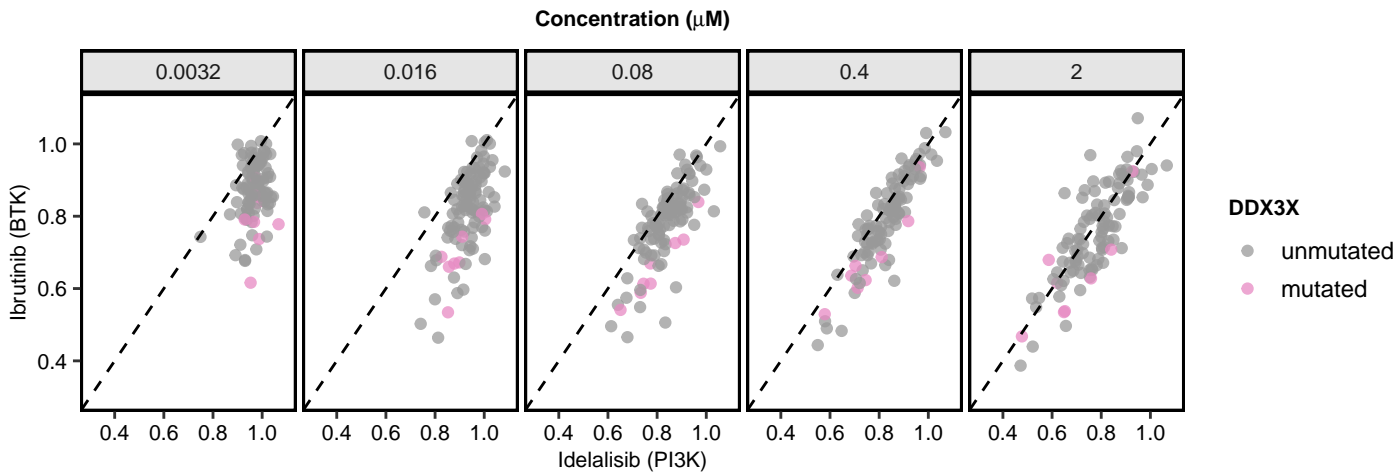


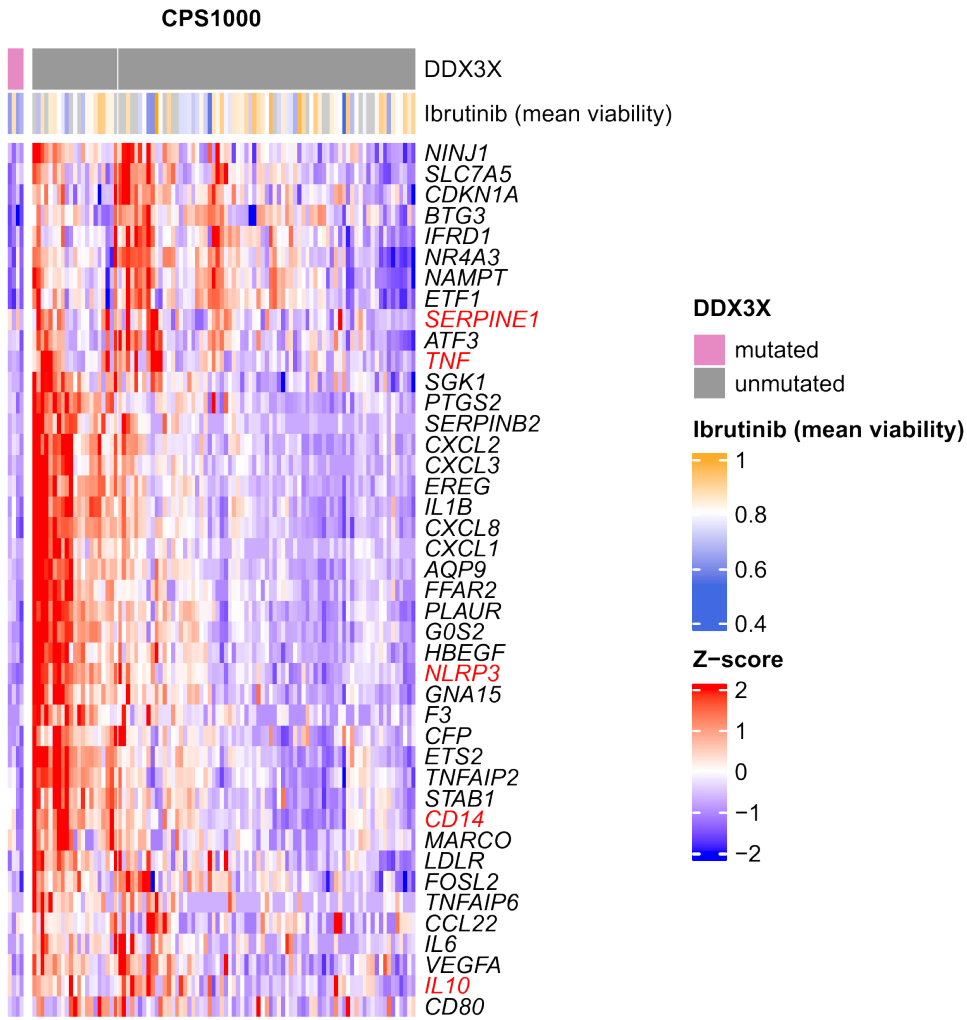
A

| ID | Sex | IGHV | DNA mutation | Amino acid alteration | Exon | Type of alteration | Allele frequency |
|-------|-----|------|----------------|-----------------------|------|----------------------|------------------|
| P0293 | M | U | c.845dupG | p.C282fs | 9 | Frameshift insertion | 0.86 |
| P0538 | M | U | c.1115_1122del | p.E372fs | 10 | Frameshift deletion | 1.00 |
| P0696 | F | U | c.A991G | p.M331V | 10 | Nonsynonymous SNV | 0.33 |
| P0711 | M | U | c.C1229G | p.S410C | 12 | Nonsynonymous SNV | 0.17 |
| P0880 | F | U | c.C1184T | p.T395I | 11 | Nonsynonymous SNV | 0.18 |
| P0987 | M | U | c.C1120T | p.Q374X | 10 | Stopgain | 0.45 |
| P1027 | M | U | c.T1256G | p.L419R | 11 | Nonsynonymous SNV | 0.94 |
| P1075 | M | U | c.C625T | p.Q209X | 6 | Stopgain | 0.96 |

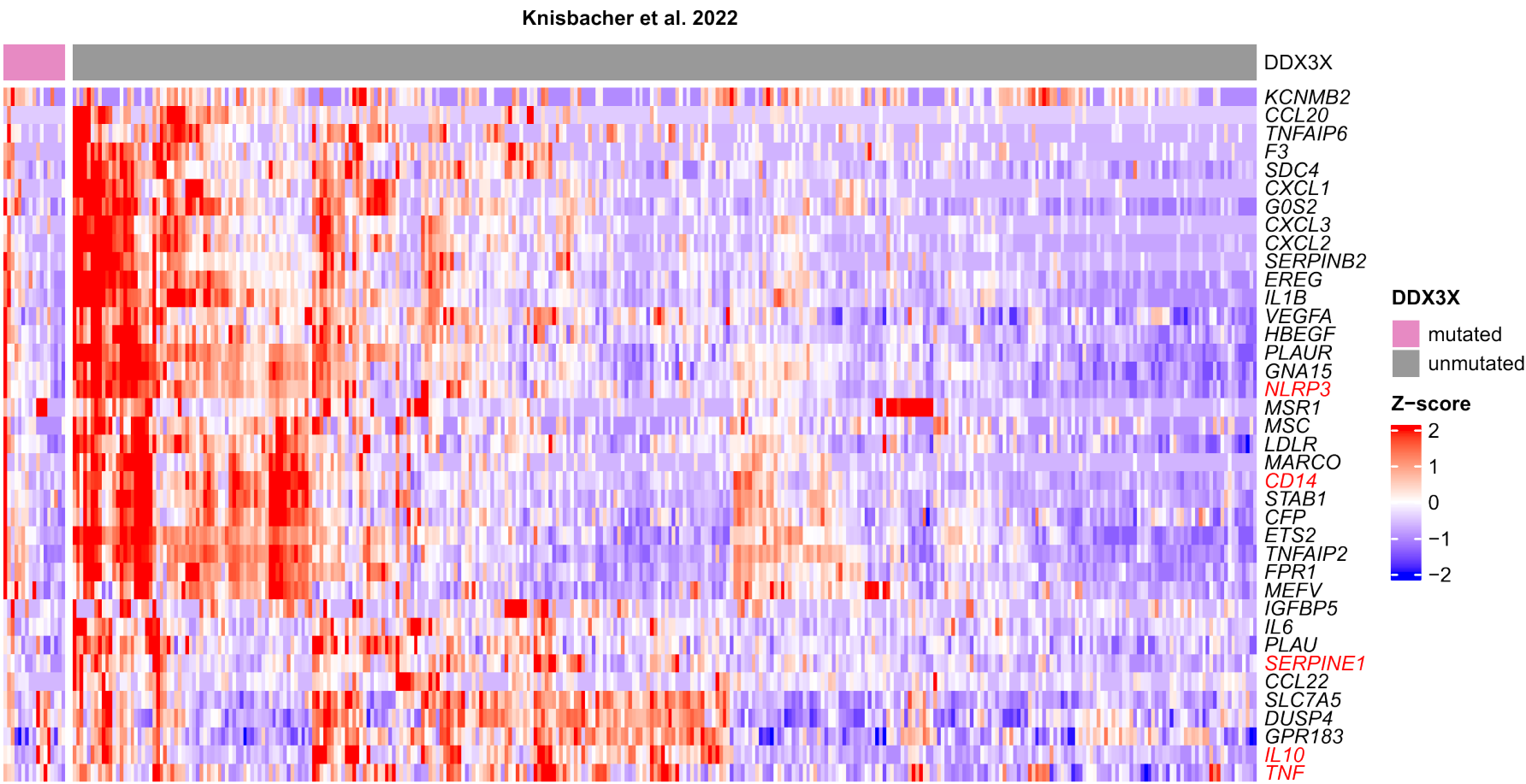
B



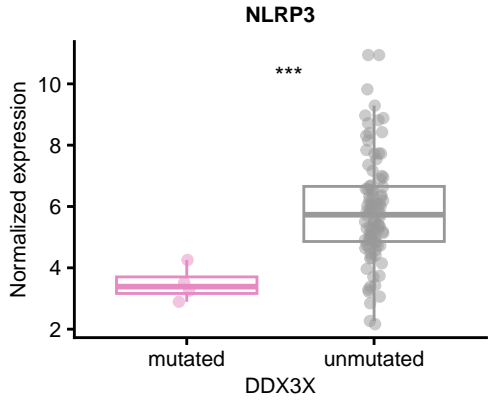
C



D



E



F

