**Supplementary File S1**

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| Model parameter | Sampled param. | Sampling distribution and sampling results |
| Vaccine efficacy V1 for age group 0.5-2 (baseline value 0.498) | RR1 = 1-V1 | Normal distribution of ln(RR1) with µ=-0.689 and =0.0669, resulting in a 95% log-normal sample range from 0.421 to 0.548 for V1 |
| Vaccine efficacy V2 for age group 3-8(baseline value 0.554) | RR2 = 1-V2 | Normal distribution of ln(RR2) with µ=-0.807 and =0.1586, resulting in a 95% log-normal sample range from 0.403 to 0.674 for V1 |
| Vaccine efficacy V3for age group 9-15(baseline value 0.690) | RR3 = 1-V3 | Normal distribution of ln(RR3) with µ=-1.171 and =0.1826, resulting in a 95% log-normal sample range from 0.553 to 0.783 for V1 |
| Vaccine efficacy V4 for age group 16-64(baseline value 0.630) | RR4 = 1-V4 | Normal distribution of ln(RR4) with µ=-0.994 and =0.0951, resulting in a 95% log-normal sample range from 0.557 to 0.693 for V4 |
| Vaccine efficacy V5 for age group 65+(baseline value 0.580) | RR5 = 1-V5 | Normal distribution of ln(RR5) with µ=0.868 and =0.2280, resulting in a 95% log-normal sample range from 0.350 to 0.735 for V5 |
| B lineage cross protection factor B after vaccination or infection(baseline value 0.60) | B | Beta distribution of R with =57 and =38, resulting in a 95% beta-distributed sample range from 0.50 to 0.70 for R |
| Multiplication factor M for vaccine efficacy against a mismatched drift variant(baseline value 0.60) | M | Beta distribution of M with =57 and =38, resulting in a 95% beta-distributed sample range from 0.50 to 0.70 for M |
| Average duration D1 between two consecutive A(H1N1) drift variants(baseline value 7 years) | D1 | Normal distribution of ln(D1) with µ=1.95 and =0.0786, resulting in a 95% log-normal sample range from 6.03 to 8.22 years for D1 |
| Average duration D2 between two consecutive A(H3N2) drift variants(baseline value 3.5 years) | D2 | Normal distribution of ln(D2) with µ=1.25 and =0.0786, resulting in a 95% log-normal sample range from 2.99 to 4.06 years for D2 |
| Average duration D3 between two consecutive B/Victoria drift variants(baseline value 7 years) | D3 | Normal distribution of ln(D3) with µ=1.95 and =0.0786, resulting in a 95% log-normal sample range from 6.00 to 8.24 years for D3 |
| Average duration D4 between two consecutive B/Yamagata drift variants(baseline value 7 years) | D4 | Normal distribution of ln(D4) with µ=1.95 and =0.0786, resulting in a 95% log-normal sample range from 6.00 to 8.15 years for D4 |
| Remaining immunity R against newly arrived drift variants(baseline value 0.60) | R | Beta distribution of R with =57 and =38, resulting in a 95% beta-distributed sample range from 0.50 to 0.69 for R |
| Immunity loss rate I after infection(baseline value 1/9.13 years) | 1/I | Normal distribution of ln(1/I) with µ=2.21 and =0.353, resulting in a 95% log-normal sample range from 4.45 to 18.24 years for 1/I |
| Difference of vaccine prices P | P | Uniform distribution for P from 0 to 4.8 USD |
| Multiplication factor of hospital admissions H | H | Normal distribution of H with µ=1.0 and =0.1, resulting in a 95% normal sample range from 0.806 to 1.204 for H |
| Multiplication factor for case fatality F | F | Normal distribution of F with µ=1.0 and =0.1, resulting in a 95% normal sample range from 0.808 to 1.200 for F |
| Multiplication factor S for the proportion of vaccinees who take a second dose of the vaccine | S | Normal distribution of S with µ=1.0 and =0.1, resulting in a 95% normal sample range from 0.816 to 1.201 for S |
| Costs per outpatient Co | Co | Uniform distribution for Co from 94.5 to 175.5 USD(i.e. baseline value ± 30%) |
| Costs per hospitalization CH | CH | Uniform distribution of CH from 1,699.6 to 3,156.4 USD(i.e. baseline value ± 30%) |
| Costs per death CD | CD | Uniform distribution of CD from 6,426 to 11,934 USD(i.e. baseline value ± 30%) |
| Monthly wage W | W | Uniform distribution of W from 1,934.52 to 3,557.58 USD(i.e. baseline value ± 30%) |
| Discount rate d | d | Uniform distribution of d from 0 to 4% |

Table A1. Sampling distributions and sampling results for the probabilistic sensitivity analysis.