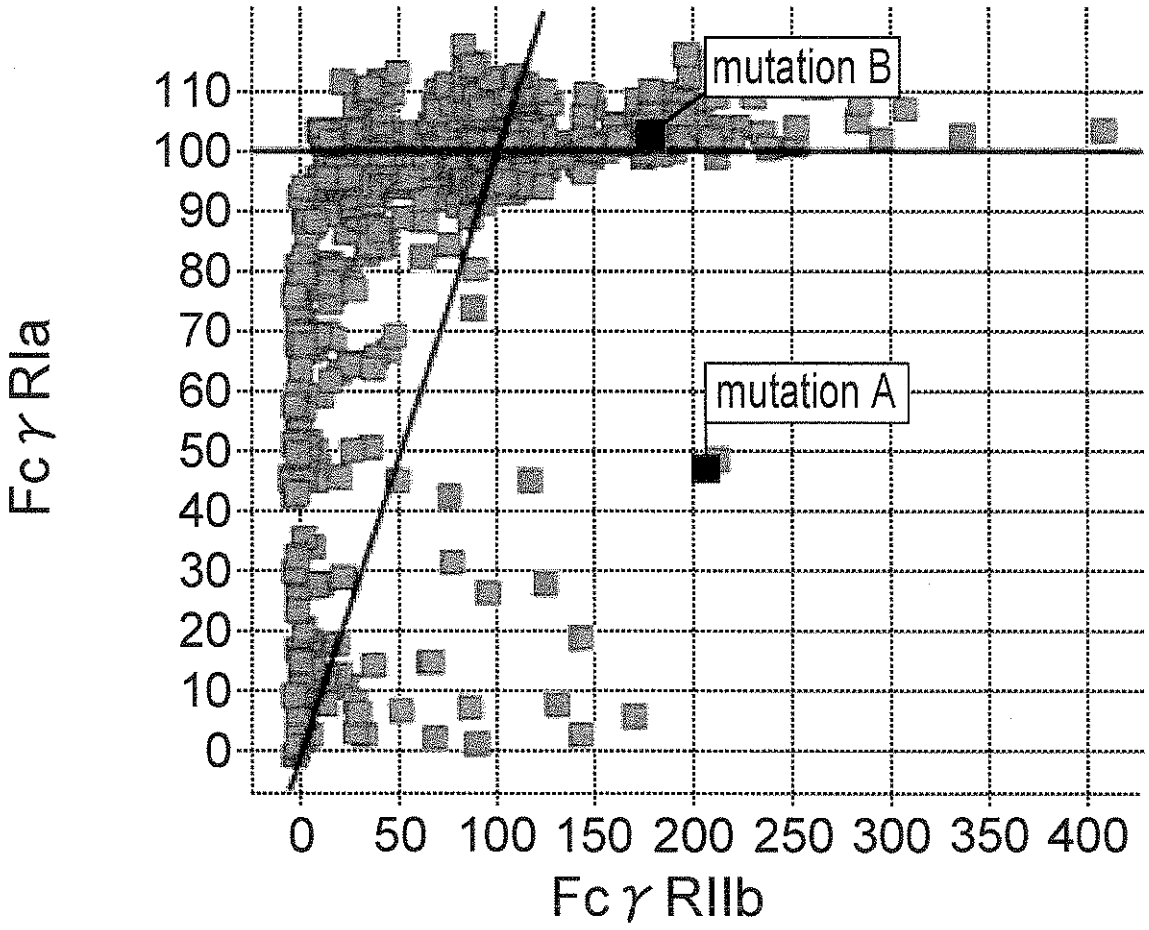

mutation B
mutation A
110
100
90
80
70
60
50
40
30
20
10
0
0
50
100
150
200
250
300
350
400
Fc γ RIa
Fc γ RIIb

FIG. 1

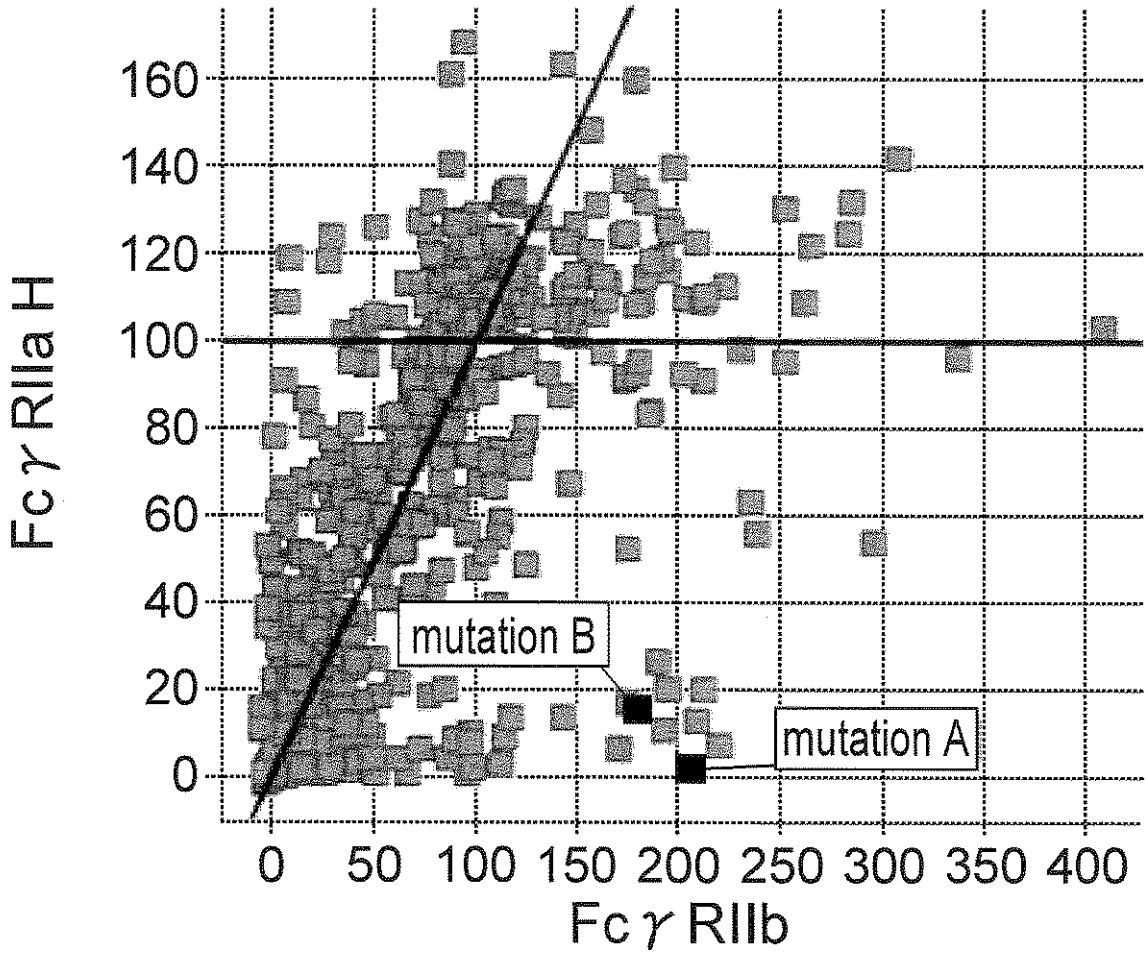

160
140
120
100
80
60
40
20
0
Fc γ RIIa H
mutation B
mutation A
0
50
100
150
200
250
300
350
400
Fc γ RIIb

FIG. 2

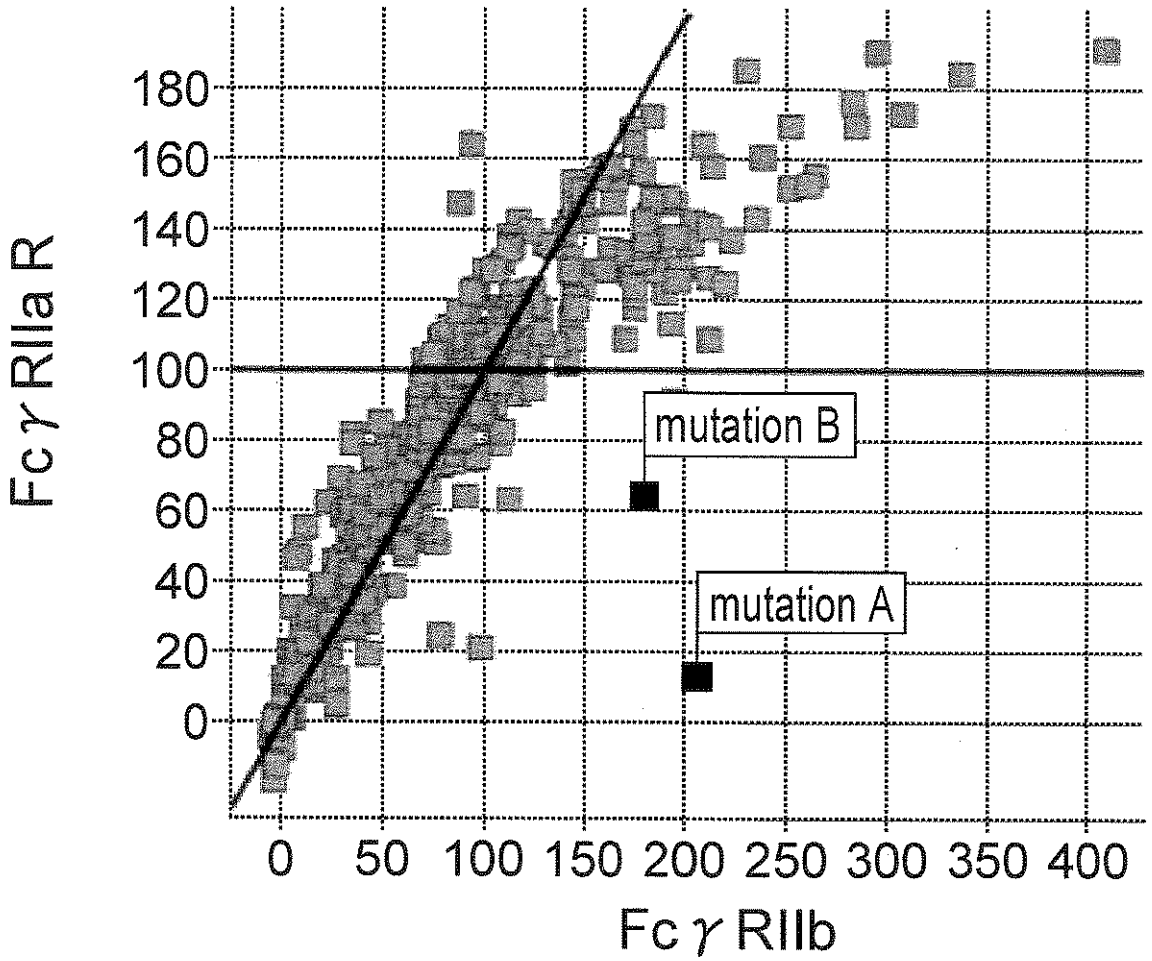

180
160
140
120
100
80
60
40
20
0
0
50
100
150
200
250
300
350
400
Fc γ RIIa R
Fc γ RIIb
mutation B
mutation A

FIG. 3

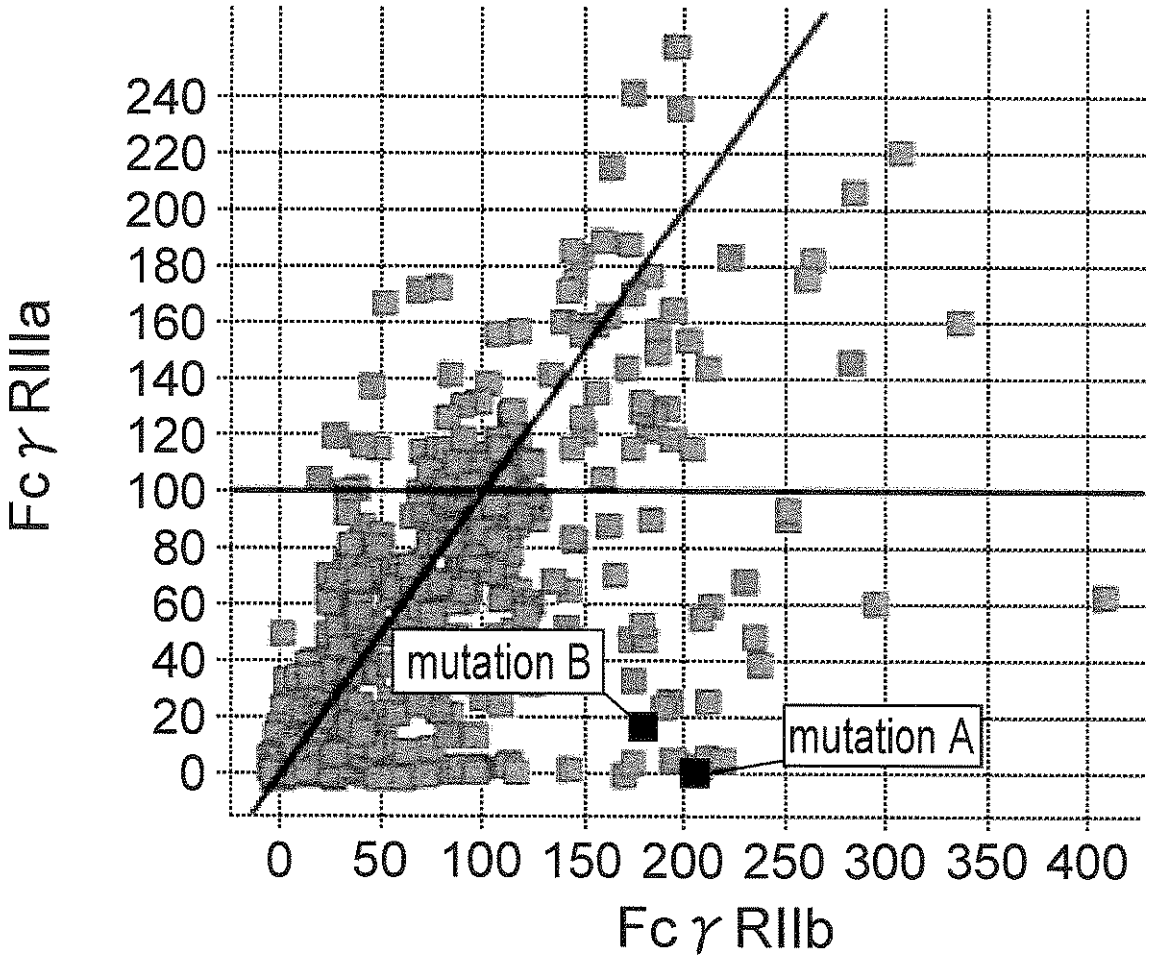

240
220
200
180
160
140
120
100
80
60
40
20
0
Fc γ RIIIa
0
50
100
150
200
250
300
350
400
Fc γ RIIb
mutation B
mutation A

FIG. 4

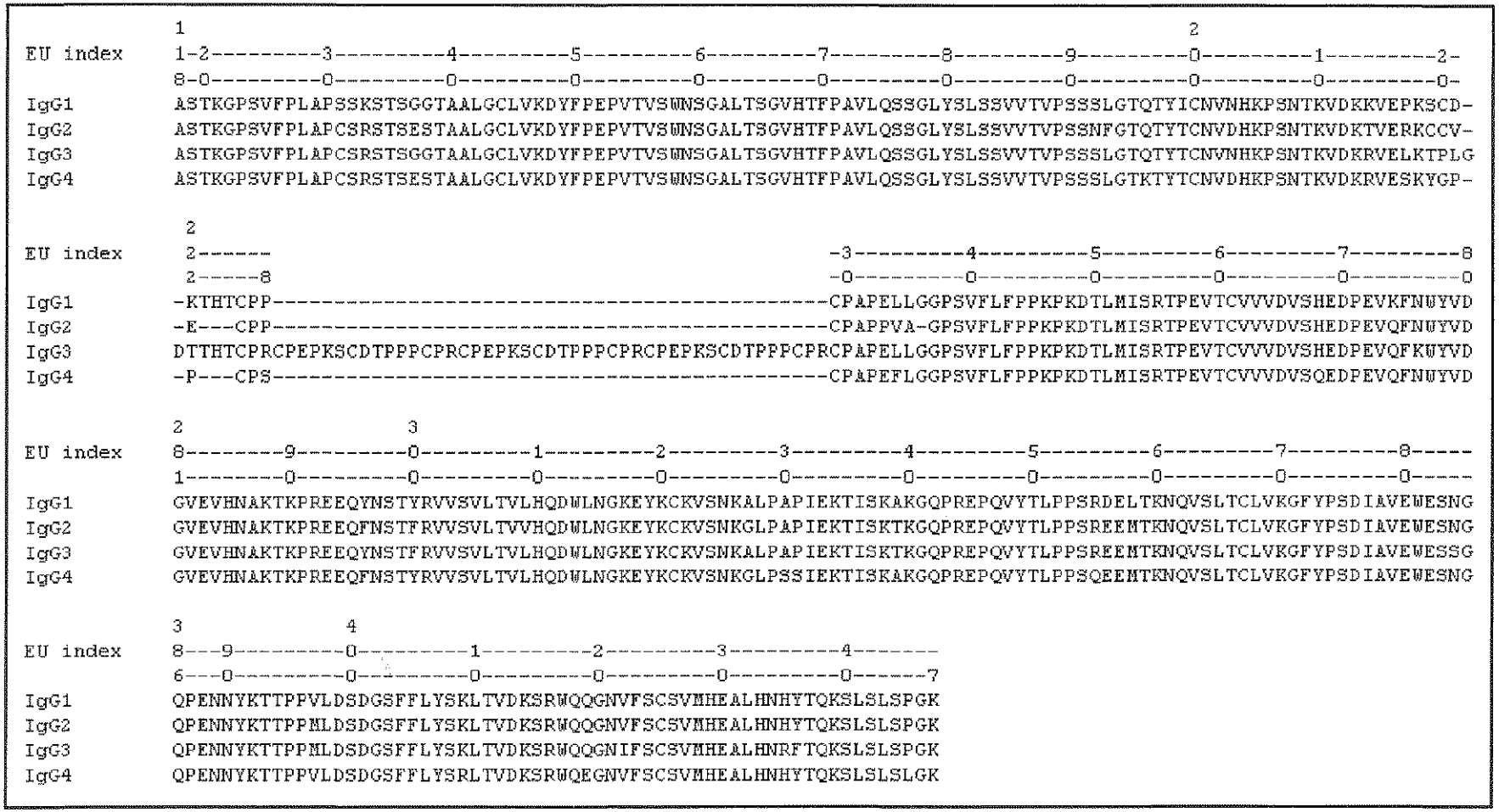

EU index
IgG1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCD-
IgG2 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCV-
IgG3 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVELKTPLG
IgG4 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGP-
EU index
IgG1 -KTHTCPP-----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
IgG2 -E---CPP-----CPAPPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVD
IgG3 DTTHTCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVD
IgG4 -P---CPS-----CPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVD
EU index
IgG1 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG
IgG2 GVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
IgG3 GVEVHNAKTKPREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSG
IgG4 GVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNG
EU index
IgG1 QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
IgG2 QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
IgG3 QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPGK
IgG4 QPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

FIG. 5

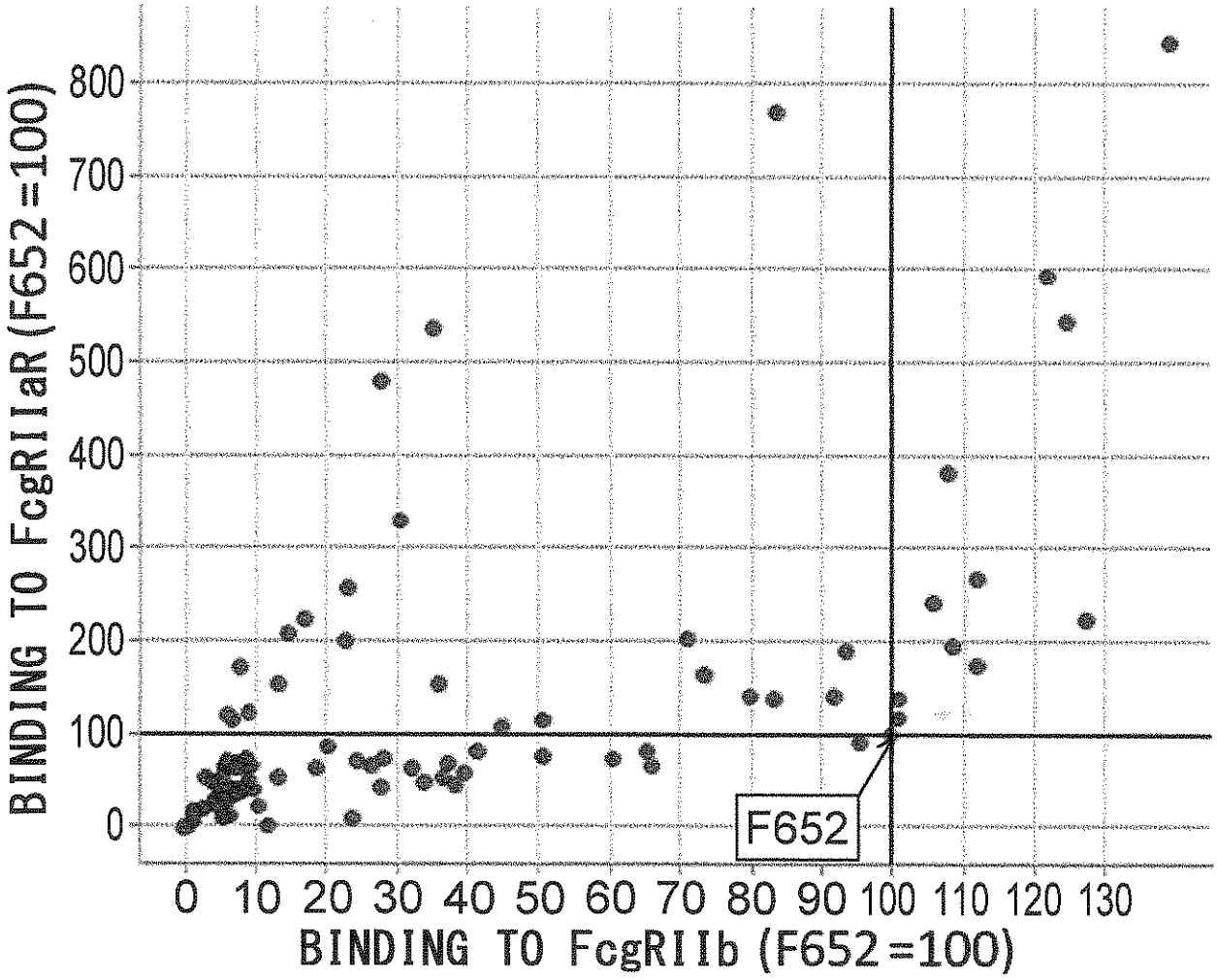

BINDING TO FcgRIIaR (F652=100)
800
700
600
500
400
300
200
100
0
F652
0 10 20 30 40 50 60 70 80 90 100 110 120 130
BINDING TO FcgRIIb (F652=100)

FIG. 6

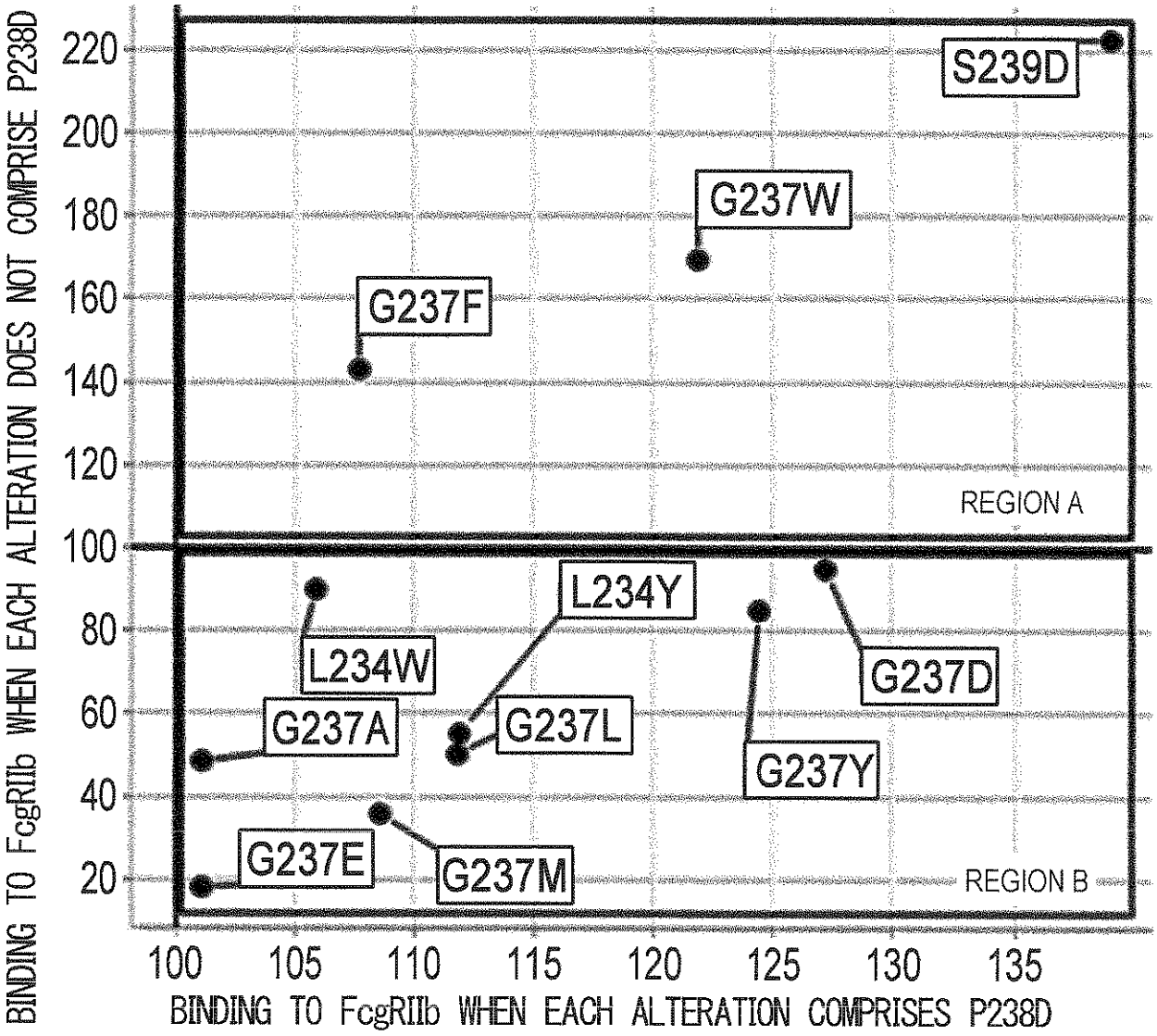

BINDING TO FcgRIIb WHEN EACH ALTERATION DOES NOT COMPRISE P238D
220
200
180
160
140
120
100
80
60
40
20
S239D
G237W
G237F
REGION A
L234Y
L234W
G237D
G237A
G237L
G237Y
G237E
G237M
REGION B
100
105
110
115
120
125
130
135
BINDING TO FcgRIIb WHEN EACH ALTERATION COMPRISES P238D

FIG. 7

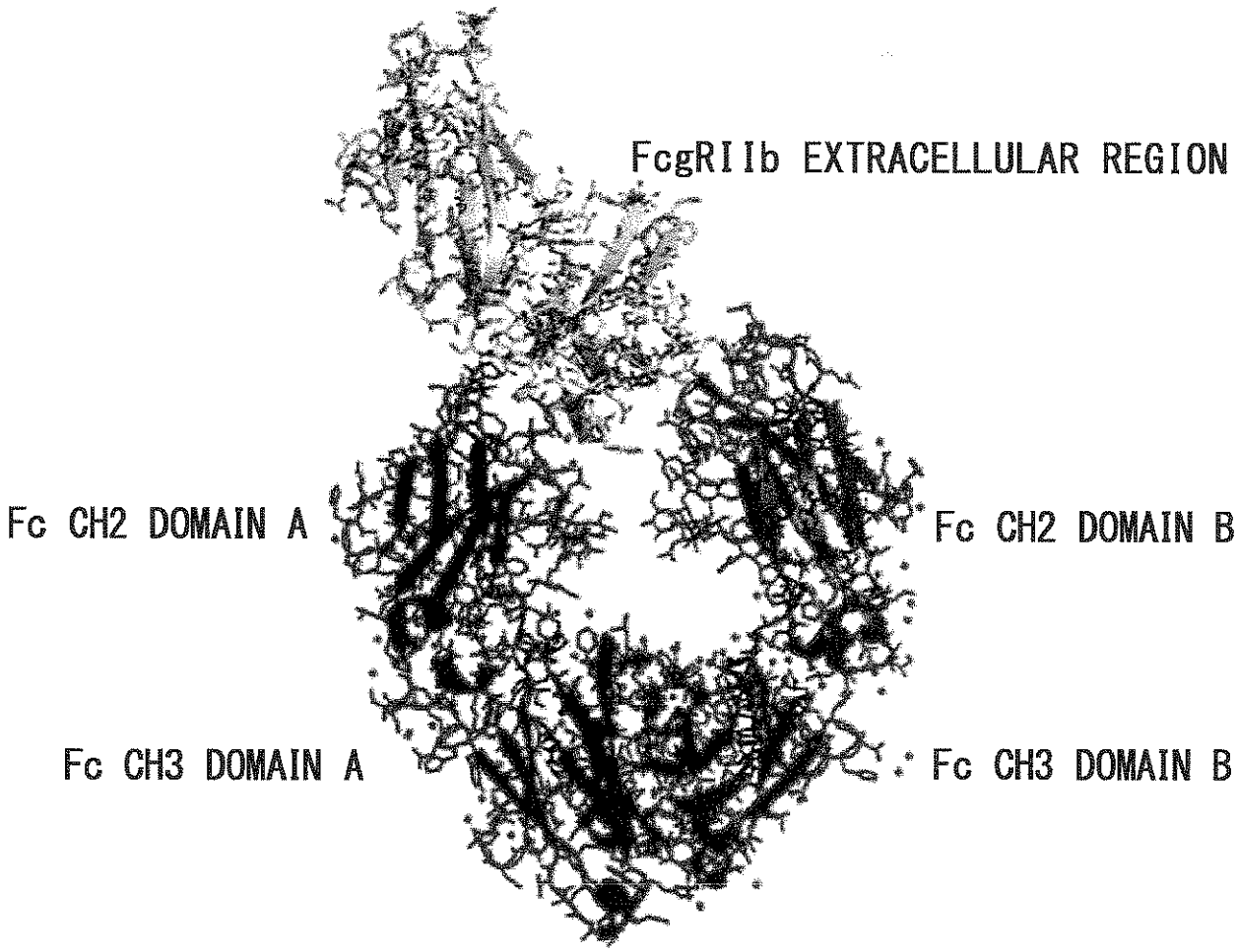
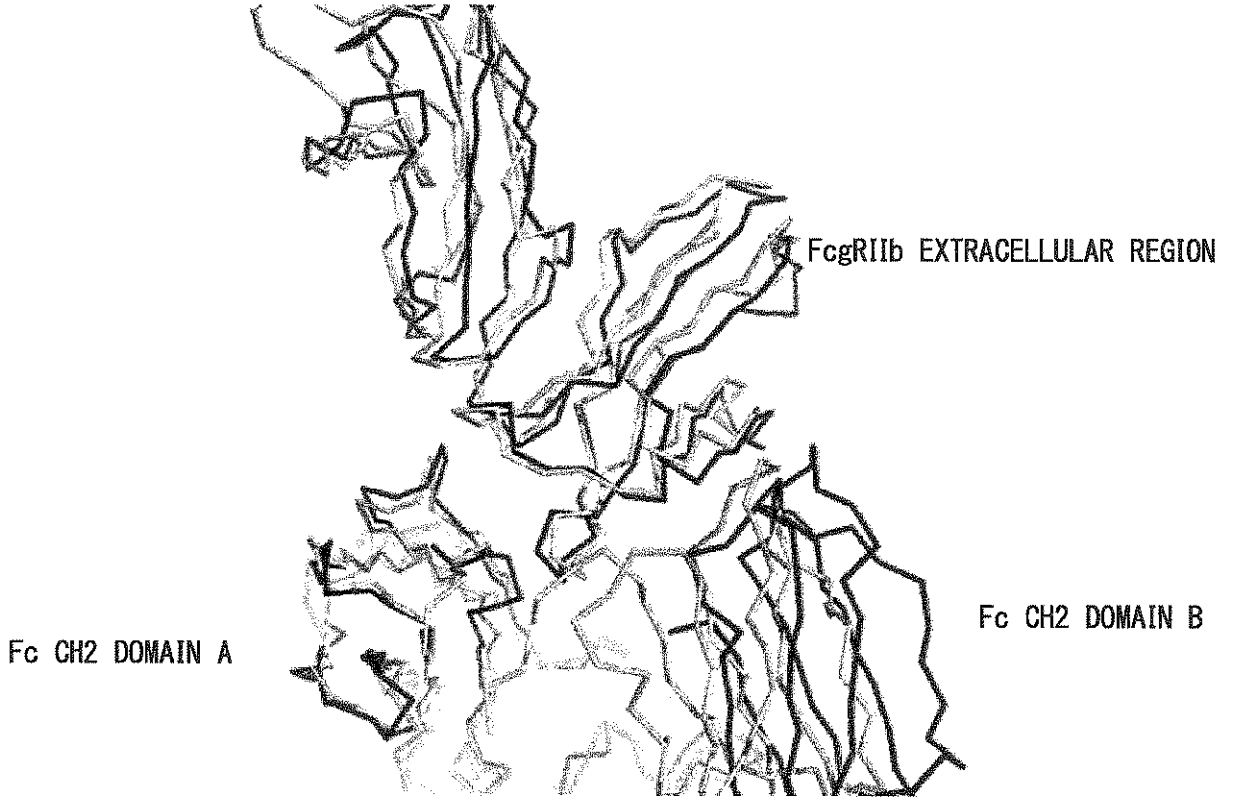
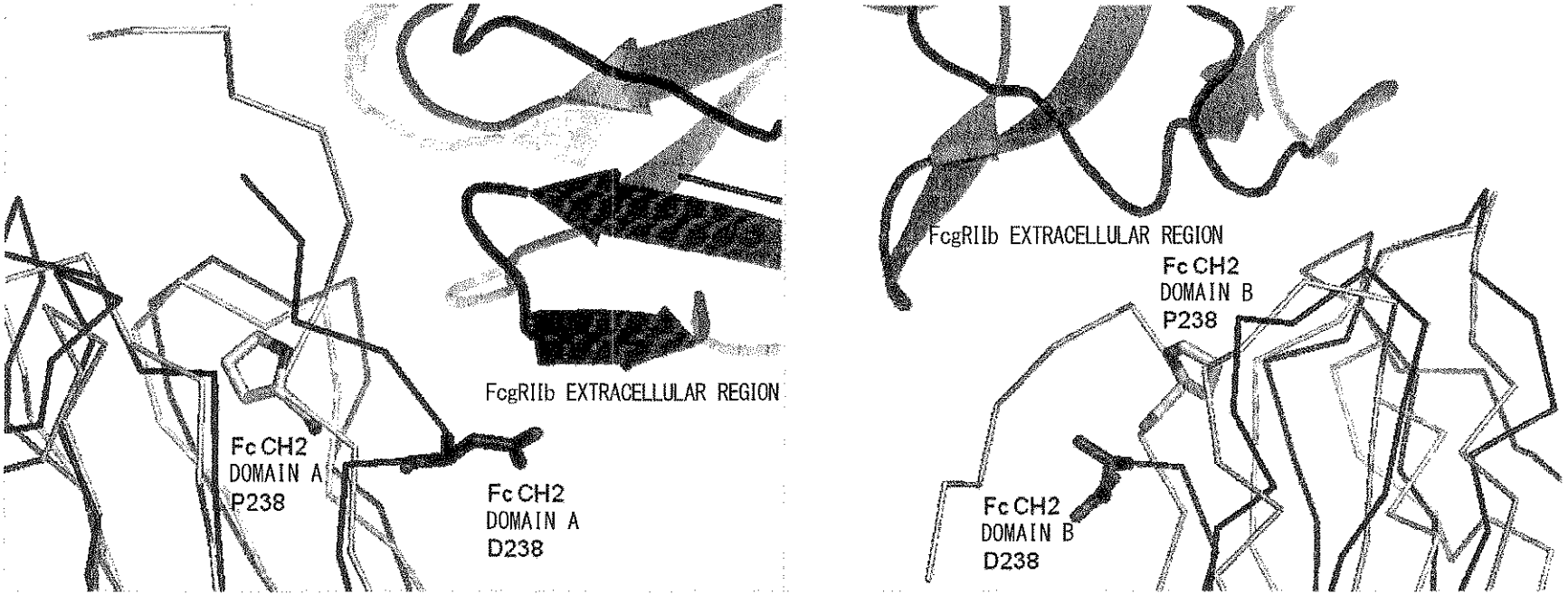

FcgRIIb EXTRACELLULAR REGION
Fc CH2 DOMAIN A
Fc CH2 DOMAIN B
Fc CH3 DOMAIN A
Fc CH3 DOMAIN B

FIG. 8



BLACK CRYSTAL STRUCTURE OF Fc(P238D)/Fcγ RIIb EXTRACELLULAR REGION COMPLEX
GRAY MODEL STRUCTURE OF Fc(WT)/Fcγ RIIb EXTRACELLULAR REGION COMPLEX

FIG. 9



BLACK CRYSTAL STRUCTURE OF Fc(P238D)/FcγRIIb EXTRACELLULAR REGION COMPLEX

GRAY MODEL STRUCTURE OF Fc(WT)/FcγRIIb EXTRACELLULAR REGION COMPLEX

FIG. 10

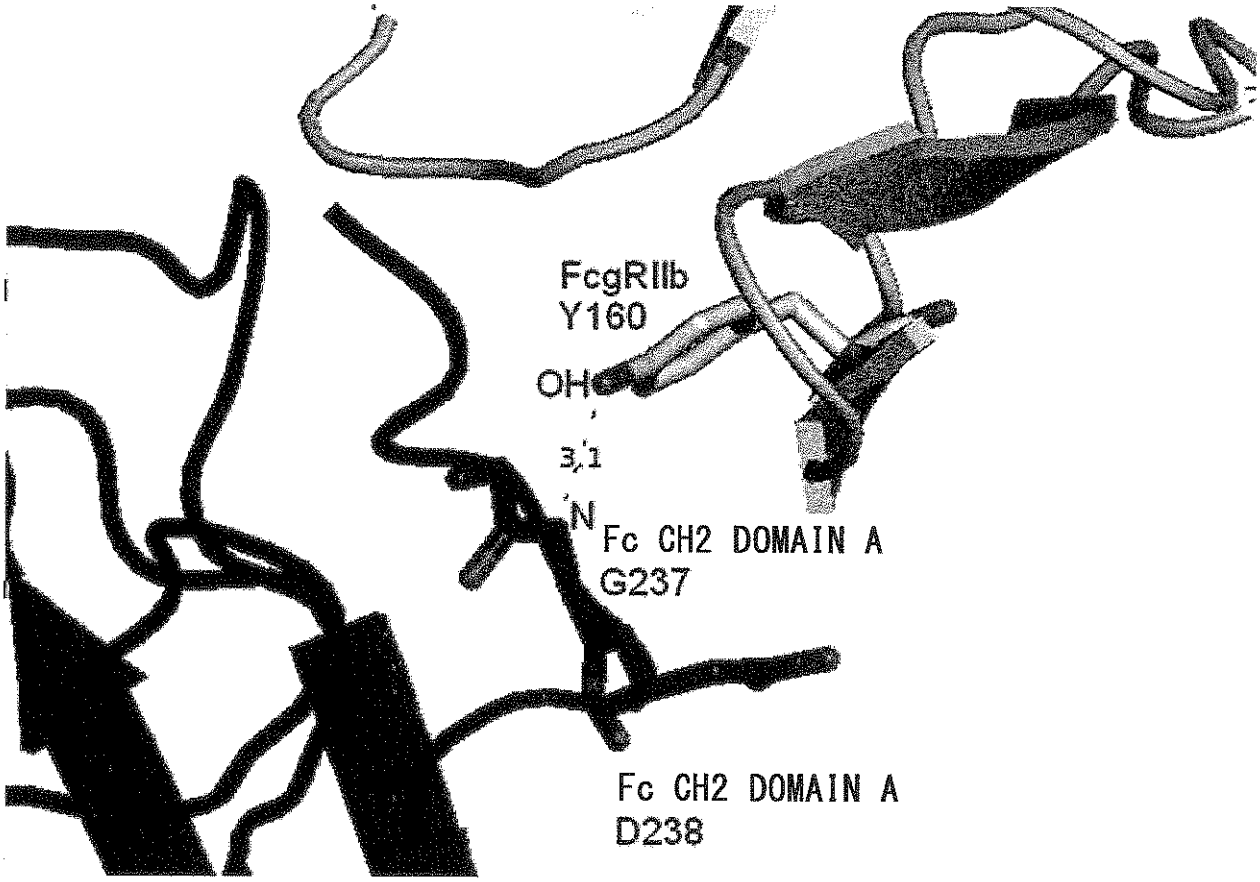


FIG. 11

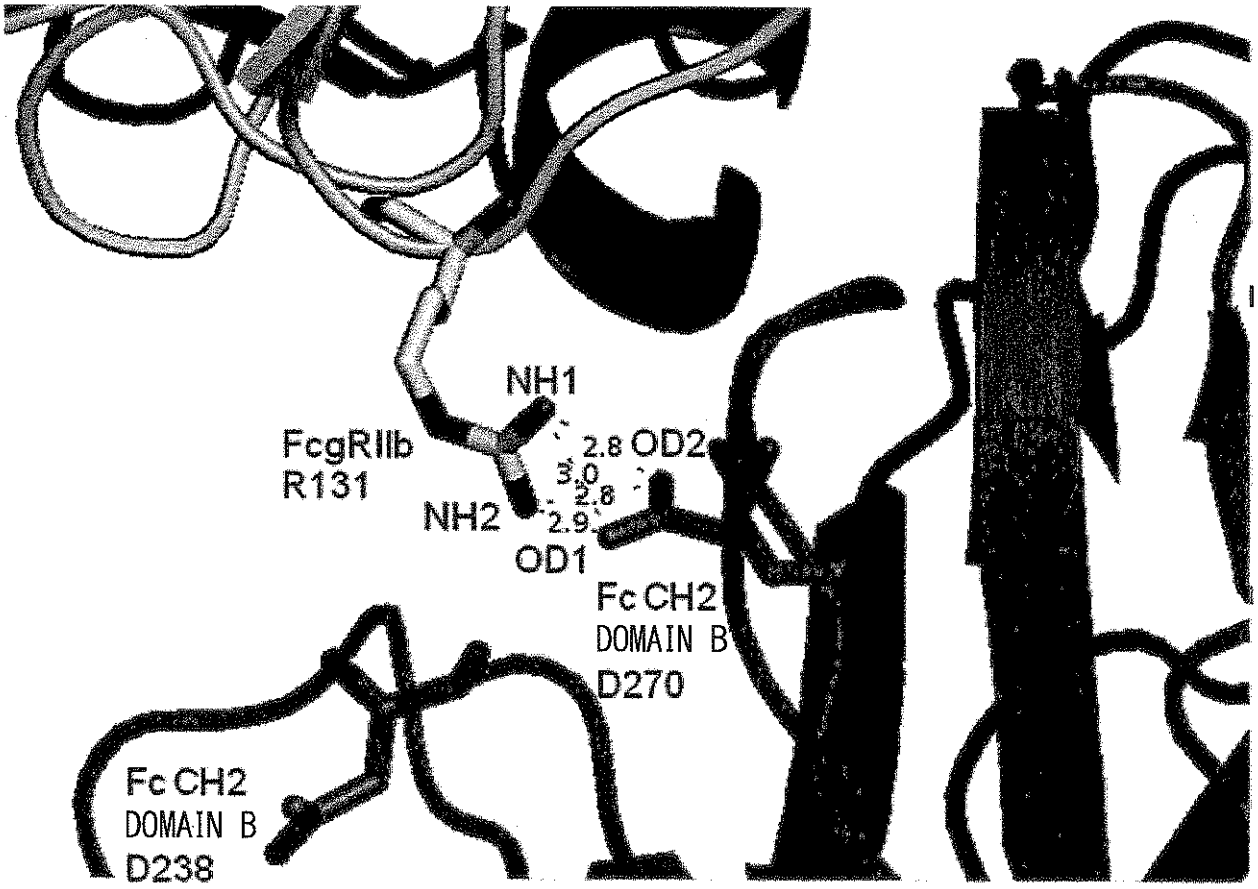

NH1
FcgRIIb
R131
2.8 OD2
3.0
2.8
NH2
2.9
OD1
Fc CH2
DOMAIN B
D270
Fc CH2
DOMAIN B
D238

FIG. 12

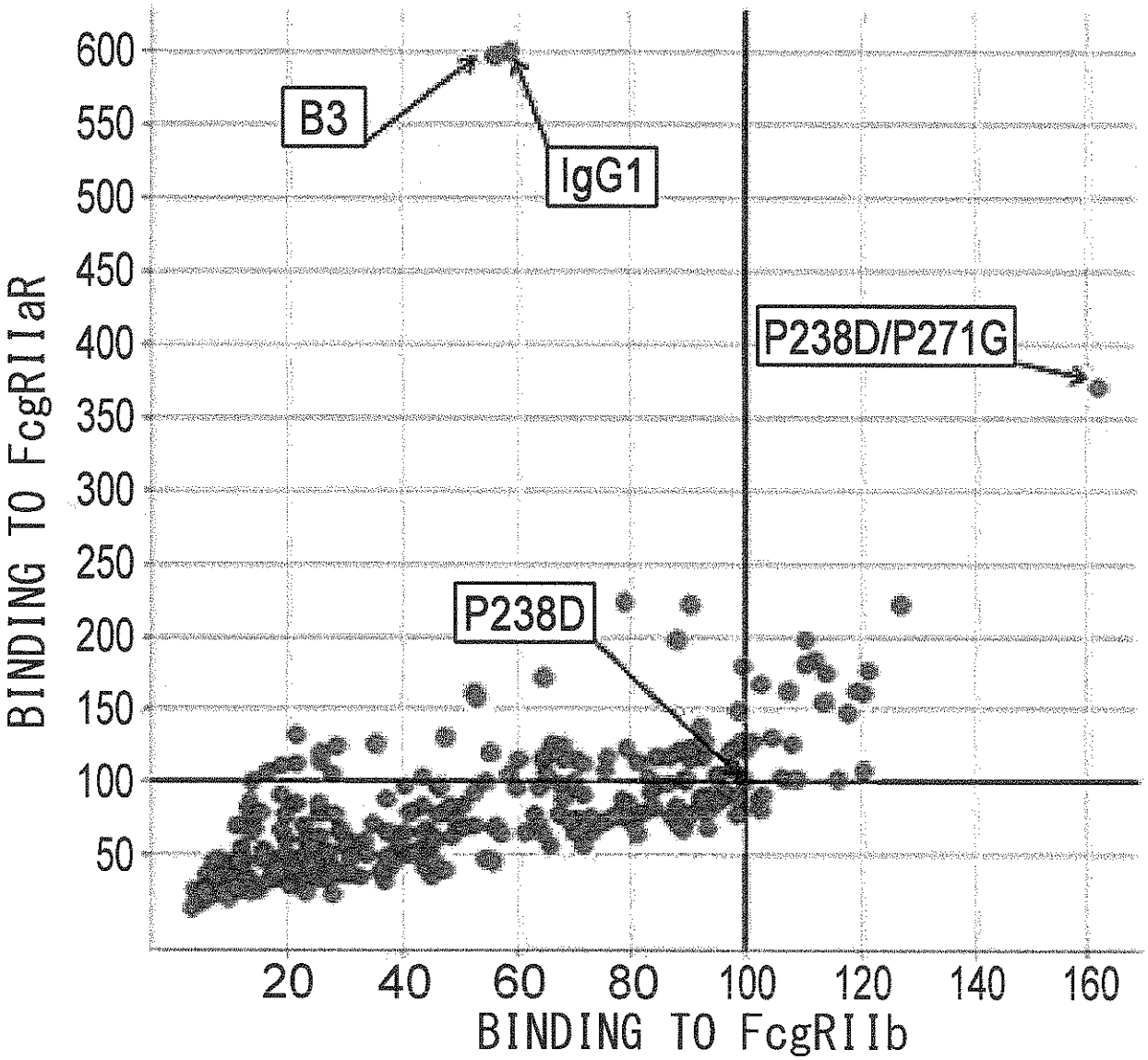

600
550
500
450
400
350
300
250
200
150
100
50
B3
IgG1
P238D/P271G
P238D
BINDING TO FcgRIIaR
20
40
60
80
100
120
140
160
BINDING TO FcgRIIb

FIG. 13

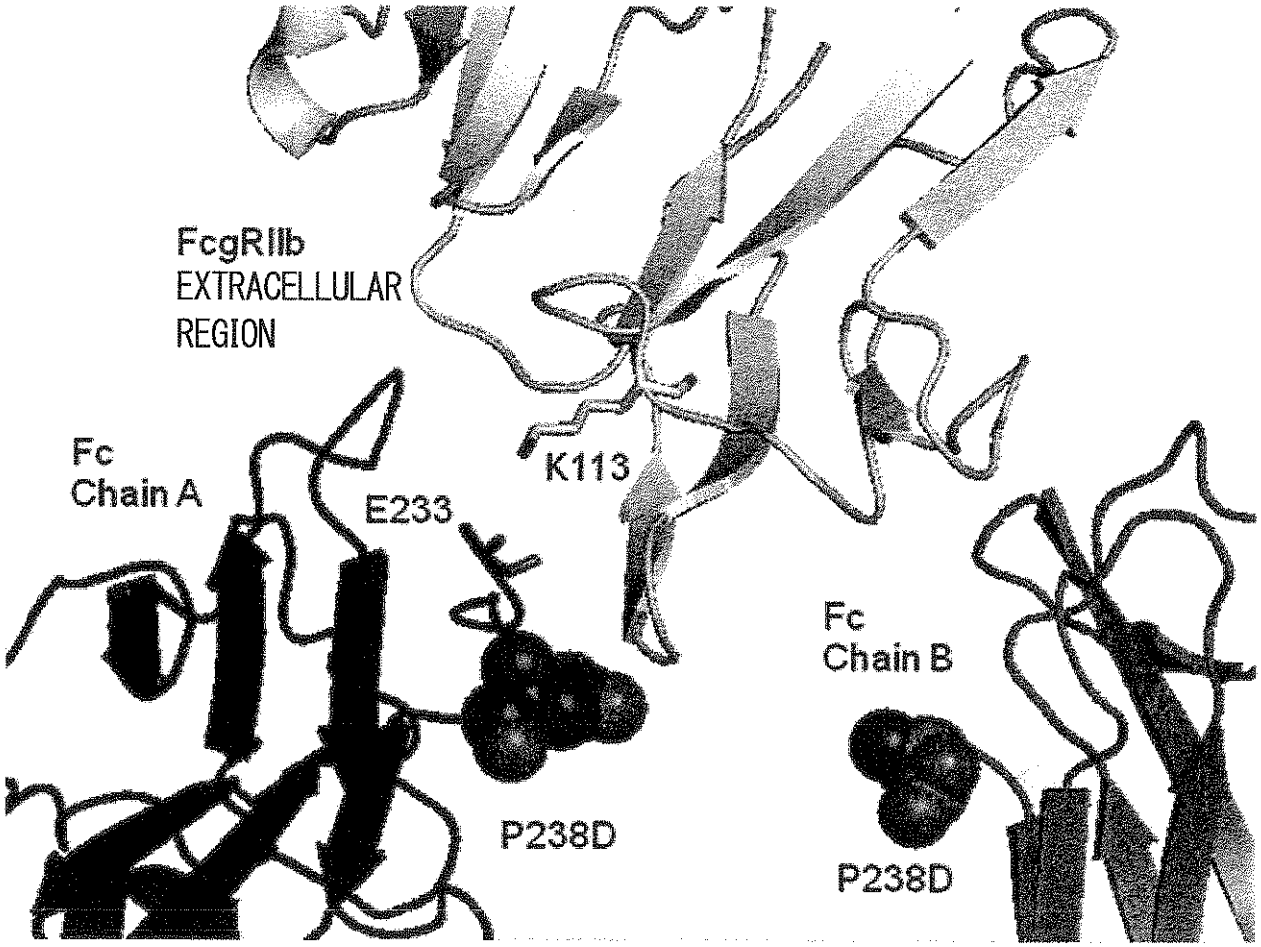

FcgRIIb
EXTRACELLULAR
REGION
Fc
Chain A
E233
K113
Fc
Chain B
P238D
P238D

FIG. 14

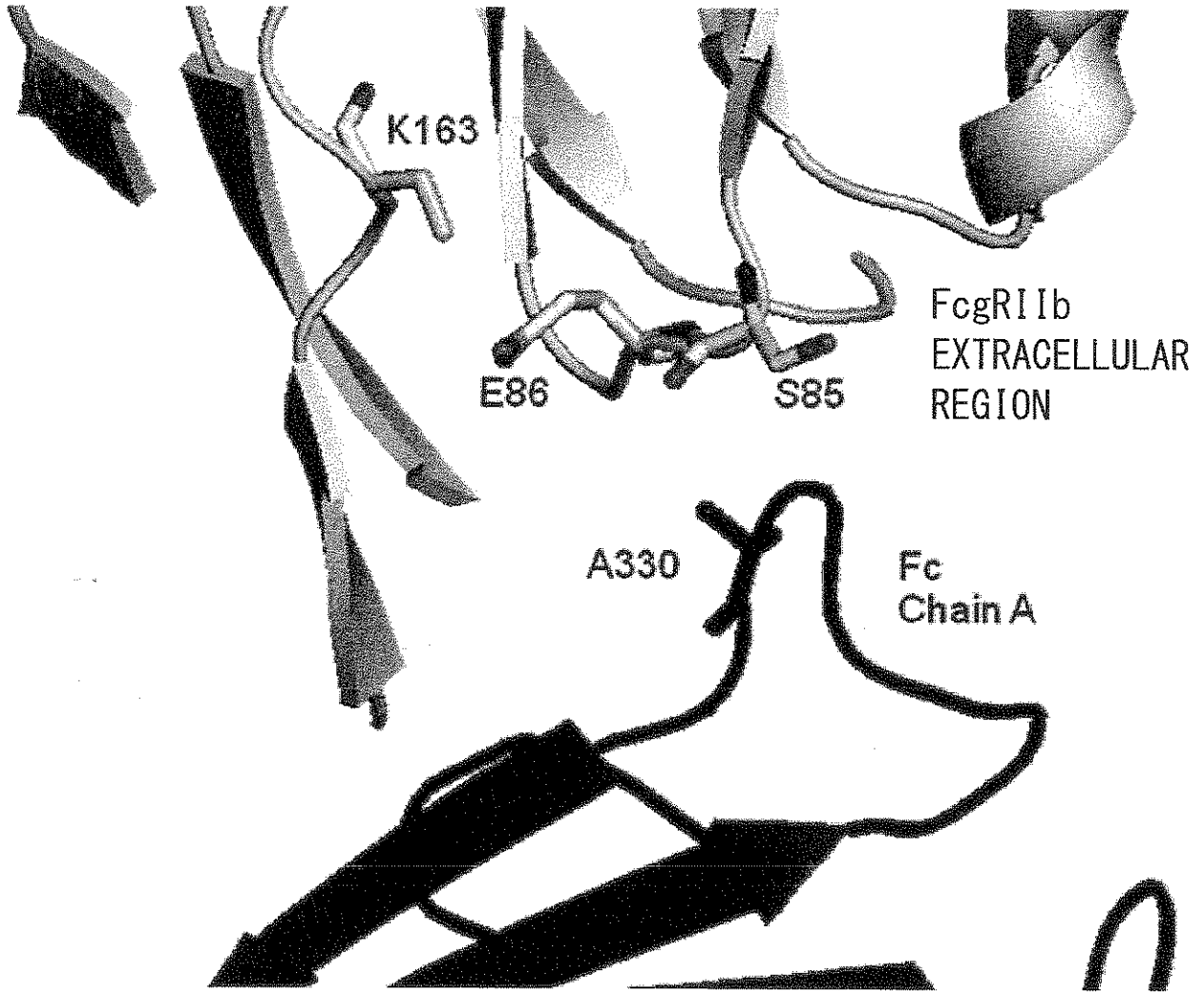
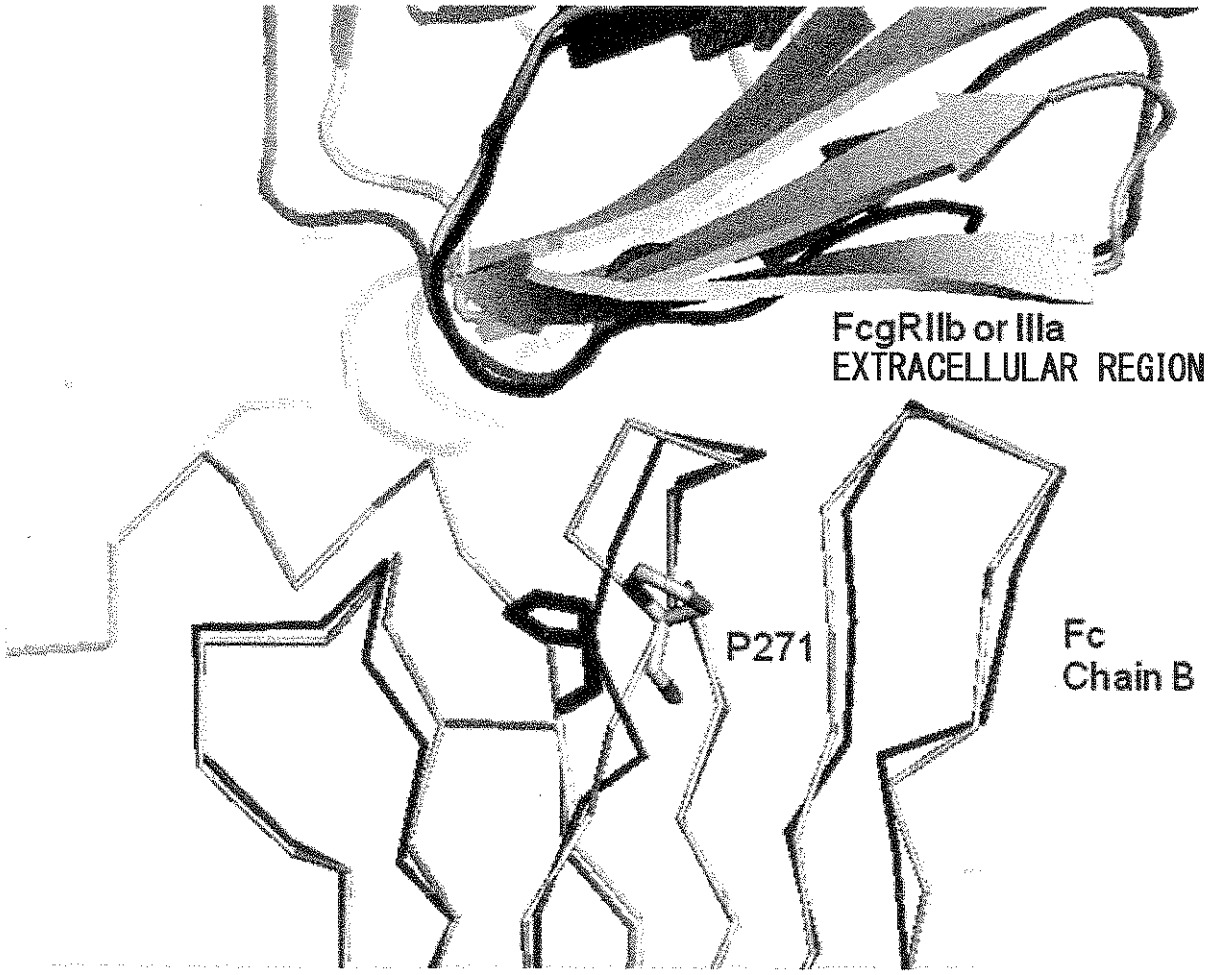


FIG. 15



BLACK CRYSTAL STRUCTURE OF Fc(P238D)/FcγRIIb EXTRACELLULAR REGION COMPLEX
GRAY CRYSTAL STRUCTURE OF Fc(WT)/FcγRIIIa EXTRACELLULAR REGION COMPLEX (PDB code: 3SGJ)

FIG. 16