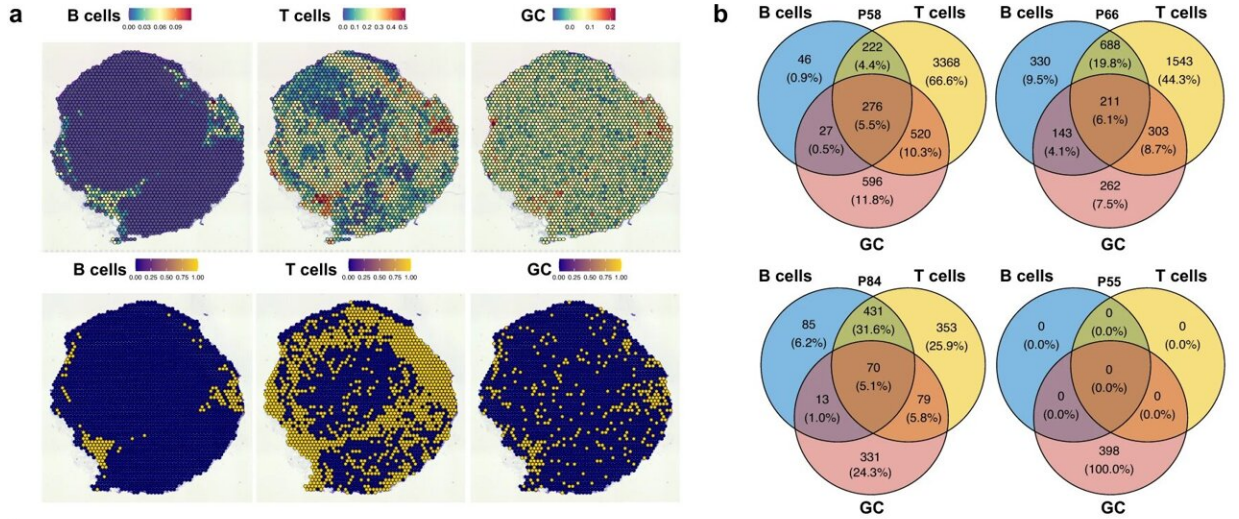
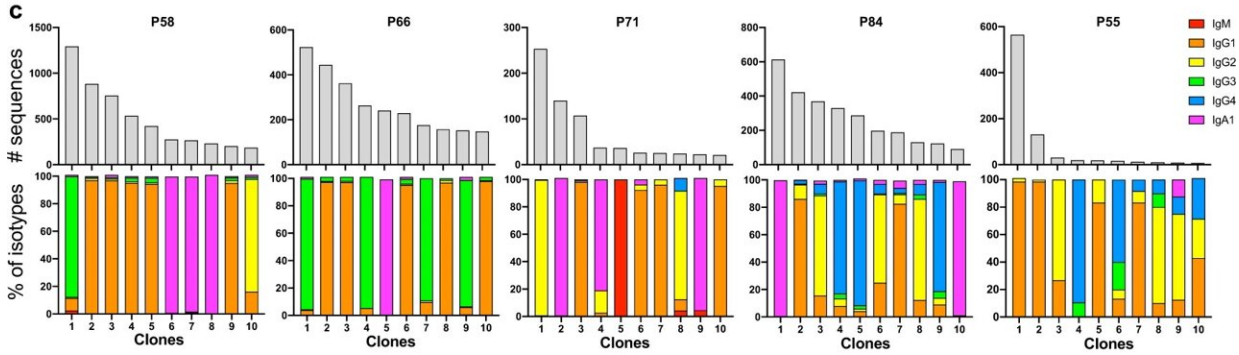
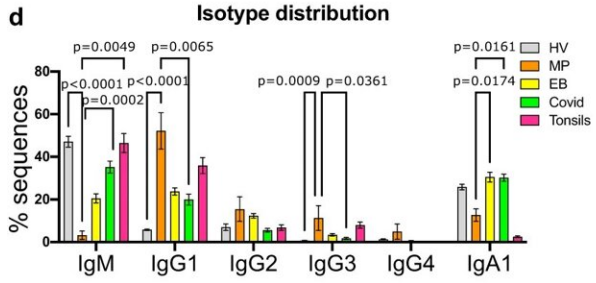
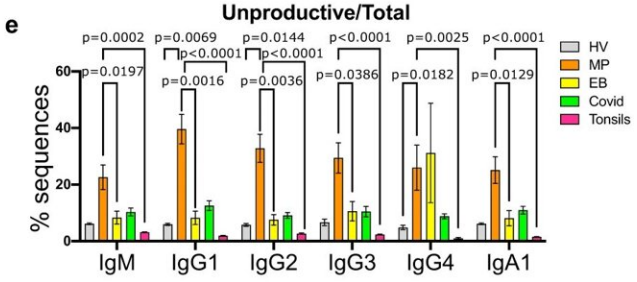
Study uncovers how B cells react to skin cancer

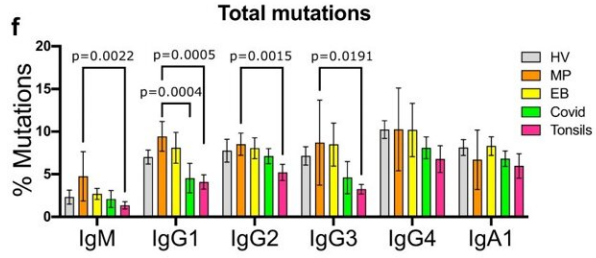
June 8 2023

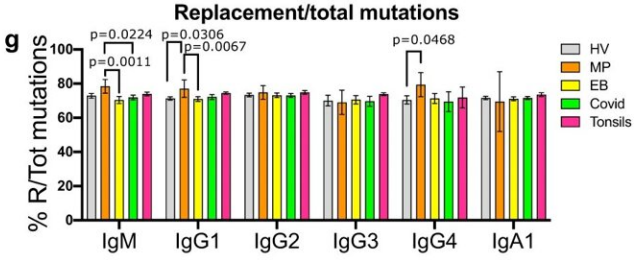

a
B cells
T cells
GC
b
B cells P58 T cells
46 (0.9%)
222 (4.4%)
3368 (66.6%)
276 (5.5%)
27 (0.5%)
520 (10.3%)
596 (11.8%)
GC
B cells P66 T cells
330 (9.5%)
688 (19.8%)
1543 (44.3%)
211 (6.1%)
143 (4.1%)
303 (8.7%)
262 (7.5%)
GC
B cells P84 T cells
85 (6.2%)
431 (31.6%)
353 (25.9%)
70 (5.1%)
13 (1.0%)
79 (5.8%)
331 (24.3%)
GC
B cells P55 T cells
0 (0.0%)
0 (0.0%)
0 (0.0%)
0 (0.0%)
0 (0.0%)
0 (0.0%)
398 (100.0%)
GC

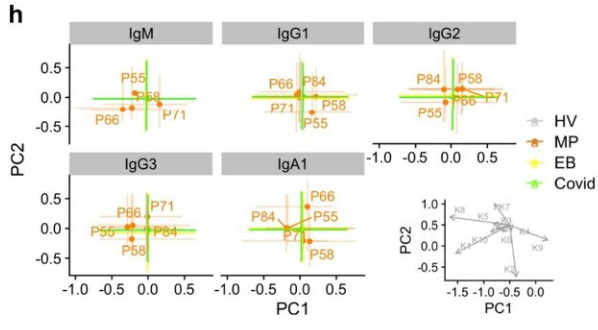

c
P58
P66
P71
P84
P55
sequences
% of isotypes
Clones
IgM
IgG1
IgG2
IgG3
IgG4
IgA1

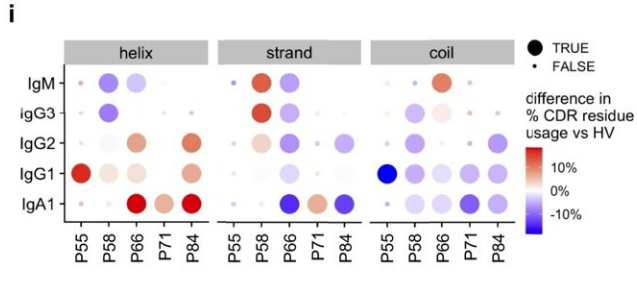

d
Isotype distribution
% sequences
p=0.0049
p=0.0065
p<0.0001
p<0.0001
p=0.0002
p=0.0009
p=0.0361
p=0.0161
p=0.0174
HV
MP
EB
Covid
Tonsils
IgM
IgG1
IgG2
IgG3
IgG4
IgA1


e
Unproductive/Total
% sequences
p=0.0002
p=0.0069
p=0.0144
p<0.0001
p<0.0001
p<0.0001
p=0.0025
p<0.0001
p=0.0197
p=0.0016
p=0.0036
p=0.0386
p=0.0182
p=0.0129
HV
MP
EB
Covid
Tonsils
IgM
IgG1
IgG2
IgG3
IgG4
IgA1


f
Total mutations
% Mutations
p=0.0022
p=0.0005
p=0.0004
p=0.0015
p=0.0191
HV
MP
EB
Covid
Tonsils
IgM
IgG1
IgG2
IgG3
IgG4
IgA1


g
Replacement/total mutations
% R/Tot mutations
p=0.0224
p=0.0306
p=0.0011
p=0.0067
p=0.0468
HV
MP
EB
Covid
Tonsils
IgM
IgG1
IgG2
IgG3
IgG4
IgA1


h
IgM
IgG1
IgG2
IgG3
IgA1
PC2
PC1
HV
MP
EB
Covid


i
helix
strand
coil
TRUE
FALSE
difference in % CDR residue usage vs HV
10%
0%
-10%
IgM
IgG3
IgG2
IgG1
IgA1
P55
P58
P66
P71
P84

Spatial transcriptomic coupled with high throughput intratumoral antibody repertoire analyses suggest an active but aberrant B cell response. **a** Representative image of spatial transcriptomic deconvolution of B cells, T cells and B cell germinal center (GC) signatures. Top panels, signature score per spot; bottom panels, binarized values using 50% (B cells and T cells) and 85% (GC) threshold. **b** Venn diagrams representing the number of spots with B cells, T cells or GC signatures and their combinations. **c** Bar chart representing the absolute number of sequences (top panels) and the proportion of isotypes in the top 10 clones (bottom panels) showing CSR, per tumor. **d–g** Bar charts representing: **d** isotype distribution; **e** % of unproductive sequences; and **f** % of total mutations, and **g** % of replacement/total mutations in the V region of unique sequences from melanoma patients' tumor (MP, $n = 5$) compared to healthy volunteers' blood (HV, $n = 9$), ebola patient (EB, $n = 12$), SARS-CoV-2 patient (COVID-19, $n = 16$) and healthy tonsils (Tonsils, $n = 8$) repertoires. Statistical significance was calculated with non-parametric ANOVA compared to MP. Error bars SEM of biologically independent samples. **h** Principal component analysis (PCA) of heavy chain CDR3 characteristics in terms of Kidera factors. Dots depict median PC1/2 and colored lines depict inter-quartile range. **i** Comparison of the proportion of α-helical, β-strand and coil amino acid structures in the CDR3 sequences of the MP compared to HV repertoire data. *P*