

**Archives of Virology**

ELECTRONIC SUPPLEMENTARY MATERIAL

**Hepatitis C virus quasispecies in chronically infected children subjected to  
interferon-ribavirin therapy**

**Magdalena Figlerowicz<sup>2\*\*</sup>, Paulina Jackowiak<sup>1\*\*</sup>, Piotr Formanowicz<sup>1,3</sup>, Paweł Kędziora<sup>3</sup>,**

**Magdalena Alekska<sup>1</sup>, Nelli Malinowska<sup>1</sup>, Jacek Błażewicz<sup>1,3</sup>, Marek Figlerowicz<sup>1\*</sup>**

1 - Institute of Bioorganic Chemistry Polish Academy of Sciences, Noskowskiego 12/14, 61-704  
Poznań, Poland

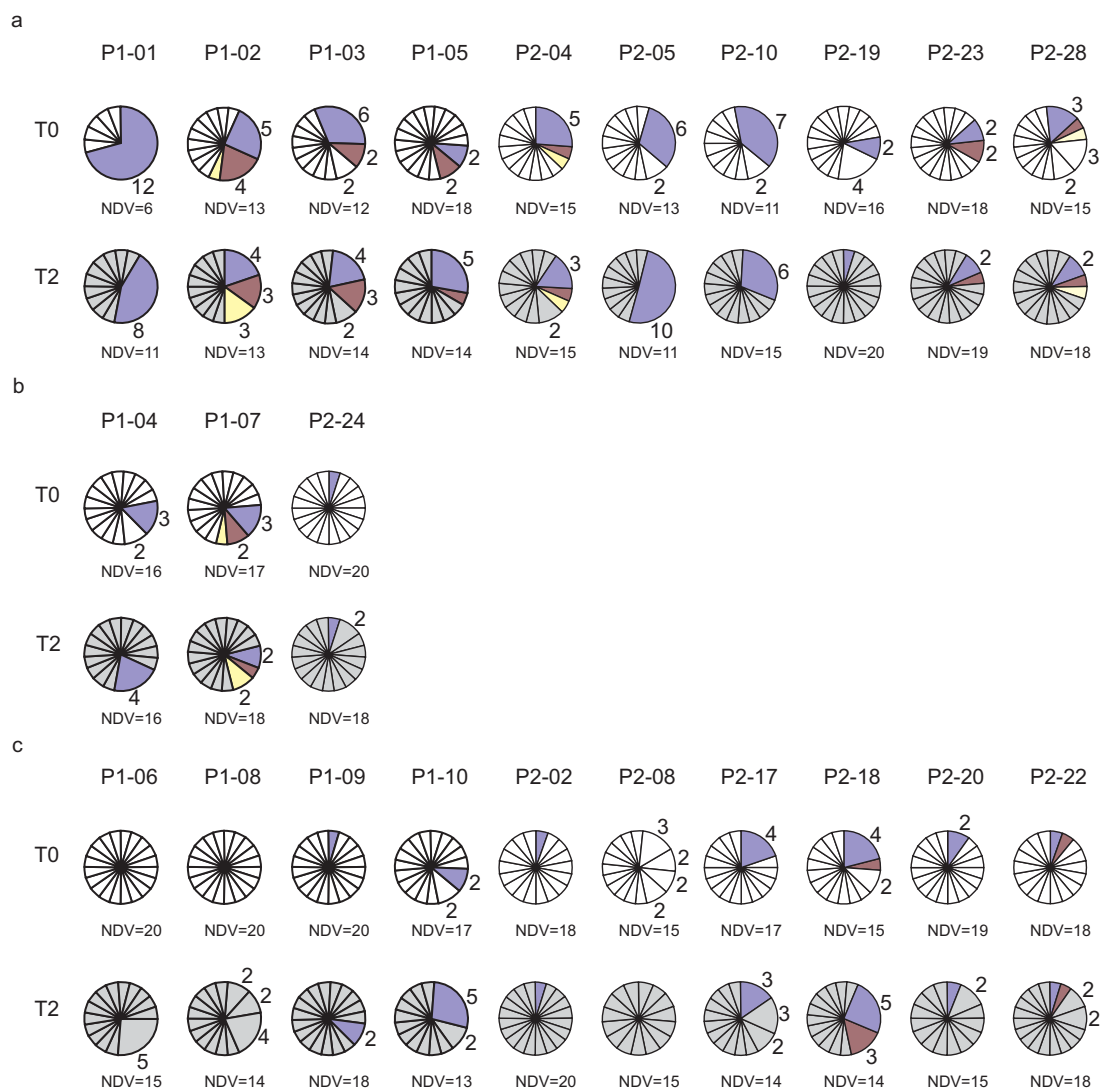
2 – Department of Infectious Diseases and Child Neurology, Karol Marcinkowski University of  
Medical Sciences, Szpitalna 27/33, 60-572 Poznań, Poland

3 – Institute of Computing Science, Poznań University of Technology, Piotrowo 3A, 60-965  
Poznań, Poland

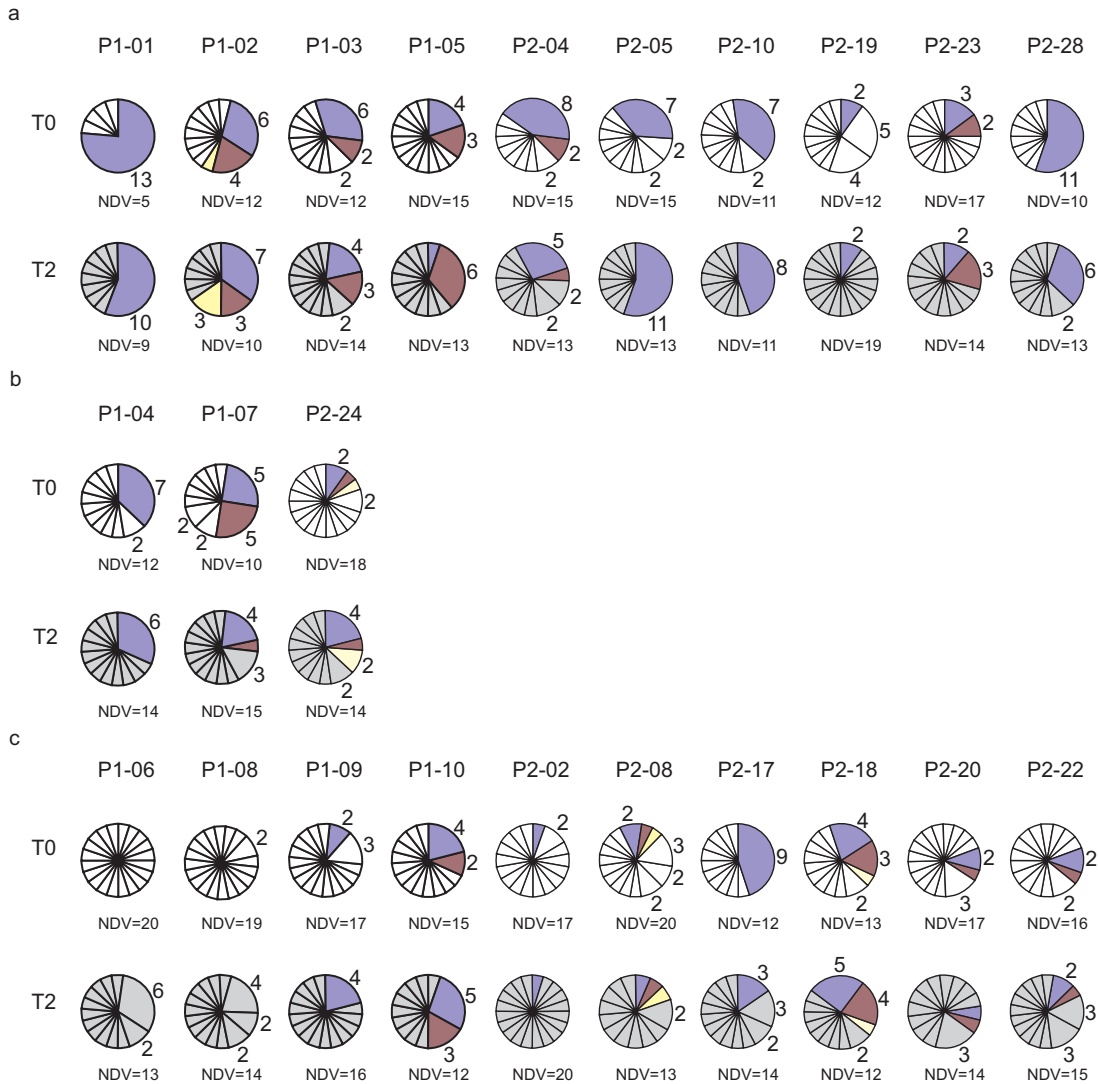
**\* Corresponding author:**

Prof. Marek Figlerowicz  
Institute of Bioorganic Chemistry  
Polish Academy of Sciences  
Noskowskiego 12/14  
61-704 Poznań  
Poland  
tel.: +48-61-8528503 e. 103,142  
fax: +48-61-8520532  
e-mail: [marekf@ibch.poznan.pl](mailto:marekf@ibch.poznan.pl)

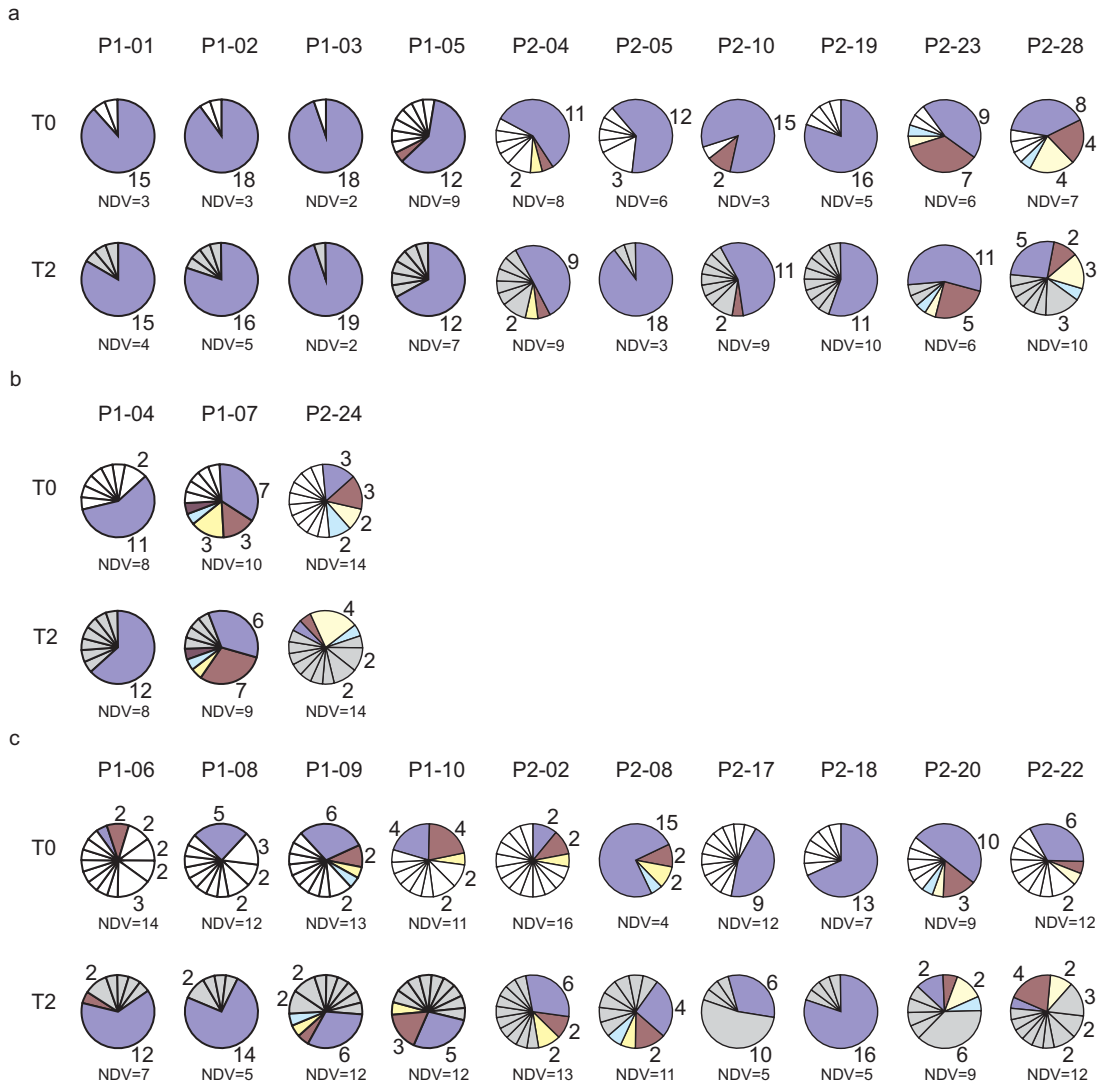
\*\* Both authors equally contributed to these studies



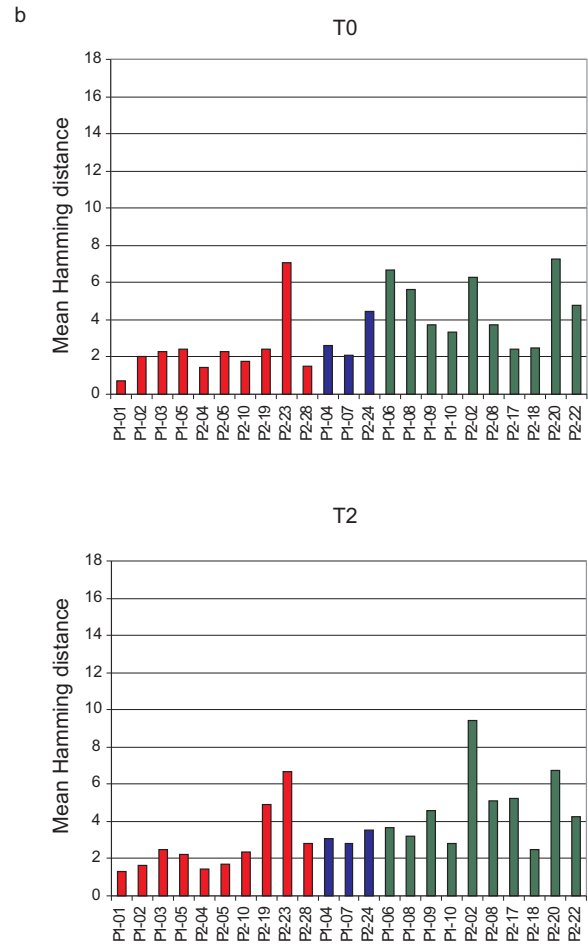
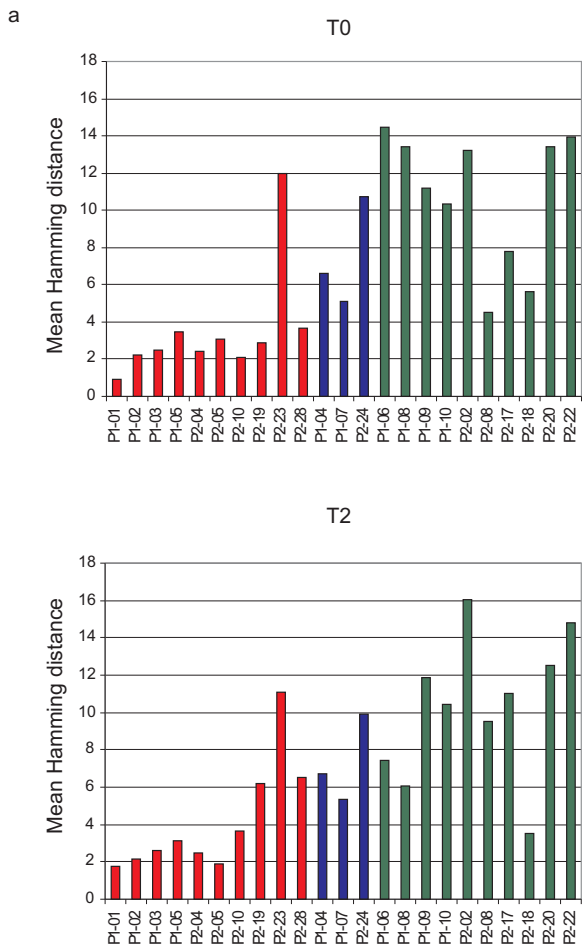
**Online Resource 1** Number of different variants identified in all analyzed HCV populations (determined based on the amino acid sequences encoded by the entire E1/E2 amplicon). Circular diagrams show the composition of the individual HCV populations isolated at T0 and T2 from non-responders (a), transient responders (b) and sustained responders (c). Every single variant is represented by one sector. Sectors representing variants identified exclusively at T0 or at T2 are white or gray, respectively. With other colors are marked the sectors representing the identical variants found both at T0 and at T2 in one patient (not in different patients). Numbers accompanying diagrams indicate how frequently each variant was identified (the lack of a number indicates that the sequence was found only once). The number of different variants (NDV) in each population is given below the diagram



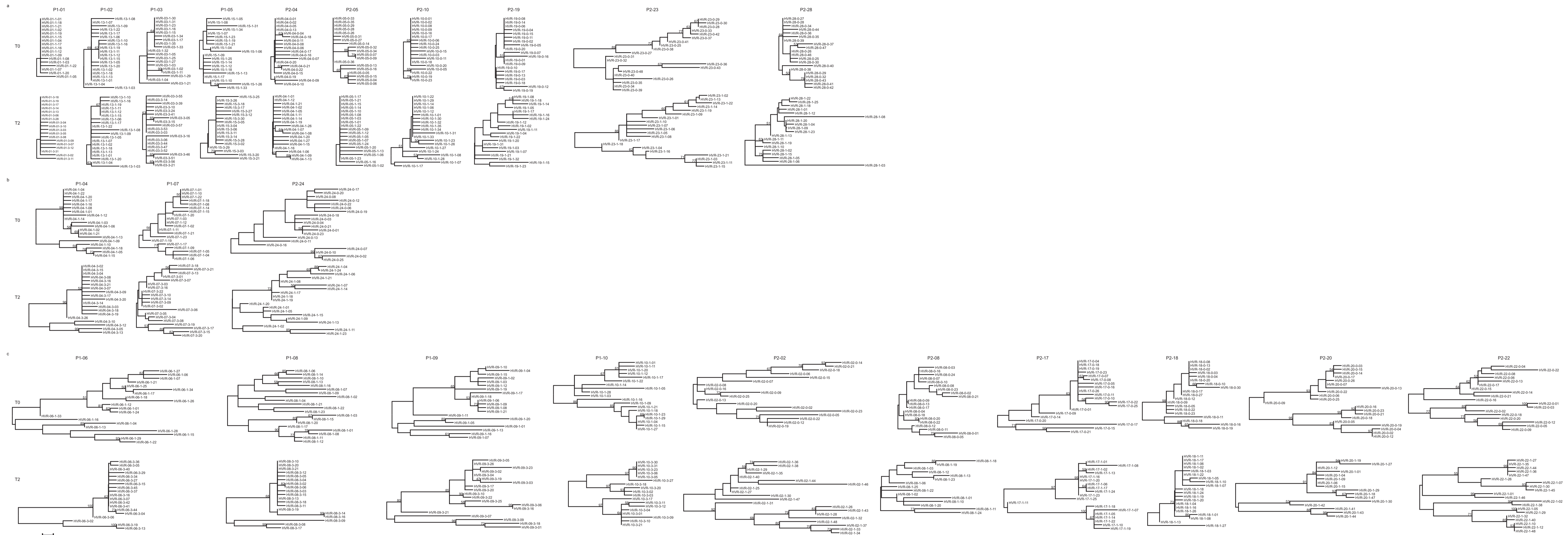
**Online Resource 2** Number of different variants identified in all analyzed HCV populations (determined based on the amino acid sequence encoded by the non-HVR1 portion of E1/E2 amplicon). For details, see legend for Online Resource 1



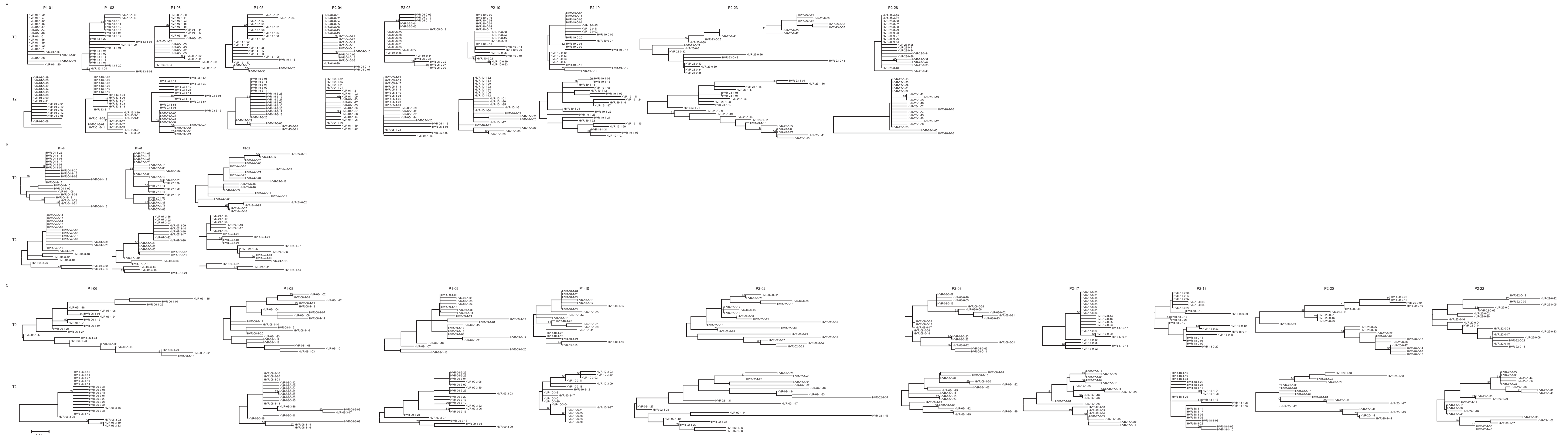
**Online Resource 3** Number of different variants identified in all analyzed HCV populations (determined based on the HVR1 amino acid sequence). For details, see legend for Online Resource 1



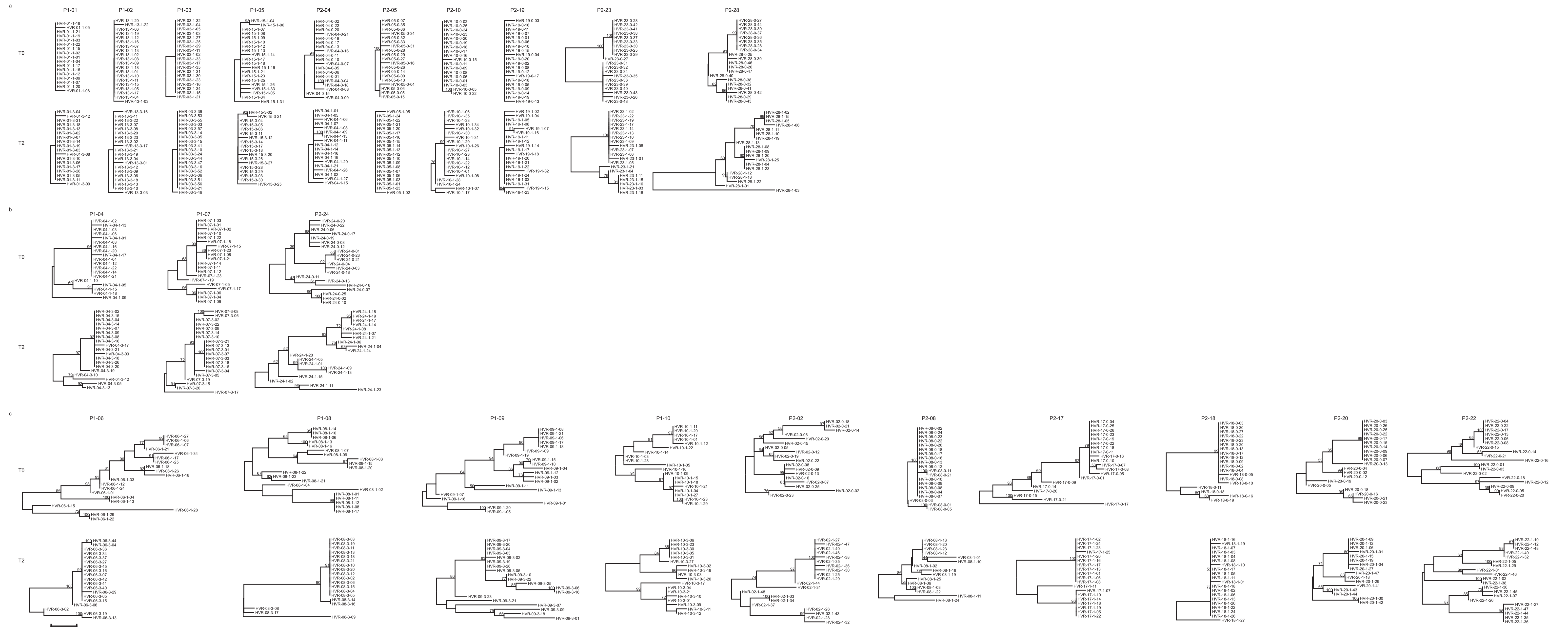
**Online Resource 4** Genetic diversity of the entire E1/E2 fragment (a) and its non-HVR1 portion (b) (determined based on the amino acid sequence). Mean Hamming distance was calculated separately for each viral population based on 20 clones randomly selected at T0 and T2. The colors of the bars correspond to the three types of the patients' response to the treatment: red - no response, blue - transient response and green - sustained response



**Online Resource 5** Phylogenetic analysis of individual HCV quasispecies (based on amino acid sequences encoded by the entire E1/E2 amplicon). Phylogenetic trees were constructed separately for each population isolated either at T0 or at T2. (a) non-responders, (b) transient responders and (c) sustained responders. The percentage of trees in which the variants clustered together is indicated above the branches (values lower than 50% were removed). Branch lengths are measured in the number of substitutions per site

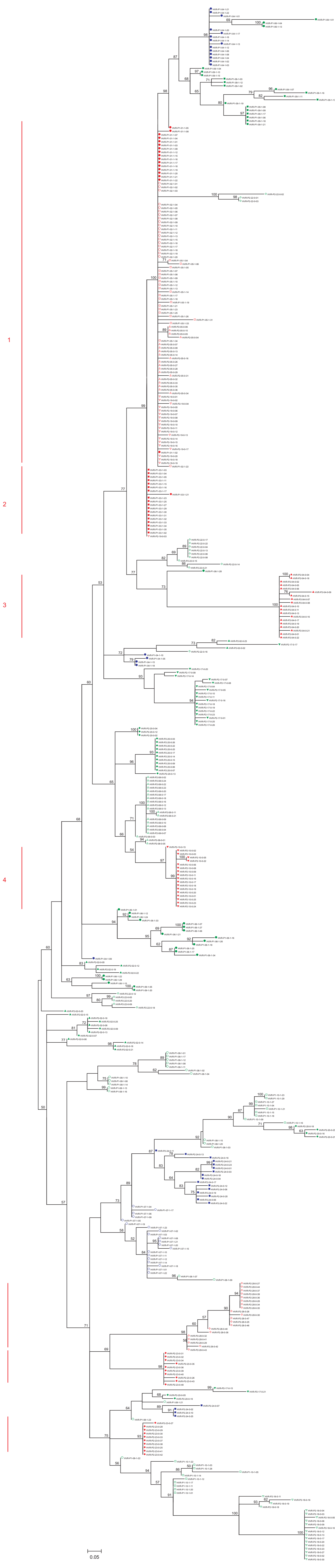


**Online Resource 6** Phylogenetic analysis of individual HCV quasispecies (based on the amino acid sequences encoded by the non-HVR1 portion of E1/E2 amplicon). For details, see legend for Online Resource 5



**Online Resource 7** Phylogenetic analysis of individual HCV quasispecies (based on the HVR1 amino acid sequences). For details, see legend for Online Resource 5





**Online Resource 8** Integrated phylogenetic tree constructed for all HVR1 variants identified in 23 examined HCV quasispécies at T0. The individual amino acid sequences are named according to the following schema: *HVR-patient-number-clone-number*; e.g. HVR-P1-03-1-21, where 'P1-03' indicates patient number, while '1-21' refers to clone number. In addition, the names are accompanied by geometrical symbols, where one symbol refers to all sequences representing the same quasispécies. The symbols are colored along with patients' response to the therapy: red – no response and blue – transient response and green – sustained response. Clusters grouping sequences detected in non-responders are marked with red line and numbers 1 to 7. The percentage of trees in which the variants clustered together is indicated above the branches (values lower than 50% were removed). Branch lengths are measured in the number of substitutions per site