

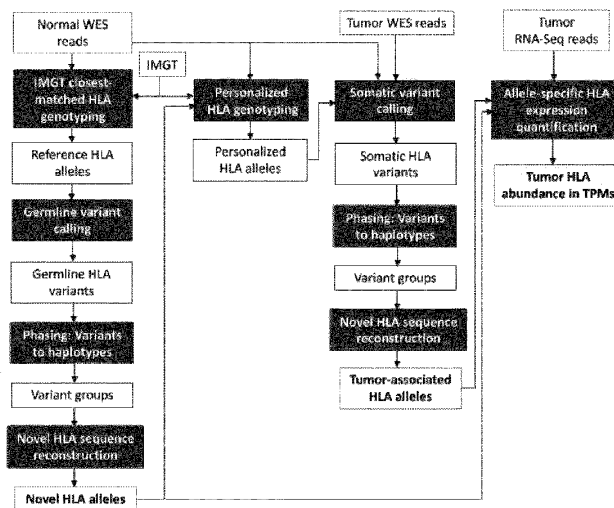


- (51) **International Patent Classification:**
G16B 20/20 (2019.01) *G16B 50/20* (2019.01)
- (21) **International Application Number:**
PCT/EP2022/052780
- (22) **International Filing Date:**
04 February 2022 (04.02.2022)
- (25) **Filing Language:** English
- (26) **Publication Language:** English
- (71) **Applicant:** NEC ONCOIMMUNITY AS [NO/NO];
Ullemchauseen 64, 0379 Oslo (NO).
- (72) **Inventors:** ANZAR, Irantz; Ullemchauseen 64, 0379
Oslo (NO). SVERCHKOVA, Angelina; Ullemchauseen
64, 0379 Oslo (NO). STRATFORD, Richard; Ullem-
chauseen 64, 0379 Oslo (NO). CLANCY, Trevor; Ullem-
chauseen 64, 0379 Oslo (NO).
- (74) **Agent:** GILL JENNINGS & EVERY LLP et al.; The
Broadgate Tower, 20 Primrose Street, London EC2A 2ES
(GB).

- (81) **Designated States** (unless otherwise indicated, for every
kind of national protection available): AE, AG, AL, AM,
AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ,
CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO,
DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN,
HR, HU, ID, IL, IN, IR, IS, IT, JO, JP, KE, KG, KH, KN,
KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD,
ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO,
NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW,
SA, SC, SD, SE, SG, SK, SL, ST, SV, SY, TH, TJ, TM, TN,
TR, TT, TZ, UA, UG, US, UZ, VC, VN, WS, ZA, ZM, ZW.
- (84) **Designated States** (unless otherwise indicated, for every
kind of regional protection available): ARIPO (BW, GH,
GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ,
UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ,
TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK,
EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV,
MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM,
TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW,
KM, ML, MR, NE, SN, TD, TG).

(54) **Title:** METHOD FOR HLA TYPING

Figures
Figure 1



(57) **Abstract:** The present invention relates to a method for characterising the HLA status of a genetic sample obtained from a subject, comprising the steps of: i. carrying out DNA or RNA sequencing on said genetic sample obtained from said subject; ii. aligning the obtained sequence with one or more reference HLA allele sequences; iii. Applying a variant calling technique to identify the presence of or type of variant(s) in the HLA sequence of said genetic sample thereby to determine the HLA status.

[Continued on next page]

Published:

— with international search report (Art. 21(3))