

## Supporting Information

### **Naked-Eye Fingerprinting of Single Nucleotide Polymorphisms on Psoriasis Patients**

Paola Valentini<sup>1†</sup>, Alessandra Marsella<sup>1,2†</sup>, Paolo Tarantino<sup>3</sup>, Salvatore Mauro<sup>3</sup>, **Silvia Baglietto<sup>4</sup>**,  
Maurizio Congedo<sup>5</sup>, and Pier Paolo Pompa<sup>1\*</sup>

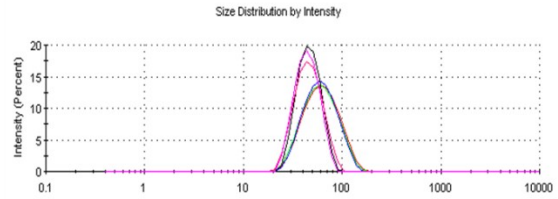
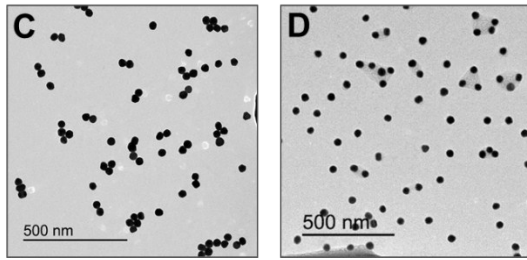
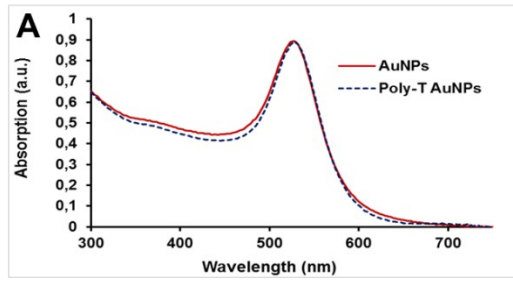
<sup>1</sup> *Nanobiointeractions&Nanodiagnostics, Istituto Italiano di Tecnologia (IIT), Via Morego, 30 – 16163 – Genova (Italy).*

<sup>2</sup> *Department of Engineering for Innovation, University of Salento, Via per Monteroni – 73100 – Lecce (Italy).*

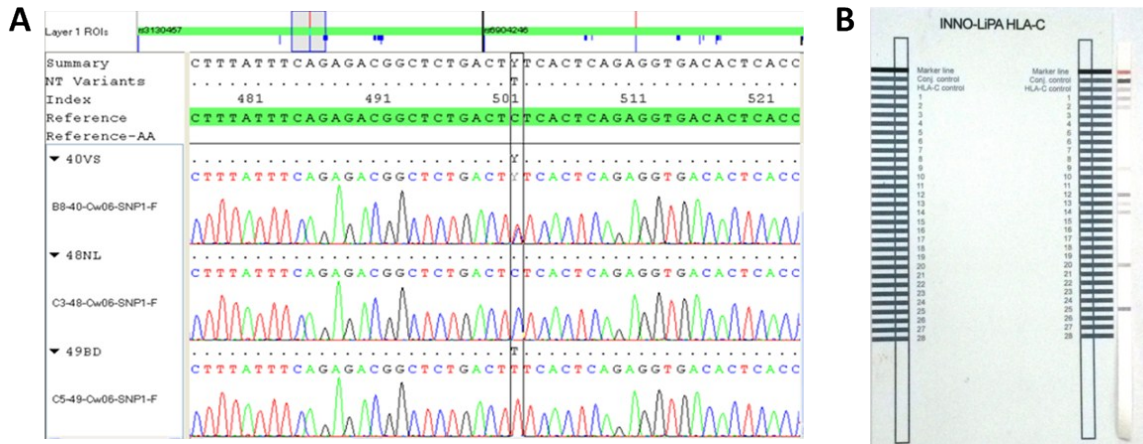
<sup>3</sup> *Laboratory of Medical Genetics, Vito Fazzi Hospital, Piazzetta Muratore – 73100 – Lecce (Italy).*

<sup>4</sup> *Pattern Analysis and Computer Vision (PAVIS), Istituto Italiano di Tecnologia (IIT), Via Morego, 30 – 16163 – Genova (Italy).*

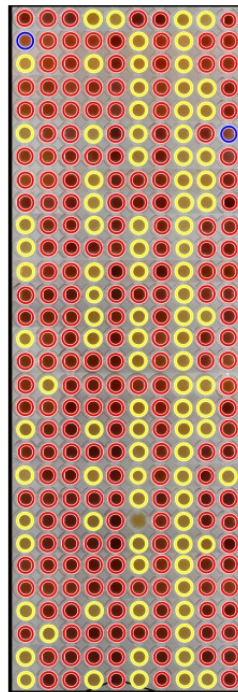
<sup>5</sup> *Department of Dermatology, Vito Fazzi Hospital, Piazzetta Muratore – 73100 – Lecce (Italy).*



**Fig. S1.** Characterization of AuNPs and PolyT-AuNPs. (A) UV-vis spectra; (B) DLS data; (C,D) TEM images of AuNPs (C) and PolyT-AuNPs (D).



**Fig. S2.** Standard reference tests for HLA genotyping. **(A)** Sequencing analysis of SNPs. Each row corresponds to a different patient; the reference sequence (green) and the nucleotide variant (column selector) are indicated. The three genotypes (heterozygous, wild-type and mutant) are clearly distinct. **(B)** Representative image of a INNO-LiPA® HLA-C line probe assay, showing the molecular typing of human leukocyte antigen (HLA) C alleles at allele group level Cw\*01 – Cw\*18. Typing and interpretation of results was performed by LiRAS software.



**Fig. S3.** Automatic color analysis of the results. A picture was analyzed by the Circular Hough Transform and by a K-means clustering algorithm, as described in Methods. The final result is a label of yellow and red circles. Unclear data are marked in blue to highlight the need for visual verification. In this picture, 298 samples out of 300 were correctly assigned by the automated analysis. The remaining 2 unclear results (<0.7 %) could be easily confirmed manually.

PCR primers						
	Sequence (5'->3')	Length	Tmelting (°C)	GC%		
HLA C*06:02	rs3130457	CCATCTACCACGCTGCTGTA	20	59.54	55.00	
		Biot - GAGGGATGCACAGCCATAGA	20	59.24	55.00	
	rs6904246	CCTCACCAGGAACTGAATCT	20	56.54	50.00	
		Biot - ACACCACAGATGGATTGGTT	20	57.02	45.00	
	rs7745906	TGGAAAGATCCCATTCAAAG	21	54.03	38.10	
		Biot - GTTTTTTGTGGGGTTCAGAT	20	54.26	40.00	
	rs10484554	CGGGAGTCCAGCAGGTC	17	59.02	70.59	
		Biot- TGCAGCAAAGCCTGGGA	17	59.07	58.82	
	TNFAIP3	rs610604	GGCAAGAATTGTAGAACCATT	21	54.43	38.10
			Biot - TCATTCTTGACTCGAACATG	20	53.38	40.00
Discriminating probes						
HLA C*06:02	rs3130457	5'GACT T TCACTCAGAG GT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3'				
		5'GACT C TCACTCAGAG GT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3'				
	rs6904246	5'CCAG G GTCCAGAATTG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3'				
		5'CCAG A GTCCAGAATTG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3'				
	rs7745906	5'CAGT G GTAGATTTTCTTAC AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3'				
		5'CAGT A GTAGATTTTCTTAC AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3'				
	rs10484554	5'TCAC T TATGACGTCTCAG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3'				
		5'TCAC C TATGACGTCTCAG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3'				
TNFAIP3	rs610604	5'AGCT C ACACTTTTCA CG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3'				
	5'AGCT A ACACTTTTCA CG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3'					

**Table S1.** Sequences of primers and discriminating probes used for the colorimetric test.

**PCR primers**

	Sequence (5'→3')	Length	Tmelting (°C)	GC%
<b>HLA C*06:02</b>	<b>rs3130457</b> TCCTCCCCTTCTCCAAACAC	20	58,94	55
	GTTTCGCCTCATCGTGGTTT	20	59,13	50
	<b>rs6904246</b> AAGAGGTTGAGAGGTTGGGG	20	58,93	55
	TCAGGGAGCAGGTGTTAGTC	20	58,73	55
	<b>rs7745906</b> AACATGTCACAGTGCTGCAG	20	59,05	50
	GCGGCAACAGAGTGAGAAC	19	59,14	57,89
<b>rs10484554</b>	CCTTGATTCAGTTTGGGGCC	20	59,1	55
	ACTCTGTCCCTGTTCTTCT	20	57,59	50
<b>TNFAIP3</b>	<b>rs610604</b> AGCAAAATACCCAACCTGAGG	21	58,19	47,62
	AGGTTCCATGGGATTCTGGG	20	59,07	55

**Table S2.** Primers used for the automated direct sequencing.

PATIENT	HLA-C allele								TNFAIP3 gene					
	rs10484554		rs3130457		rs6904246		rs7745906		Genotype	RDB <sup>a</sup>	LiRaS <sup>b</sup>	rs610604		
	COLORIMETRIC TEST	SEQUENCING	COLORIMETRIC TEST	SEQUENCING	COLORIMETRIC TEST	SEQUENCING	COLORIMETRIC TEST	SEQUENCING				COLORIMETRIC TEST	SEQUENCING	
1	C/T	C/T	T/T	T/T	A/A	A/A	G/G	G/G	NN <sup>c</sup>	12/12	1202/1214	T/T	T/T	
2	C/T	C/T	C/T	C/T	G/G	G/G	G/G	G/G	NP <sup>d</sup>	04/06	0404/0602	G/T	G/T	
3	C/C	C/C	T/T	T/T	G/G	G/G	G/G	G/G	NN	14/16	1402/1404	G/T	G/T	
4	C/T	C/T	C/T	C/T	G/G	G/G	G/G	G/G	NP	01/06	0102/0602	T/T	T/T	
5	C/T	C/T	C/T	C/T	G/G	G/G	G/G	G/G	NP	04/06	0401/0602	T/T	T/T	
6	C/C	C/C	T/T	T/T	G/G	G/G	G/G	G/G	NN	04/04	0401/0401	G/T	G/T	
7	C/T	C/T	C/T	C/T	G/G	G/G	G/G	G/G	NP	06/15	0602/1502	T/T	T/T	
8	C/T	C/T	T/T	T/T	A/G	A/G	G/G	G/G	NN	04/06	0411/0611	T/T	T/T	
9	C/T	C/T	T/T	T/T	A/G	A/G	G/G	G/G	NN	08/12	0805/0812	T/T	T/T	
10	C/C	C/C	T/T	T/T	G/G	G/G	G/G	G/G	NN	02/07	0202/0208	G/T	G/T	
11	C/C	C/C	C/T	C/T	G/G	G/G	G/G	G/G	NN	07/07	0701/0706	G/T	G/T	
12	C/C	C/C	T/T	T/T	G/G	G/G	G/G	G/G	NN	04/15	0401/1501	G/T	G/T	
13	C/T	C/T	T/T	T/T	A/G	A/G	G/G	G/G	NN	04/12	0407/1202	G/T	G/T	
14	C/T	C/T	T/T	T/T	G/G	G/G	G/G	G/G	NP	06/17	0602/1701	T/T	T/T	
15	C/C	C/C	T/T	T/T	G/G	G/G	G/G	G/G	NN	07/16	0701/1601	G/T	G/T	
16	C/T	C/T	C/T	C/T	G/G	G/G	G/G	G/G	NP	04/06	0401/0602	G/T	G/T	
17	T/T	T/T	C/T	C/T	A/G	A/G	G/G	G/G	NP	06/12	0602/1202	T/T	T/T	
18	C/T	C/T	C/T	C/T	G/G	G/G	G/G	G/G	NP	01/06	0102/0602	T/T	T/T	
19	C/C	C/C	T/T	T/T	G/G	G/G	G/G	G/G	NN	04/07	0401/0701	T/T	T/T	
20	C/T	C/T	C/T	C/T	G/G	G/G	G/G	G/G	NP	04/06	0401/0602	G/T	G/T	
21	C/C	C/C	T/T	T/T	G/G	G/G	G/G	G/G	NN	04/15	0401/1511	G/G	G/G	
22	C/T	C/T	C/T	C/T	G/G	G/G	G/G	G/G	NP	04/06	0401/0602	G/T	G/T	
23	C/C	C/C	T/T	T/T	G/G	G/G	G/G	G/G	NN	05/15	0501/1507	G/T	G/T	
24	C/C	C/C	C/T	C/T	G/G	G/G	G/G	G/G	NN	07/08	0706/0801	T/T	T/T	
25	C/T	C/T	C/T	C/T	G/G	G/G	G/G	G/G	NP	01/06	0102/0602	G/T	G/T	
26	C/T	C/T	C/T	C/T	A/G	A/G	G/G	G/G	NN	08/14	0803/1404	G/T	G/T	
27	C/C	C/C	T/T	T/T	G/G	G/G	G/G	G/G	NN	04/16	0407/1601	G/T	G/T	
28	T/T	T/T	C/T	C/T	A/G	A/G	G/G	G/G	NP	06/12	0602/1202	G/T	G/T	
29	C/C	C/C	C/T	C/T	G/G	G/G	G/G	G/G	NN	08/15	0801/1509	G/T	G/T	
30	C/C	C/C	T/T	T/T	G/G	G/G	G/G	G/G	NN	05/05	0501/0501	T/T	T/T	

<sup>a</sup>RDB = Reverse Dot Blot C\* test results for both allele (two digits)  
<sup>b</sup>LiRaS = prediction of C\* status from RDB results using the LiRaS software (four digits)  
<sup>c</sup>NN = Negative for C\*06:02 on both chromosomes  
<sup>d</sup>NP = Heterozygote for C\*06:02

**Table S3.** Detailed results of the SNPs genotypization by colorimetric test, sequencing, and reverse dot blot test, for each patient.