Impact of HCV *Core* gene quasispecies on hepatocellular carcinoma risk among HALT-C Trial patients

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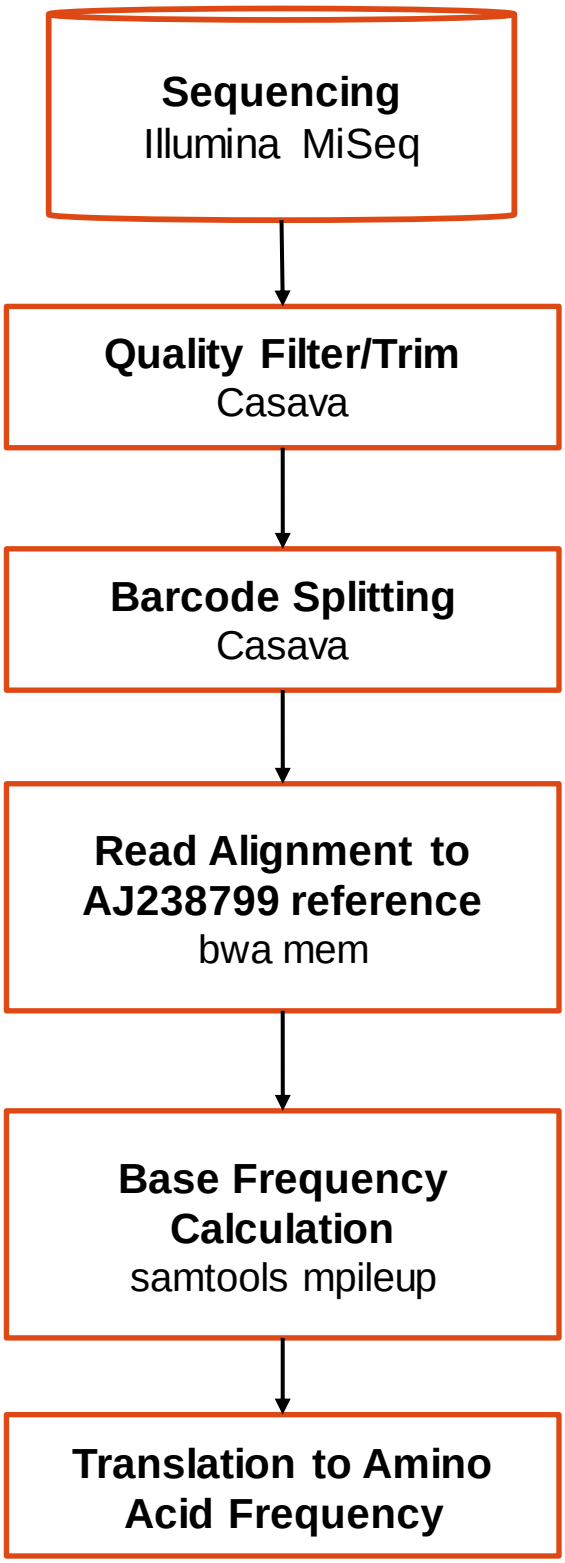
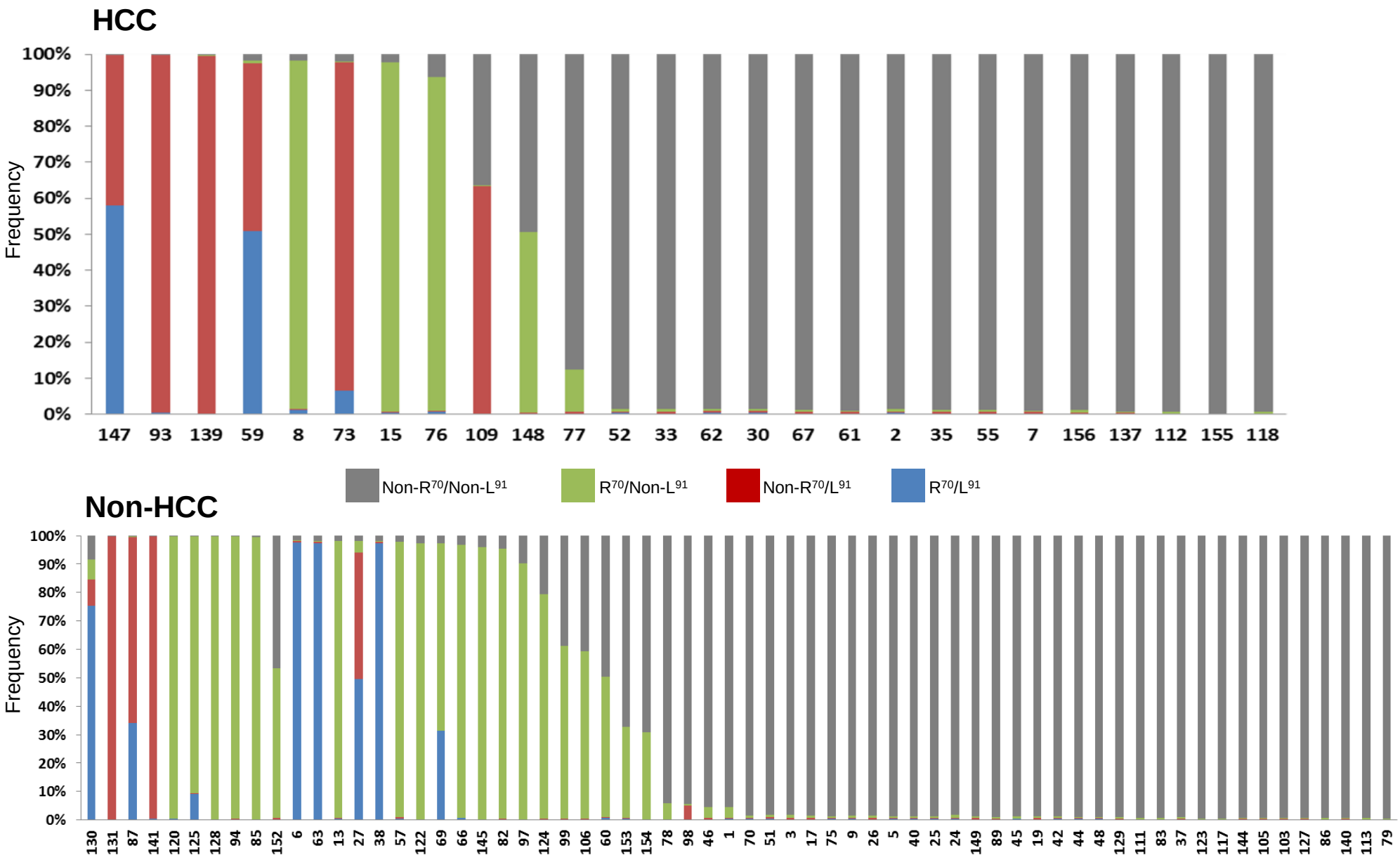


Supple. Fig. 1. Workflow of bioinformatic analysis for processing sequence reads obtained by Illumina-MiSeq deep-sequencing.



Suppl. Fig. 2. Distribution of core "haplotypes" (pairs of amino acids at positions 70 and 91 encoded in the same viral RNA) in patients who developed HCC or not (non-HCC). The X axis indicate patient IDs while the Y axis serves as a reference to indicate the percentage of intra-patient haplotypes. By analyzing the association between each core haplotype (Non-R^{70}/Non-L^{91}, R^{70}/Non-L^{91}, Non-R^{70}/L^{91} and R^{70}/L^{91}) and HCC, none of the haplotypes were significantly associated with HCC.

CONSORT 2010 checklist of information to include when reporting a randomised trial*

Section/Topic	Item No	Checklist item	Reported on page No
Title and abstract			
	1a	Identification as a randomised trial in the title	1
	1b	Structured summary of trial design, methods, results, and conclusions (for specific guidance see CONSORT for abstracts)	2
Introduction			
Background and objectives	2a	Scientific background and explanation of rationale	3 - 4
	2b	Specific objectives or hypotheses	4 - 5
Methods			
Trial design	3a	Description of trial design (such as parallel, factorial) including allocation ratio	5 – 7 and suppl.file
	3b	Important changes to methods after trial commencement (such as eligibility criteria), with reasons	5 – 7 and suppl.file
Participants	4a	Eligibility criteria for participants	5 – 7 and suppl.file
	4b	Settings and locations where the data were collected	5 – 7 and suppl.file
Interventions	5	The interventions for each group with sufficient details to allow replication, including how and when they were actually administered	5 – 7 and suppl.file
Outcomes	6a	Completely defined pre-specified primary and secondary outcome measures, including how and when they were assessed	5 – 7 and suppl.file
	6b	Any changes to trial outcomes after the trial commenced, with reasons	5 – 7 and suppl.file
Sample size	7a	How sample size was determined	5 – 7 and suppl.file
	7b	When applicable, explanation of any interim analyses and stopping guidelines	5 – 7 and suppl.file
Randomisation:			5 – 7 and suppl.file

Sequence generation	8a	Method used to generate the random allocation sequence	5 – 7 and suppl.file
	8b	Type of randomisation; details of any restriction (such as blocking and block size)	5 – 7 and suppl.file
Allocation concealment mechanism	9	Mechanism used to implement the random allocation sequence (such as sequentially numbered containers), describing any steps taken to conceal the sequence until interventions were assigned	5 – 7 and suppl.file
Implementation	10	Who generated the random allocation sequence, who enrolled participants, and who assigned participants to interventions	5 – 7 and suppl. file
Blinding	11a	If done, who was blinded after assignment to interventions (for example, participants, care providers, those assessing outcomes) and how	5 – 7 and suppl.file
	11b	If relevant, description of the similarity of interventions	suppl.file
Statistical methods	12a	Statistical methods used to compare groups for primary and secondary outcomes	8 - 9
	12b	Methods for additional analyses, such as subgroup analyses and adjusted analyses	8 - 9
Results			
Participant flow (a diagram is strongly recommended)	13a	For each group, the numbers of participants who were randomly assigned, received intended treatment, and were analysed for the primary outcome	Suppl. File of HALT-C protocol
	13b	For each group, losses and exclusions after randomisation, together with reasons	Suppl. File of HALT-C protocol
Recruitment	14a	Dates defining the periods of recruitment and follow-up	Suppl. File of HALT-C protocol
	14b	Why the trial ended or was stopped	Suppl. File of HALT-C protocol
Baseline data	15	A table showing baseline demographic and clinical characteristics for each group	Table 1 (P. 21)
Numbers analysed	16	For each group, number of participants (denominator) included in each analysis and whether the analysis was by original assigned groups	Table 1 and pages 9 - 12
Outcomes and estimation	17a	For each primary and secondary outcome, results for each group, and the estimated effect size and its precision (such as 95% confidence interval)	9 – 12 and tables 2, 3

			and 4
	17b	For binary outcomes, presentation of both absolute and relative effect sizes is recommended	9 – 12 and tables 2, 3 and 4
Ancillary analyses	18	Results of any other analyses performed, including subgroup analyses and adjusted analyses, distinguishing pre-specified from exploratory	NA
Harms	19	All important harms or unintended effects in each group (for specific guidance see CONSORT for harms)	NA
Discussion			
Limitations	20	Trial limitations, addressing sources of potential bias, imprecision, and, if relevant, multiplicity of analyses	13 - 14
Generalizability	21	Generalisability (external validity, applicability) of the trial findings	13 - 14
Interpretation	22	Interpretation consistent with results, balancing benefits and harms, and considering other relevant evidence	14 - 15
Other information			
Registration	23	Registration number and name of trial registry	5 - 6
Protocol	24	Where the full trial protocol can be accessed, if available	Suppl.file
Funding	25	Sources of funding and other support (such as supply of drugs), role of funders	20

*We strongly recommend reading this statement in conjunction with the CONSORT 2010 Explanation and Elaboration for important clarifications on all the items. If relevant, we also recommend reading CONSORT extensions for cluster randomised trials, non-inferiority and equivalence trials, non-pharmacological treatments, herbal interventions, and pragmatic trials. Additional extensions are forthcoming: for those and for up to date references relevant to this checklist, see www.consort-statement.org.