\mu\text{g}/\text{mL}$ ) for 24 h for changes in CD40, CD80, CD86, CD83, HLA-DR and CCR7. Each experimental construct was compared to the empty-vector control, filled histograms, and infected cells were gated on GFP prior to analysis.



**Supplemental Table S2. ANOVA test values**

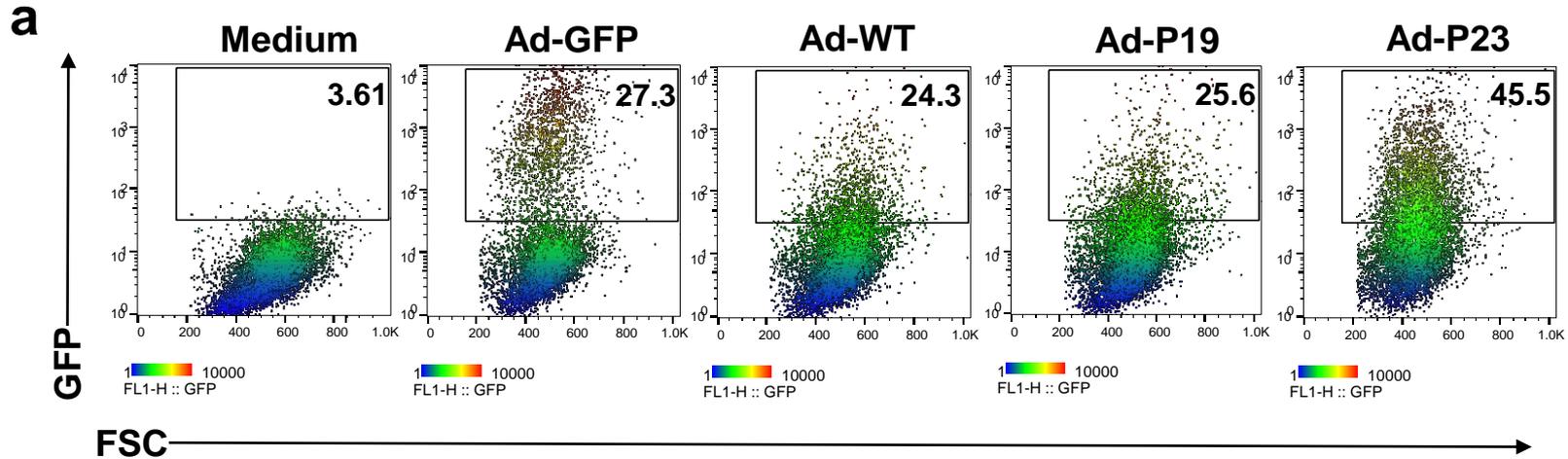
	Ad-GFP vs				
	WT	DN-WT	Ad-P19	Ad-P20	Ad-P23
TNF $\alpha$	0.9998	>0.9999	<b>0.0002</b>	0.9987	0.1033
IL-12p70	0.9985	>0.9999	<b>&lt;0.0001</b>	>0.9999	<b>0.0752</b>
IL-10	0.9926	0.9963	0.9176	0.9406	0.4258
IL-8	0.5549	0.9999	<b>0.0005</b>	0.8661	<b>0.0048</b>
IFN $\gamma$	0.9996	0.9998	<b>0.0002</b>	0.9999	<b>0.0559</b>

	Ad-GFP vs			
	WT	DN-WT	Ad-P19	Ad-P23
Proliferation	0.3939	0.3638	<b>&lt;0.0001</b>	<b>&lt;0.0001</b>
Lysis	0.3906	0.7983	<b>&lt;0.0001</b>	<b>0.0028</b>
Migration	0.6277	<b>&lt;0.0001</b>	<b>&lt;0.0001</b>	0.117

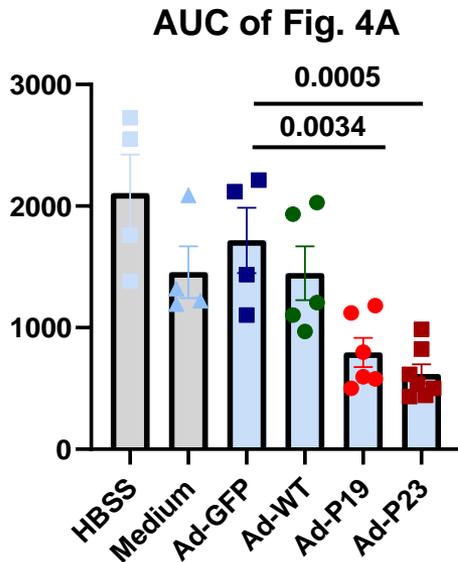
ELISPOT	Ad-GFP vs		
	Ad-WT	Ad-P19	Ad-P23
	<b>0.9995</b>	<b>0.1658</b>	<b>0.0026</b>

ANOVA analysis of figures 2b, 3a, 3b, 3c and 4b. Yellow denotes p value is significant. Note that two bolded p-values in Ad-P23 close to significant.

Supplemental Figure S3



**b**



a) GFP expression flow cytometric analysis of bone marrow DCs from animal experiment in Figure 4 transfected with Nothing (medium), Ad-GFP, Ad-WT, Ad-P19, and Ad-P23 (representative figure). b) representation of calculation of area under the curve (AUC) for animals as in “a”. The significance was measured with ANOVA (shown) against Ad-GFP as control). The AUC was performed with animals that survived to the end of the study.

<b>Supplemental Table S3. Paired student t-test values</b>					
<i>Day 7</i>	Medium	Ad-GFP	Ad-WT	Ad-p19	Ad-P23
HBSS vs	0.227012	0.155804	0.00562	0.000243	0.132482
Med vs		0.168829	0.085582	0.126083	0.544817
AdGFP vs			0.168767	0.193095	0.720357
<i>Day 10</i>					
HBSS vs	0.838925	0.2088	0.191246	0.000179	0.003925
Med vs		0.003124	0.111424	0.004858	0.008461
AdGFP vs			0.7023	0.021071	0.02903
<i>Day 14</i>					
HBSS vs	0.087598	0.120166	0.100367	0.000196	0.000718
Med vs		0.450491	0.163527	0.008035	0.002613
AdGFP vs			0.245815	0.011623	0.004682
<i>Day 18</i>					
HBSS vs	0.064465	0.202463	0.016984	0.000607	0.003114
Med vs		0.088198	0.955855	0.009669	0.009832
AdGFP vs			0.1784	0.001072	0.001837
<i>Day 21</i>					
HBSS vs	0.069485	0.260954	0.061666	0.003163	0.007203
Med vs		0.104447	0.671304	0.001028	0.002993
AdGFP vs			0.549291	0.004537	0.001536
<i>Day 25</i>					
HBSS vs	0.13873	0.055627	0.09018	0.010939	0.00984
Med vs		0.259094	0.111343	0.003299	0.001504
AdGFP vs			0.22362	0.008242	0.002021
<i>Day 28</i>					
HBSS vs	0.225245	0.053565	0.042643	0.01083	0.014383
Med vs		0.943765	0.008639	0.022113	0.012809
AdGFP vs			0.082507	0.063996	0.017233

Paired student t-test analysis of tumor volume comparisons in Figure 4a. Yellow denotes p value is significant.

### Supplemental Table S4. Mutagenesis Primers

Primer name	Sequence
PCDNA3	5'-AATACGACTCACTATAGGGA-3'
	5'-GGACAGTGGGAGTGGCACCTTCCA-3'
DAP12 P7	5'-GTAGACAACCGACCTCTGACC -3
	5'-AGGTCGGTTGTCTACAGCGAC -3'
DAP12 P8	5'-CGCTCATTGTATTCCGGCCTCTGTGC -3'
	5'- CAGAGGCCGGAATACAAATGAGCGGCC -3'
DAP12 P9	5'-ACCGAGTCGCCTGATC AGGAGCTCCA -3'
	5'-GAGCTCCTGATCAGGCGACTCGGT -3'
DAP12 P10	5'-CGCTCATTCTCTTCCGGCCTCTGTGT -3'
	5'-CAGAGGCCGGAAGAGAAATGAGCGGCC -3'
DAP12 P11	5'-TCGGATGTCGACAGCGACCTCAAC -3'
	5'-GTGTTGAGGTCGCTGTCGACATCC -3'
DAP12 P17	5'-CAGAGGTCGGTTCGCTACAGCGACCTC-3'
	5'-GTCGCTGTAGCGAACCGACCTCTGACC-3'
DAP12 P18	5'-CAGAGGTCGCATGTCTACAGCCACCTCAA CAC-3'
	5'-TG TTGAGGTGGCTGTAGACATGCGAC CTCTGAC-3'
DAP12 P19	5'-GATGTCTACAGCAA CCTCAACACA CAGAG-3'
	5'-CTGTGTGTTGAGGTTGCTGTAG ACATCCG-3'
DAP12 P20	5'-ACCGAGTCGCCTTGTGAGGAGCTCCAGG-3'
	5'-TGGAGCTCCTGACAAGGCGACTCGGTCTC-3'
DAP12 P21	5'-GTCGGATGTCTGCAGCGACCTCAACACAC-3'
	5'-GTTGAGGTCGCTGCAGACATCCGACCTC-3'
DAP12 P22	5'-GATGTCTACAGCGACTACAACAC ACAGAG-3'
	5'-GCCTCTGTGTGTTGTAGTCGCTGTAGAC-3'
DAP12 P23	5'-GTCTACAGCGACCTCAAAACAC AGAGGC-3'
	5'-CGGCCTCTGTGTTTTGAGGTCGCTG TAG-3'