

Additional File 2: Supplementary results for the article *Interventions to control nosocomial transmission of SARS-CoV-2: a modelling study*

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I. Results on transmission routes

Our results show that for the considered simulation scenarios most of the nosocomial transmissions of the SARS-CoV-2 variant is mainly driven by transmissions between patients and HCWs (Figure S4). This is expected as we assumed that there is no direct contact between patients and the majority of contacts of HCWs are with patients. Furthermore, for most of the intervention scenarios, over 90% of transmissions occur in non-COVID wards where no use of PPE is assumed in the baseline scenario (Figure S6). Since in our model infected patients are transferred to COVID wards and infected HCWs are assumed to self-isolate immediately upon symptom onset, most transmissions take place during the pre-symptomatic stage of an infected individual (dark-grey bars in Figure S7). This is in line with a French study where secondary cases were exposed mainly in the pre-symptomatic phase.¹⁵ When PPE is used throughout the hospital or HCWs are screened assuming a perfect test sensitivity, most transmissions are prevented (Figure 5 of the main text). In particular, transmissions that occur during non-symptomatic states in non-COVID wards are significantly reduced, decreasing their contribution to the overall number of transmissions (Figure S6-Figure S7).

II. Results of sensitivity analyses

We evaluate the changes of our results with respect to changes in our model parameters. We present the results and corresponding plots for the effective reproduction number R_E , the total number of nosocomial transmissions, and daily number of absent HCWs. The remaining plots can be found online: https://github.com/htahir2/covid_intra-hospital_model.git

PPE effectiveness

We performed two sensitivity analyses to test the impact of PPE effectiveness values on our results:

- a) 50% effective PPE
- b) 70% effective PPE

Our sensitivity analyses show that the effective reproduction numbers and the total number of nosocomial transmissions increase with lower PPE effectiveness and decrease with higher PPE effectiveness, in particular for the “PPE in all wards” intervention scenario (compare Figure S8-S7, Figures Figure S11-Figure S12, and Figures 4-5 of the main text). A similar effect can be observed for the daily percentage of HCW absenteeism (compare Figure S10, Figure S13, and Figure 6 of the main text). The relative impact of the different interventions on the reproduction number in comparison to the baseline scenario are similar to what we have observed in our main analysis. The only difference is that for a low value of PPE effectiveness of 50%, screening every three days with time-invariant perfect sensitivity is more effective in reducing the effective reproduction number, especially for pre-symptomatic HCWs. However, the use of 50% effective PPE in all wards still decreases the effective reproduction number more than the remaining interventions.

Reproduction number

We performed a sensitivity analysis to test the impact of equal reproduction numbers of symptomatically and asymptotically infected individuals on our results (Figure S14-Figure S16). Furthermore, we show the model results for the reproduction numbers resulting from calibrating our model to data on the number of occupied beds by COVID-19 patients at the UMCU (Figure S17-Figure S19). Our sensitivity analyses show that the effective reproduction numbers, the total number of nosocomial transmissions as well as the daily percentage of HCW absenteeism increase with increasing basic reproduction number. In particular, when the reproduction number of asymptotically infected individuals is as high as the one of symptomatically infected individuals, the respective effective reproduction numbers for asymptomatic patients and HCWs increase. The impact on the overall effective reproduction number is smaller, however, still notable. Qualitatively, our conclusions regarding the relative effect of the considered infection control interventions remain unchanged. For low reproduction numbers as it was the case for the nosocomial spread of the wild-type SARS-CoV-2 variant at UMCU, the numbers of nosocomial transmissions are very small and hence the relative impact of the intervention scenarios in comparison to each other and to the baseline scenario is smaller than for higher reproduction numbers. However, the qualitative conclusions remain unchanged.

Increased HCW-to-HCW contact rate

In our main analysis, we assume that HCWs meet other HCWs once every hour. In this sensitivity analysis, we relax this assumption by increasing the contact rates between HCWs to once every 30 minutes and evaluate the impact on our results (Figure S20-Figure S22). The effective reproduction numbers, the total number of nosocomial transmissions, and the daily percentage of HCW absenteeism increase when the contact rate between HCWs is increased. In particular, the effective reproduction numbers for HCWs increase but not those for symptomatic patients (Figure S20). Qualitatively, our conclusions with respect to the impact of the interventions on the hospital epidemic do not change with respect to this parameter.

Test sensitivity

We performed two sensitivity analyses:

- a) assuming the test sensitivity to remain at the maximum after reaching its peak (high test sensitivity scenario) and
- b) reducing the test sensitivity curve of the main analysis by 15% (low test sensitivity scenario).

The respective test sensitivity curves varying from time since infection are shown in Additional File 1: Figure S1. There are only minor differences in our results for both sensitivity scenarios (Figure S23-Figure **S25** vs Figures 4-6 of the main text).

Recovery time

To test the impact of the recovery time of infected individuals (i.e., the time after which infected individuals are set to non-infectious and recovered in the model), we performed the simulations with a stochastic (instead of fixed) implementation of the recovery times. For this sensitivity analysis we assumed the following uniform distributions for the recovery times:

- Unif(9,19) for asymptomatic and moderately symptomatically infected individuals
- Unif(30,40) for severely symptomatically infected individuals.

The parameters in brackets represent the time since infection and serve as lower and upper bounds in the uniform distribution. Qualitatively, our results do not change with respect to this parameter (Figure S29-Figure **S31**).

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Table S1. Outcome measures for baseline and intervention scenarios.

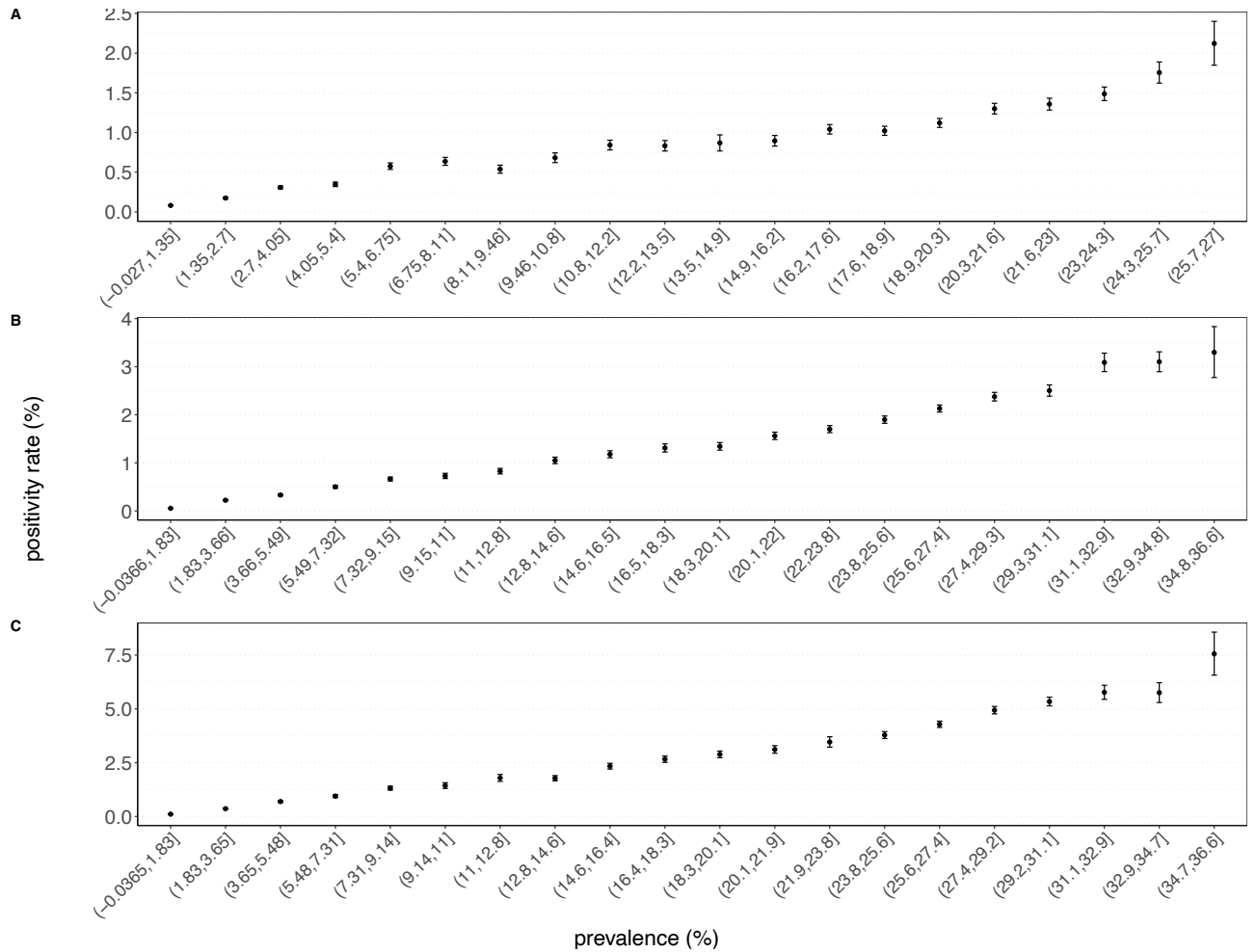
Scenario	Effective reproduction number*					Total number of nosocomial transmissions*	Peak percentage of HCW absenteeism (%) [†]	Peak positivity rates (%)*
	Overall	Symptomatic patient	Asymptomatic patient	Pre-symptomatic HCW	Asymptomatic HCW			
Baseline	0.65 (0.57, 0.71)	0.55 (0.46, 0.66)	0.40 (0.23, 0.60)	0.94 (0.79, 1.07)	0.44 (0.33, 0.54)	526.2 (362.3, 675.2)	5.4	
HCW cohorting	0.62 (0.56, 0.67)	0.50 (0.40, 0.60)	0.39 (0.17, 0.60)	0.91 (0.79, 1.04)	0.44 (0.31, 0.55)	457.9 (359, 565.1)	5.2	
PPE in all wards	0.10 (0.07, 0.14)	0.03 (0.01, 0.06)	0.03 (0.00, 0.42)	0.21 (0.13, 0.32)	0.09 (0.02, 0.18)	32.9 (21.5, 48.5)	2.3	
Screening 3 days perfect sens	0.24 (0.14, 0.32)	0.23 (0.10, 0.36)	0.53 (0.00, 1.23)	0.28 (0.19, 0.40)	0.12 (0.03, 0.24)	90.9 (47, 136.5)	5.1	1.7 (1.6, 1.8)
Screening 3 days	0.59 (0.51, 0.65)	0.53 (0.42, 0.62)	0.47 (0.24, 0.71)	0.81 (0.68, 0.92)	0.36 (0.22, 0.51)	419 (298.1, 528.7)	8.6	2.5 (2.4, 2.6)
Screening 7 days	0.63 (0.54, 0.69)	0.55 (0.47, 0.64)	0.44 (0.25, 0.64)	0.87 (0.73, 0.98)	0.39 (0.29, 0.51)	473 (353.9, 614.3)	6.6	5.1 (5, 5.3)
7-day Contact tracing perfect sens	0.44 (0.36, 0.55)	0.29 (0.21, 0.38)	0.31 (0.11, 0.61)	0.74 (0.60, 0.90)	0.36 (0.22, 0.50)	232.7 (155.9, 341.4)	4	15.1 (14.1, 16.1)
2-day Contact tracing	0.41 (0.33, 0.48)	0.27 (0.18, 0.35)	0.30 (0.08, 0.65)	0.71 (0.55, 0.84)	0.32 (0.19, 0.47)	202.9 (138.5, 269.6)	3.6	11.3 (9.4, 13.1)
7-day Contact tracing	0.39 (0.33, 0.44)	0.25 (0.17, 0.34)	0.29 (0.05, 0.61)	0.67 (0.52, 0.80)	0.31 (0.17, 0.44)	188.7 (139, 248.6)	3.9	10.4 (9.1, 11.6)

*Mean values over 100 simulation runs are given. Values in brackets are the lower and upper bounds of 95% uncertainty intervals.

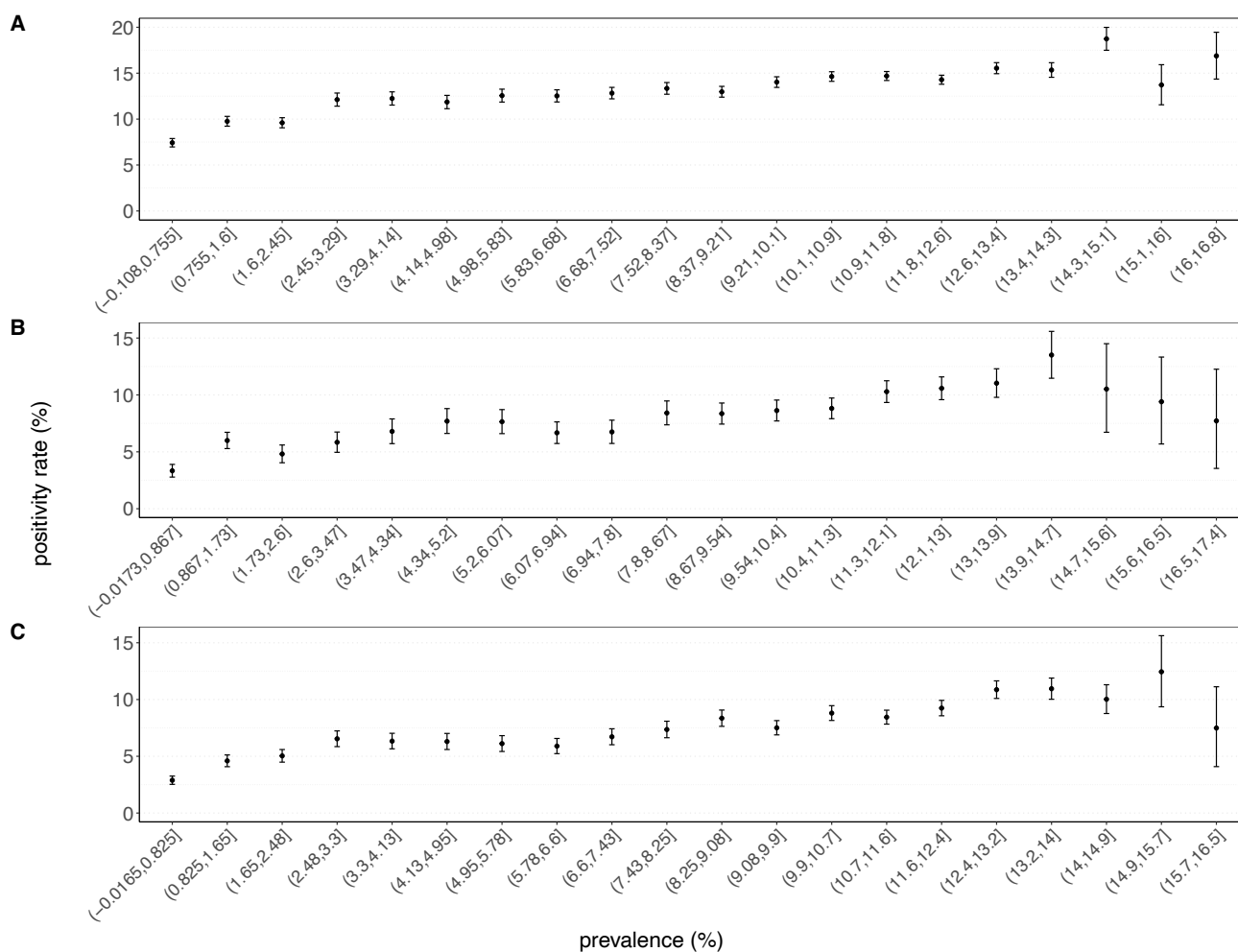
[†]7-day moving average of mean percentage (over 100 simulation runs)

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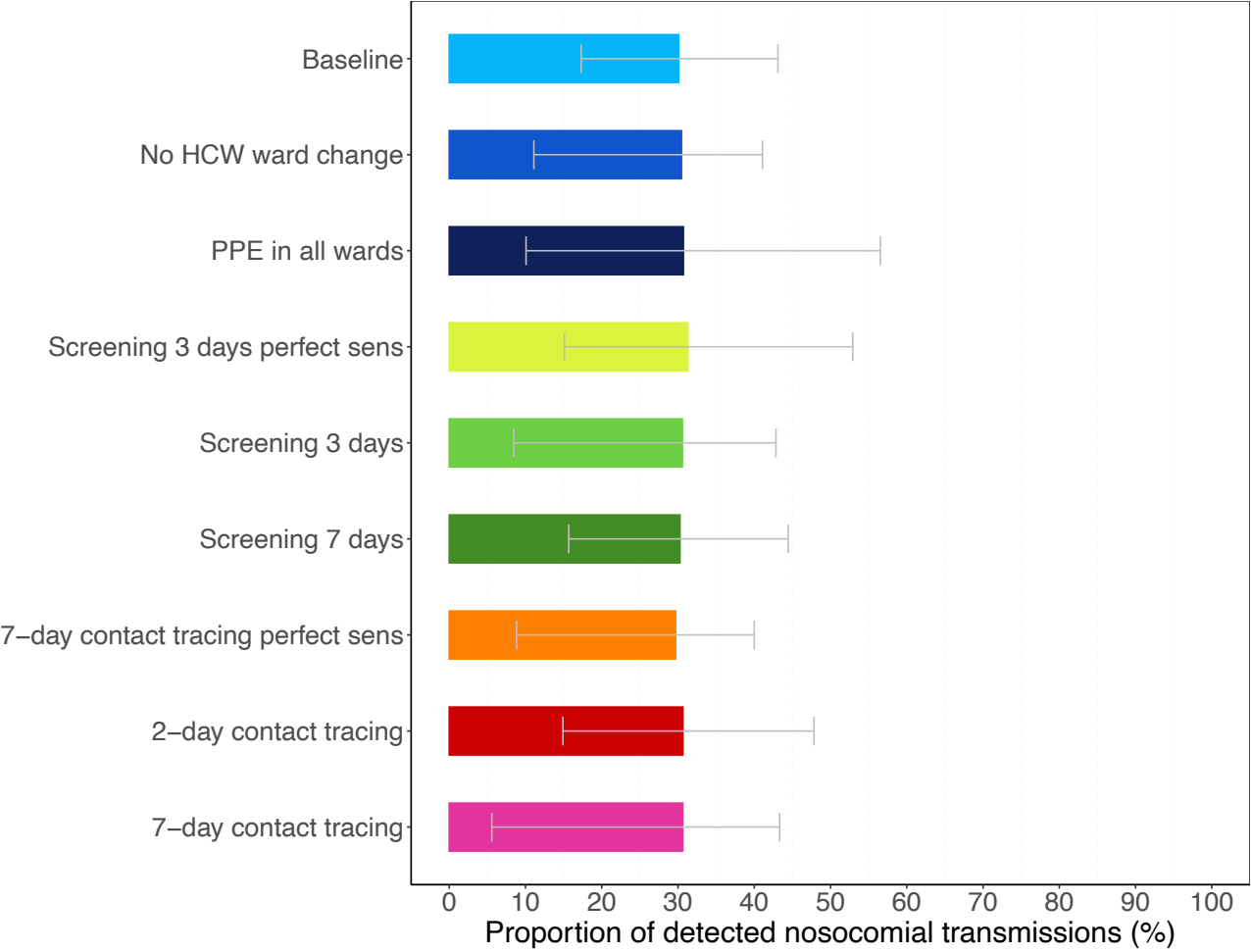
201 **Figure S1. Positivity rate of screening interventions for different prevalence ranges.** Results shown are based on
 202 $R_S=1.95$ and $R_A=0.8$ (reproduction numbers for the SARS-CoV-2 variant with 56% higher transmissibility with respect to
 203 the wild-type SARS-CoV-2 variant). (A) Screening every three days with constant perfect test sensitivity. (B) Screening
 204 every three days with imperfect, time-varying test sensitivity. (C) Screening every seven days with imperfect, time-varying
 205 test sensitivity. On each day when HCWs were screened, the number of positive tested HCWs among the total number of
 206 screened HCWs is computed. The prevalence values on the day when HCWs were screened is divided into categories. For
 207 each prevalence category, the positivity rate was computed by the total number of positive tested HCWs divided by the
 208 total number of screened HCWs (merging values of all simulations) and is shown as a point. The error bars represent the
 209 95% binomial proportion confidence intervals.



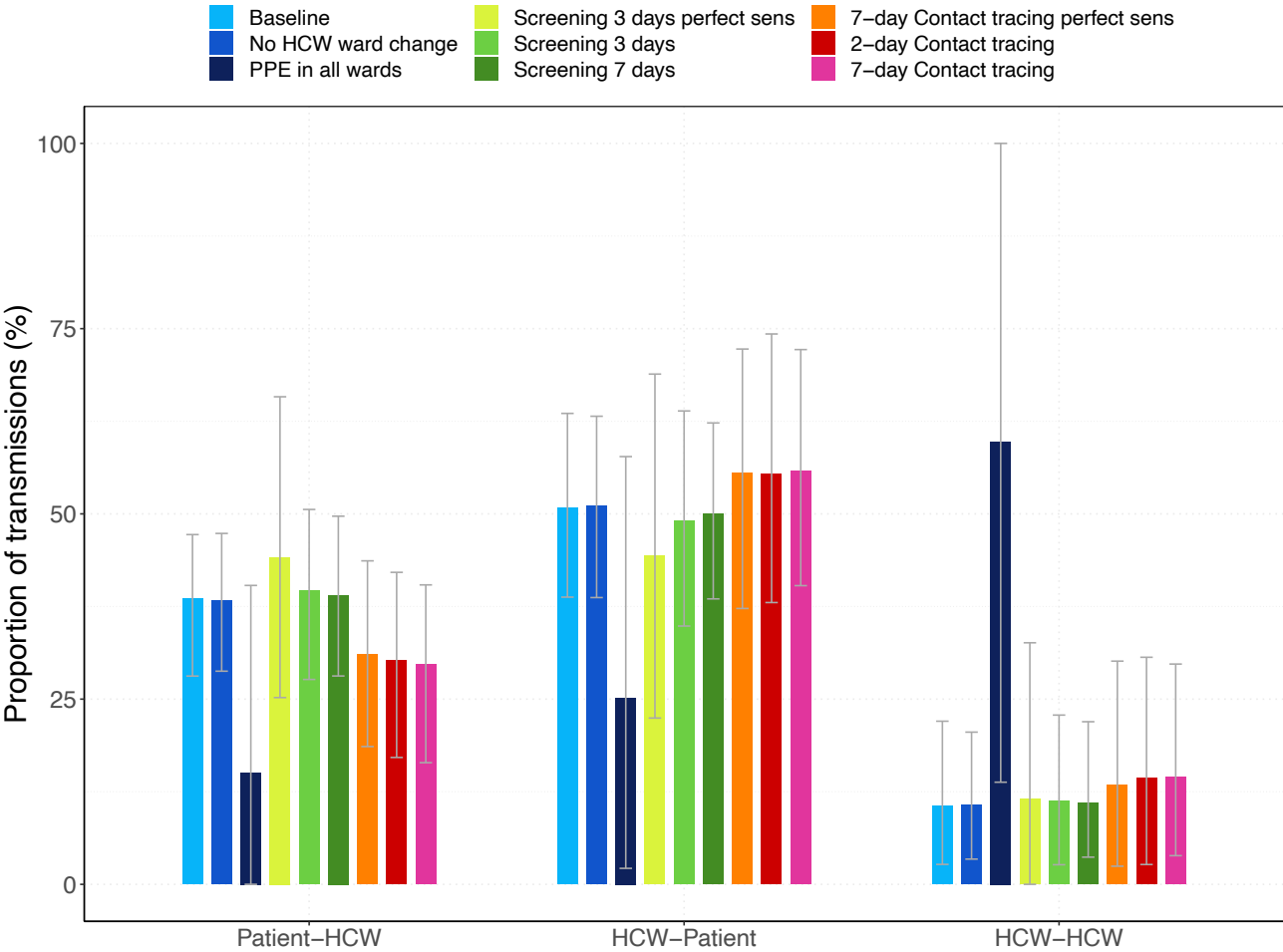
229 **Figure S2. Positivity rate of contact tracing interventions for different prevalence ranges.** Results shown are based
 230 on $R_S=1.95$ and $R_A=0.8$ (reproduction numbers for the SARS-CoV-2 variant with 56% higher transmissibility with respect
 231 to the wild-type SARS-CoV-2 variant). (A) Contact tracing of contacts two days prior to symptom onset with perfect test
 232 sensitivity. (B) Contact tracing of contacts two days prior to symptom onset with time-varying imperfect test sensitivity.
 233 (C) Contact tracing of contacts seven days prior to symptom onset with time-varying, imperfect test sensitivity. For each
 234 index case (symptomatically infected HCW), the number of positive contacts and total number of contacts that are traced
 235 is computed in each simulation. The prevalence values on the day when an index case was traced, is divided into categories.
 236 For each prevalence category, the positivity rate is computed by the total number of positive divided by the total number
 237 of traced contacts (all simulations merged) and is shown as a point. The error bars represent the binomial proportion
 238 confidence interval.



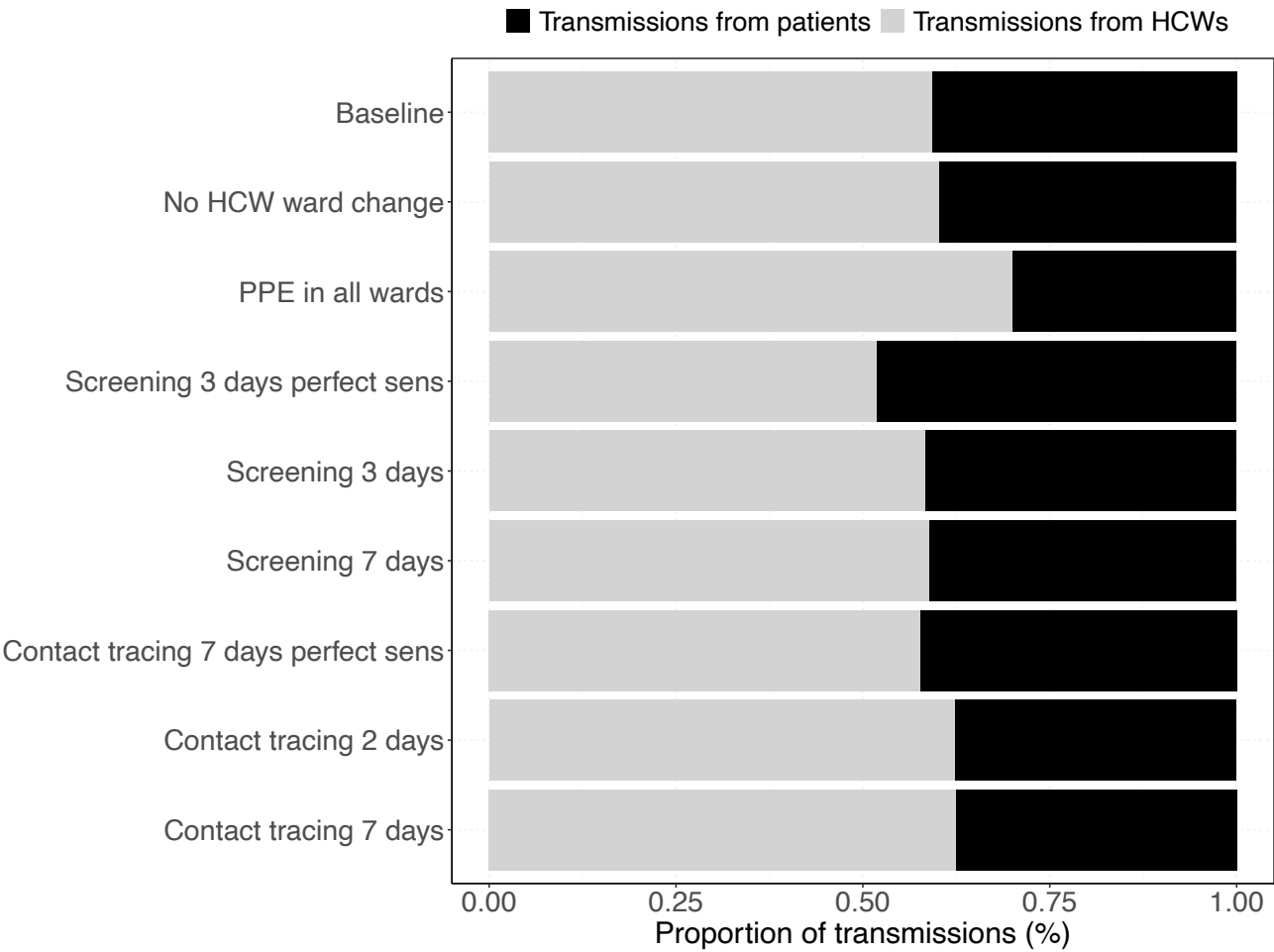
257 **Figure S3. Proportion of detected nosocomial transmissions of the SARS-CoV-2 variant for each simulation**
 258 **scenario.** Results shown are based on $R_S=1.95$ and $R_A=0.8$ (reproduction numbers for the SARS-CoV-2 variant with
 259 56% higher transmissibility with respect to the wild-type SARS-CoV-2 variant). The colored rectangular bars with black
 260 borders represent the mean proportion of patients detected with a SARS-CoV-2 infection in the hospital due to symptom
 261 onset or detection by an intervention (over 100 simulation runs). The denominator are patients either admitted with a
 262 SARS-CoV-2 infection (asymptomatic or pre-symptomatic) or acquired it in the hospital. The proportions of infected
 263 patients undetected comprise patients who are discharged to community in a pre-symptomatic or asymptomatic state. The
 264 grey error bars the respective 95% uncertainty intervals.



285 **Figure S4. Transmission route contributions for nosocomial transmissions of the SARS-CoV-2 variant for each**
 286 **simulation scenario.** Three different transmission routes are considered: From patient to HCW (Patient-HCW), from
 287 HCW to patient (HCW-patient), and from HCW to HCW (HCW-HCW). The colored rectangular bars represent the mean
 288 percentage of transmissions (averaged over 100 simulations) due to the respective transmission route for each simulation
 289 scenario. The grey error bars represent the respective 95% uncertainty intervals. For screening every 3 days and 7-day
 290 contact tracing, we considered two different test sensitivity scenarios: time-invariant perfect test sensitivity (perfect sens)
 291 and time-varying imperfect test sensitivity.

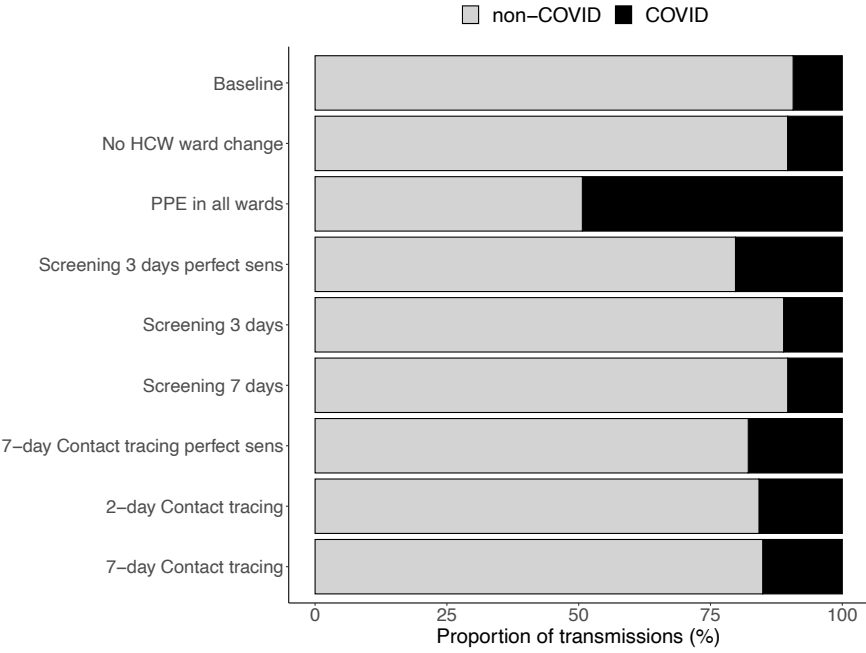


295 **Figure S5. Proportion of transmissions from HCWs and from patients for each simulation scenarios.** Mean
296 percentage of total transmissions (averaged over 100 simulation runs) that occurred from HCWs vs from patients are shown
297 in stacked bar plots. Results shown are based on $R_S=1.95$ and $R_A=0.8$ (reproduction numbers for the SARS-CoV-2 variant
298 with 56% higher transmissibility with respect to the wild-type SARS-CoV-2 variant).

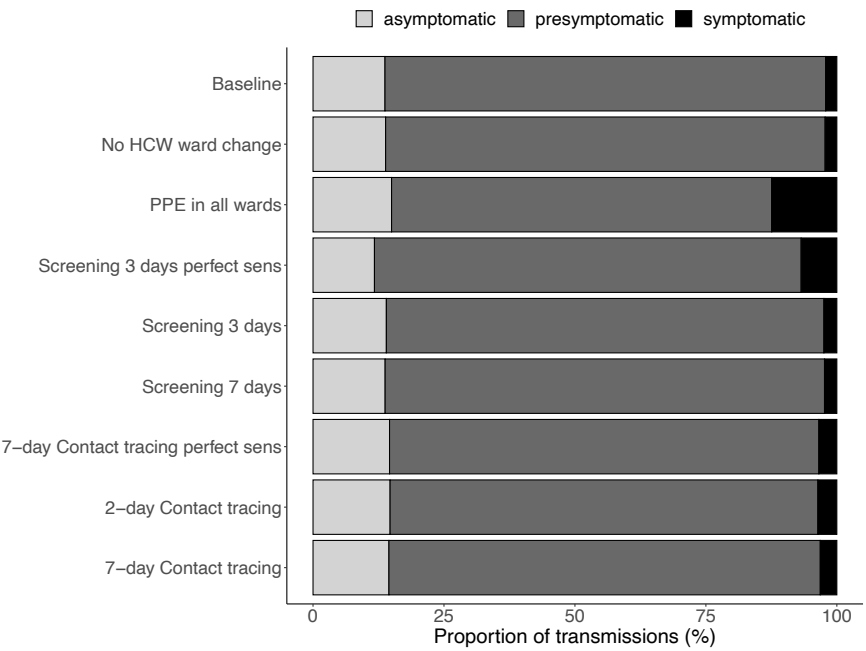


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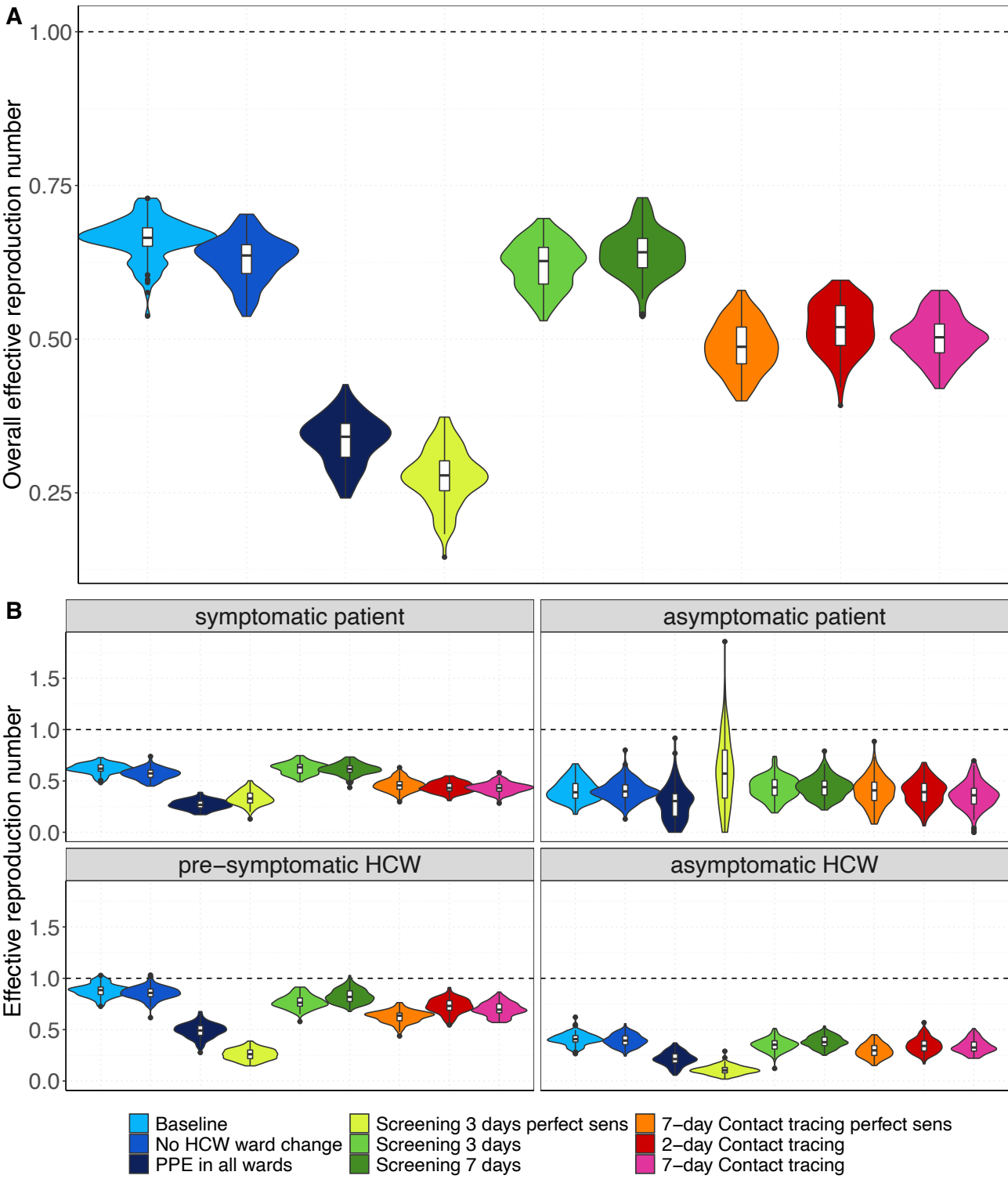
302 **Figure S6. Proportion of nosocomial transmissions in COVID- and non-COVID wards for each simulation scenario.**
 303 The mean percentages of nosocomial transmissions (averaged over 100 simulation runs) in COVID and non-COVID wards
 304 are shown in stacked bar plots. Results shown are based on $R_S=1.95$ and $R_A=0.8$ (reproduction numbers for the SARS-
 305 CoV-2 variant with 56% higher transmissibility with respect to the wild-type SARS-CoV-2 variant).



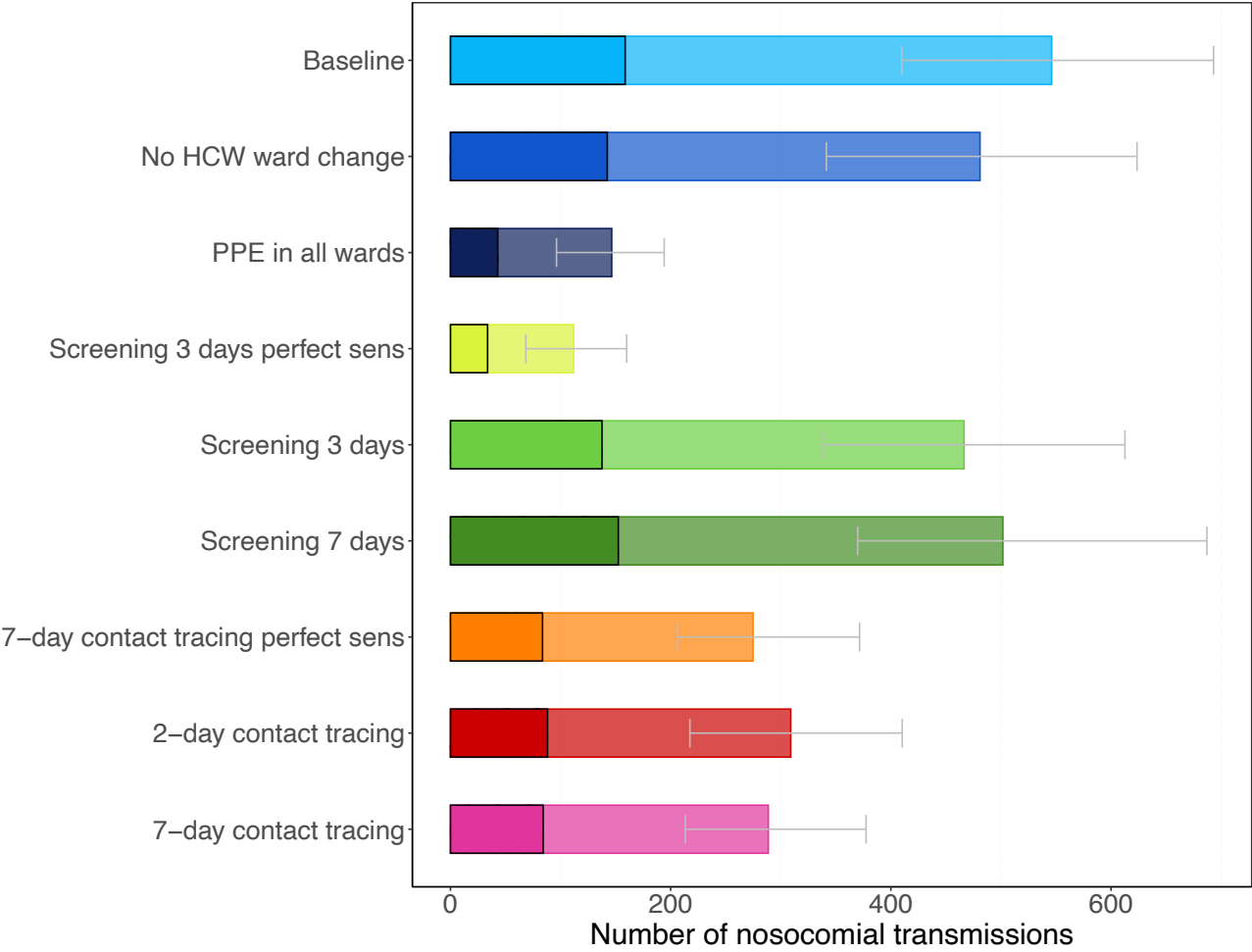
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 308 **Figure S7. Proportion of transmissions during different infection states for each simulation scenario.** The mean
 309 percentages of transmissions (averaged over 100 simulations) that occurred while the infected individual was in an
 310 asymptomatic, pre-symptomatic, or symptomatic state are shown in stacked bar plots. Results shown are based on $R_S=1.95$
 311 and $R_A=0.8$ (reproduction numbers for the SARS-CoV-2 variant with 56% higher transmissibility with respect to the wild-
 312 type SARS-CoV-2 variant).



316 **Figure S8. Effective reproduction numbers for the nosocomial spread of the SARS-CoV-2 variant for each**
 317 **simulation scenario assuming 50% effective PPE.** Results shown are based on $R_S=1.95$ and $R_A=0.8$ (reproduction
 318 numbers for the SARS-CoV-2 variant with 56% higher transmissibility with respect to the wild-type SARS-CoV-2 variant).
 319 (A) For each simulation scenario, violin and boxplots of the overall reproduction numbers (for pre-/symptomatic and
 320 asymptomatic patients and HCWs combined) are shown (over 100 simulations). (B) For each simulation scenario, violin
 321 and boxplots of the reproduction numbers for pre-/symptomatic and asymptomatic individuals are shown (over 100
 322 simulations). Note that since HCWs are assumed to immediately self-isolate upon symptom onset, the reproduction
 323 number is assigned to the pre-symptomatic state. The horizontal dashed line represents a reproduction number of 1. For screening
 324 every three days and contact tracing seven days prior to symptom onset of SARS-CoV-2 infected HCWs, we considered
 325 two different test sensitivity scenarios: time-invariant perfect test sensitivity (perfect sens) and imperfect test sensitivity
 326 varying from time since infection.

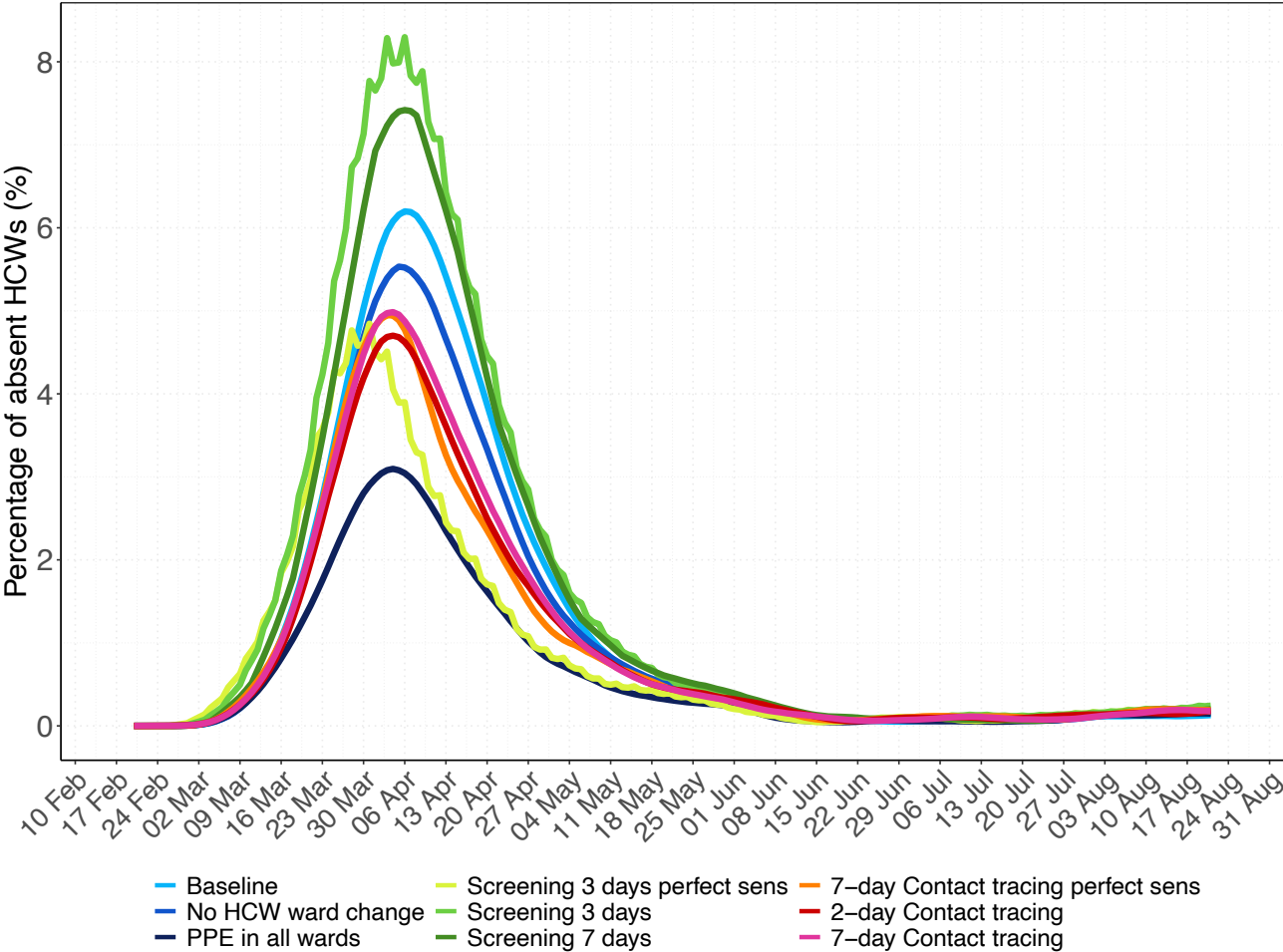


328 **Figure S9. Number of nosocomial transmissions of the SARS-CoV-2 variant for each simulation scenario assuming**
 329 **50% effective PPE.** Results shown are based on $R_S=1.95$ and $R_A=0.8$ (reproduction numbers for the SARS-CoV-2 variant
 330 with 56% higher transmissibility with respect to the wild-type SARS-CoV-2 variant). The full rectangular bar height
 331 represents the mean total number of nosocomial transmissions during the whole study period (over 100 simulation runs).
 332 The grey error bars represent the corresponding 95% uncertainty intervals. Patients that acquire a SARS-CoV-2 nosocomial
 333 infection may be diagnosed in the hospital (due to symptom onset during hospital stay or due to detection by an
 334 intervention) or discharged to the community in a pre-symptomatic or asymptomatic state. The rectangular bars with the
 335 black border represent the mean number of individuals (patients and HCWs) infected with SARS-CoV-2 and diagnosed in
 336 the hospital. The lighter rectangular bars represent the remaining mean number of patients discharged to community
 337 undiagnosed. For screening every 3 days and 7-day contact tracing, we considered two different test sensitivity scenarios:
 338 time-invariant perfect test sensitivity (perfect sens) and time-varying imperfect test sensitivity.

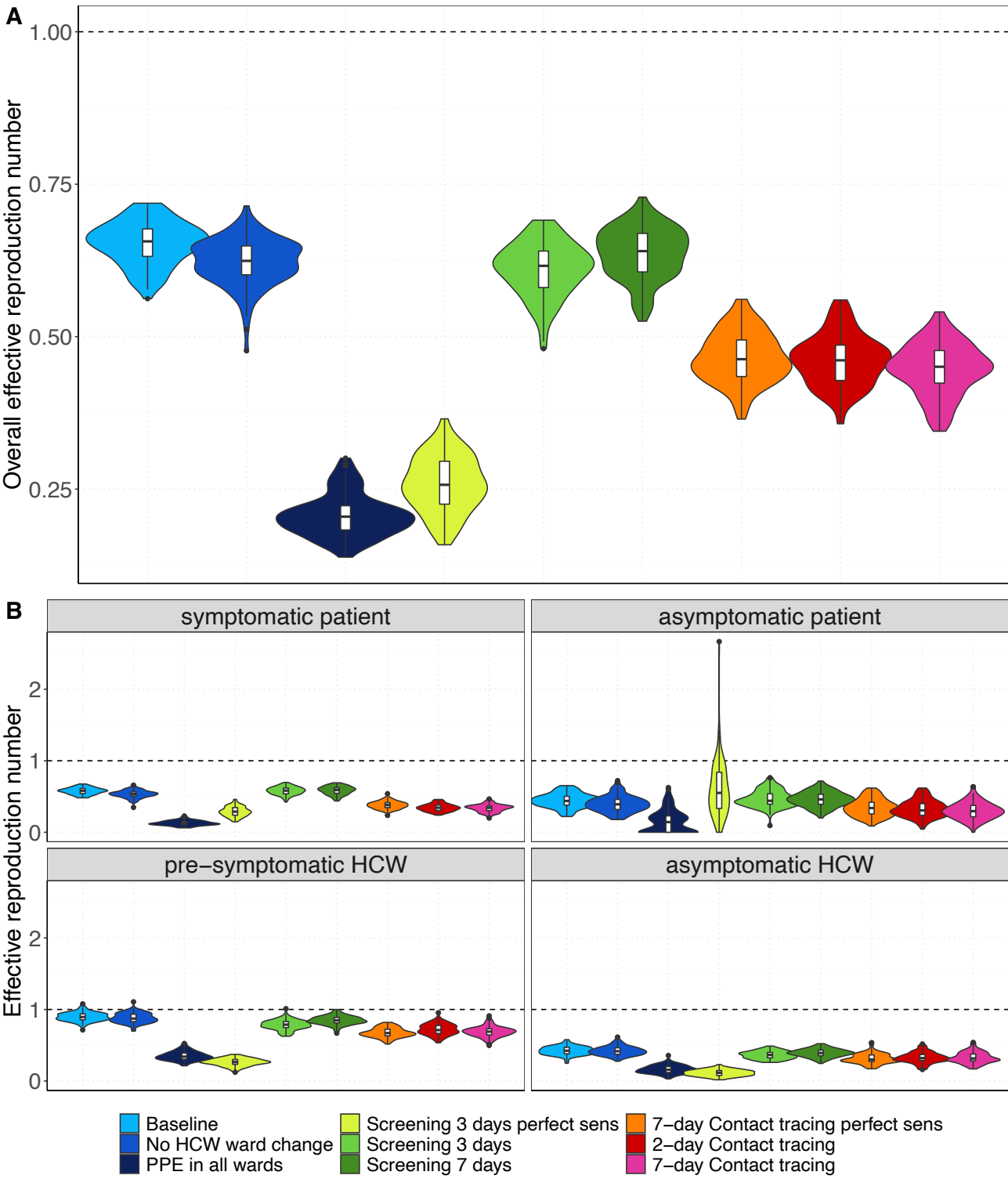


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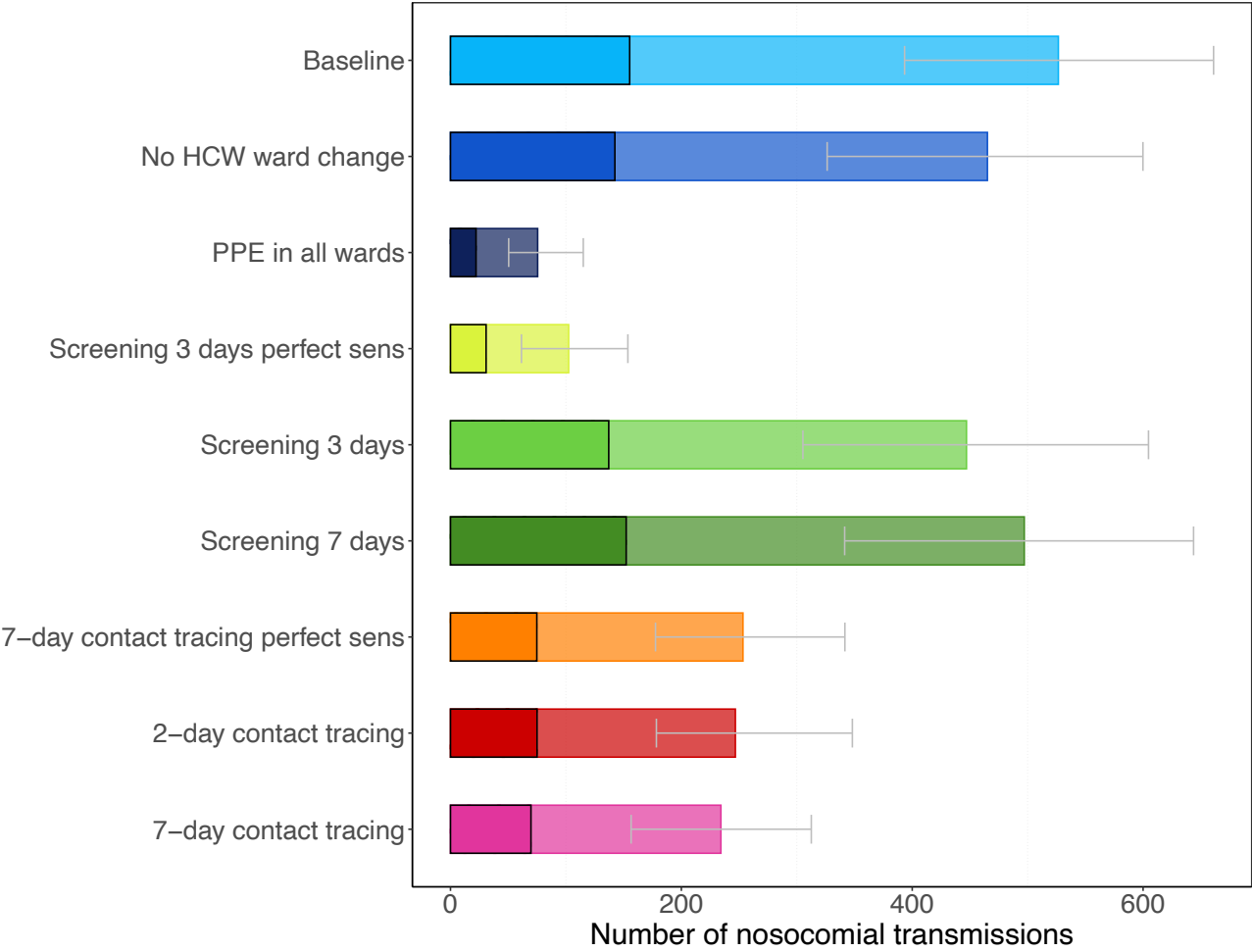
341 **Figure S10. Daily percentage of absent HCWs during the hospital epidemic for each simulation scenario assuming**
 342 **50% effective PPE.** Results shown are based on $R_S=1.95$ and $R_A=0.8$ (reproduction numbers for the SARS-CoV-2
 343 variant with 56% higher transmissibility with respect to the wild-type SARS-CoV-2 variant). The 7-day moving average
 344 of the mean percentage (over 100 simulation runs) of HCWs absent from work due to symptom onset or a detected SARS-
 345 CoV-2 infection screening or contact tracing is shown. For screening every 3 days and contact tracing 7 days prior to
 346 symptom onset of SARS-CoV-2 infected HCWs, we considered two different test sensitivity scenarios: time-invariant
 347 perfect test sensitivity (perfect sens) and time-varying imperfect test sensitivity.



350 **Figure S11. Effective reproduction numbers for the nosocomial spread of the SARS-CoV-2 variant for each**
 351 **simulation scenario assuming 70% effective PPE.** Results shown are based on $R_S=1.95$ and $R_A=0.8$ (reproduction
 352 numbers for the SARS-CoV-2 variant with 56% higher transmissibility with respect to the wild-type SARS-CoV-2 variant).
 353 (A) For each simulation scenario, violin and boxplots of the overall reproduction numbers (for pre-/symptomatic and
 354 asymptomatic patients and HCWs combined) are shown (over 100 simulations). (B) For each simulation scenario, violin
 355 and boxplots of the reproduction numbers for pre-/symptomatic and asymptomatic individuals are shown (over 100
 356 simulations). Note that since HCWs are assumed to immediately self-isolate upon symptom onset, the reproduction number
 357 is assigned to the pre-symptomatic state. The horizontal dashed line represents a reproduction number of 1. For screening
 358 every three days and contact tracing seven days prior to symptom onset of SARS-CoV-2 infected HCWs, we considered
 359 two different test sensitivity scenarios: time-invariant perfect test sensitivity (perfect sens) and imperfect test sensitivity
 360 varying from time since infection.

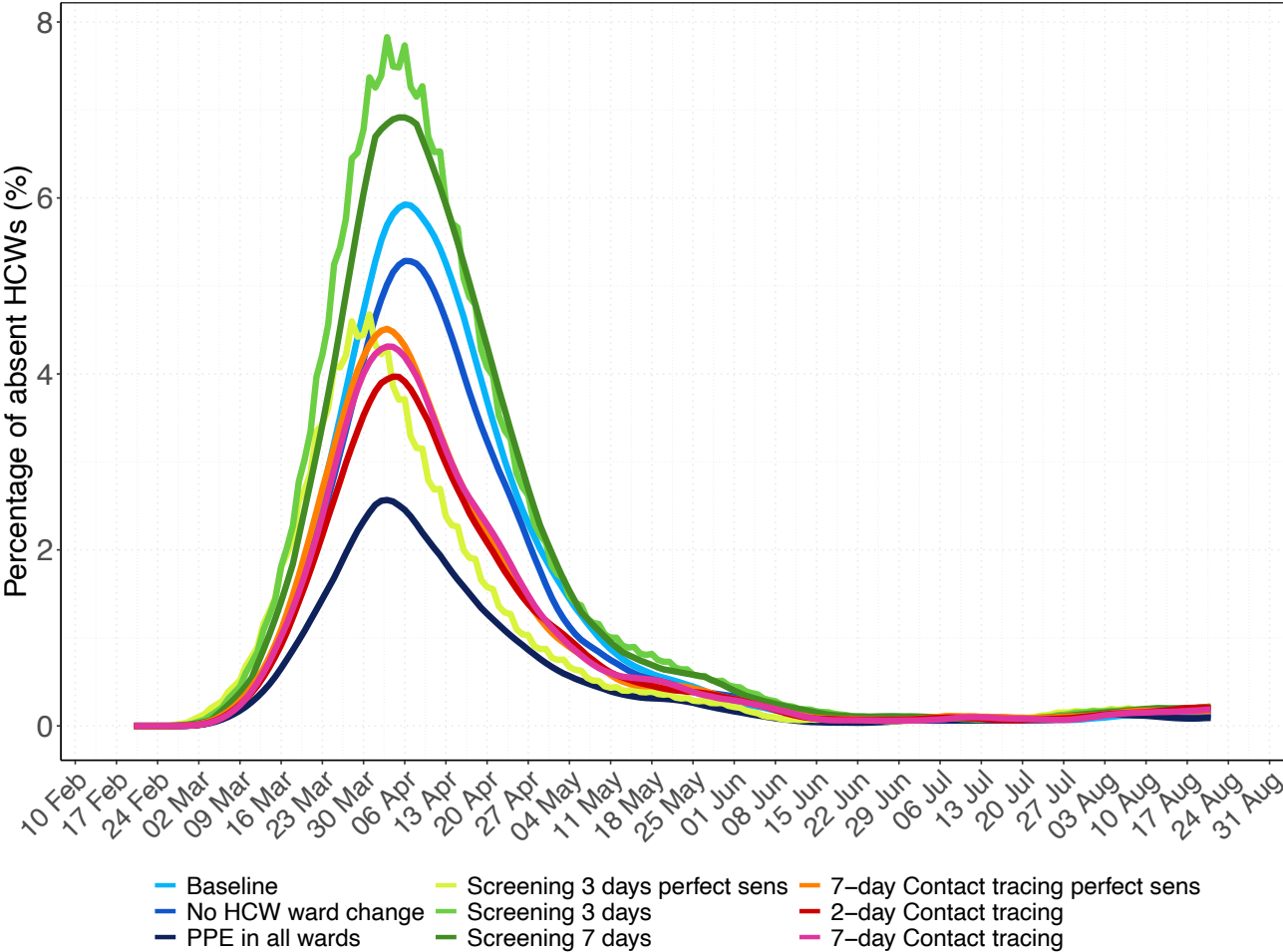


362 **Figure S12. Number of nosocomial transmissions of the SARS-CoV-2 variant for each simulation scenario assuming**
 363 **70% effective PPE.** Results shown are based on $R_S=1.95$ and $R_A=0.8$ (reproduction numbers for the SARS-CoV-2 variant
 364 with 56% higher transmissibility with respect to the wild-type SARS-CoV-2 variant). The full rectangular bar height
 365 represents the mean total number of nosocomial transmissions during the whole study period (over 100 simulation runs).
 366 The grey error bars represent the corresponding 95% uncertainty intervals. Patients that acquire a SARS-CoV-2 nosocomial
 367 infection may be diagnosed in the hospital (due to symptom onset during hospital stay or due to detection by an
 368 intervention) or discharged to the community in a pre-symptomatic or asymptomatic state. The rectangular bars with the
 369 black border represent the mean number of individuals (patients and HCWs) infected with SARS-CoV-2 and diagnosed in
 370 the hospital. The lighter rectangular bars represent the remaining mean number of patients discharged to community
 371 undiagnosed. For screening every 3 days and 7-day contact tracing, we considered two different test sensitivity scenarios:
 372 time-invariant perfect test sensitivity (perfect sens) and time-varying imperfect test sensitivity.

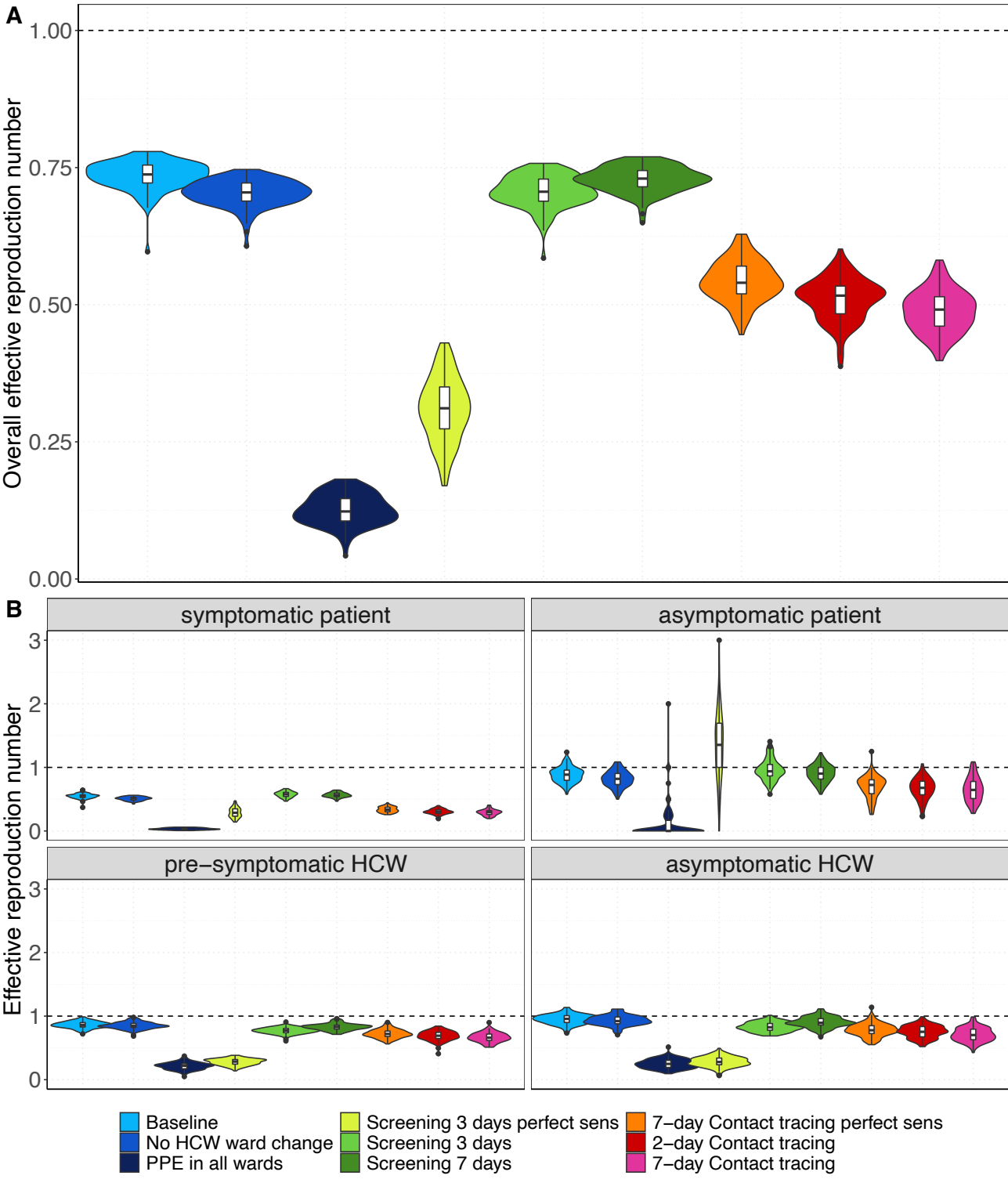


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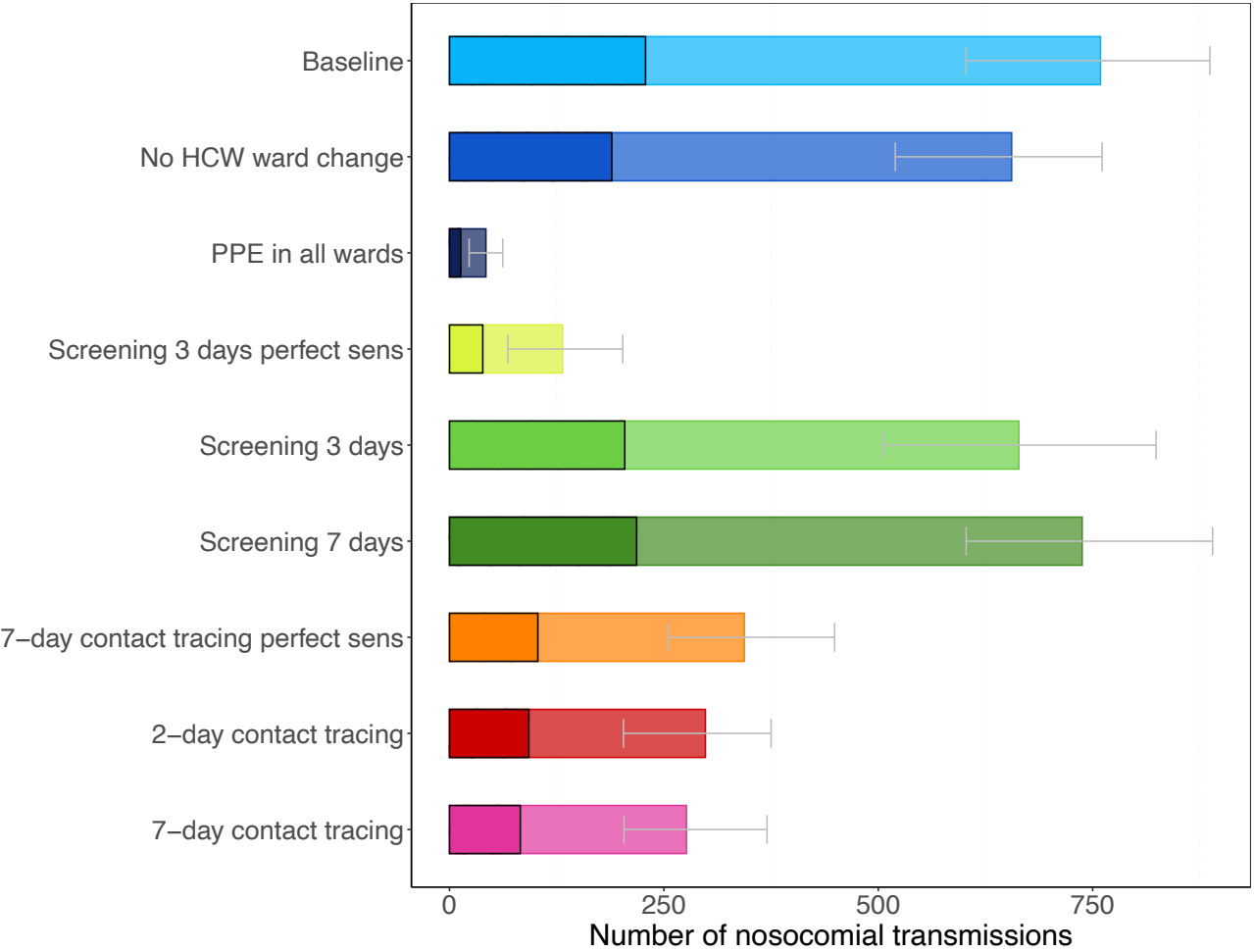
375 **Figure S13. Daily percentage of absent HCWs during the hospital epidemic for each simulation scenario assuming**
 376 **70% effective PPE.** Results shown are based on $R_S=1.95$ and $R_A=0.8$ (reproduction numbers for the SARS-CoV-2
 377 variant with 56% higher transmissibility with respect to the wild-type SARS-CoV-2 variant). The 7-day moving average
 378 of the mean percentage (over 100 simulation runs) of HCWs absent from work due to symptom onset or a detected SARS-
 379 CoV-2 infection screening or contact tracing is shown. For screening every 3 days and contact tracing 7 days prior to
 380 symptom onset of SARS-CoV-2 infected HCWs, we considered two different test sensitivity scenarios: time-invariant
 381 perfect test sensitivity (perfect sens) and time-varying imperfect test sensitivity.



384 **Figure S14. Effective reproduction numbers for the nosocomial spread of the SARS-CoV-2 variant for each**
 385 **simulation scenario assuming equal reproduction numbers for symptomatically and asymptotically infected**
 386 **individuals $R_S=1.95$ and $R_A=1.95$.** (A) For each simulation scenario, violin and boxplots of the overall reproduction
 387 numbers (for pre-/symptomatic and asymptomatic patients and HCWs combined) are shown (over 100 simulations). (B)
 388 For each simulation scenario, violin and boxplots of the reproduction numbers for pre-/symptomatic and asymptomatic
 389 individuals are shown (over 100 simulations). Note that since HCWs are assumed to immediately self-isolate upon
 390 symptom onset, the reproduction number is assigned to the pre-symptomatic state. The horizontal dashed line represents a
 391 reproduction number of 1. For screening every three days and contact tracing seven days prior to symptom onset of SARS-
 392 CoV-2 infected HCWs, we considered two different test sensitivity scenarios: time-invariant perfect test sensitivity (perfect
 393 sens) and imperfect test sensitivity varying from time since infection.

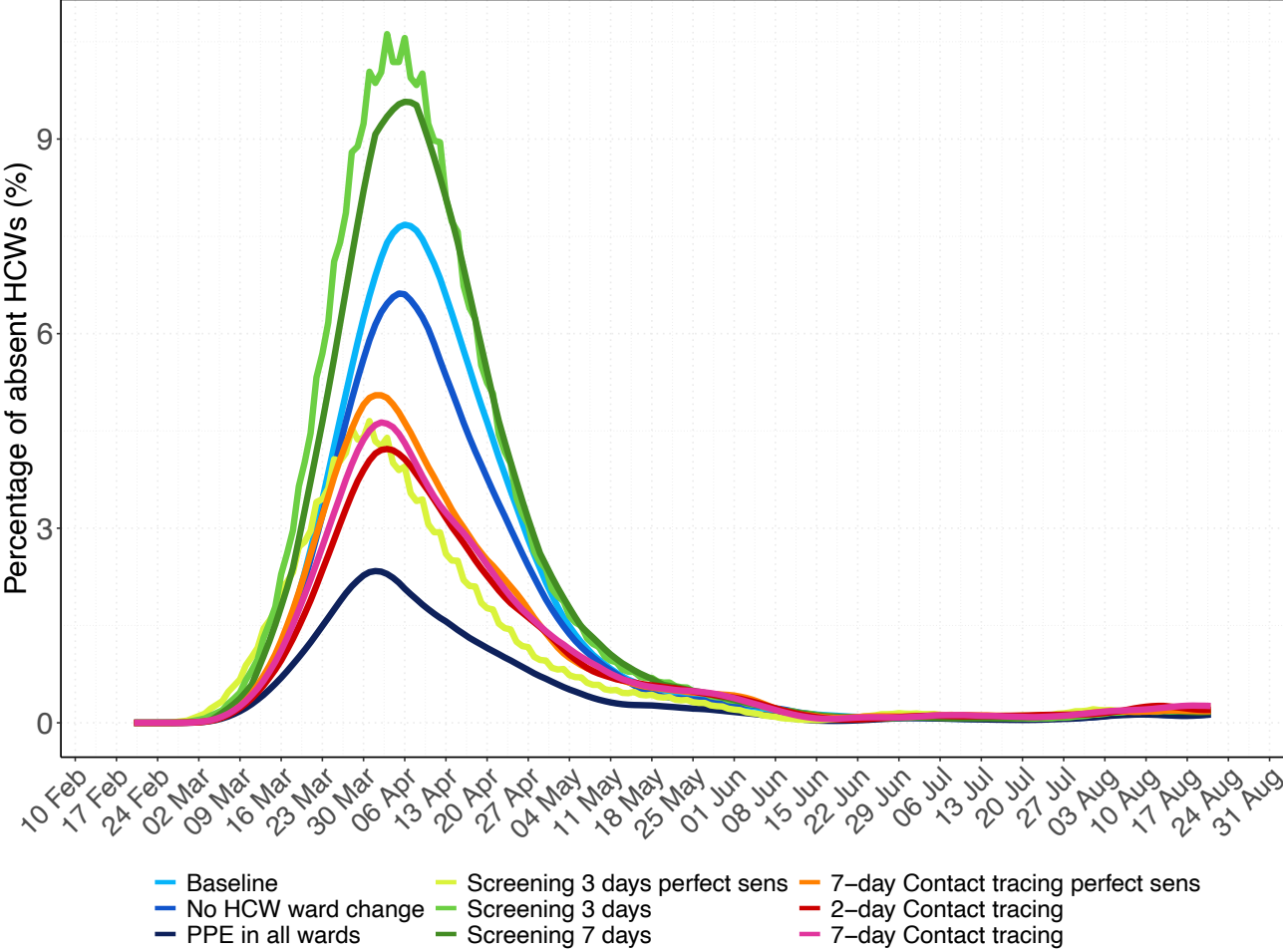


396 **Figure S15. Number of nosocomial transmissions of the SARS-CoV-2 variant for each simulation scenario assuming**
 397 **equal reproduction numbers for symptomatically and asymptotically infected individuals $R_S=1.95$ and $R_A=1.95$.**
 398 The full rectangular bar height represents the mean total number of nosocomial transmissions during the whole study period
 399 (over 100 simulation runs). The grey error bars represent the corresponding 95% uncertainty intervals. Patients that acquire
 400 a SARS-CoV-2 nosocomial infection may be diagnosed in the hospital (due to symptom onset during hospital stay or due
 401 to detection by an intervention) or discharged to the community in a pre-symptomatic or asymptomatic state. The
 402 rectangular bars with the black border represent the mean number of individuals (patients and HCWs) infected with SARS-
 403 CoV-2 and diagnosed in the hospital. The lighter rectangular bars represent the remaining mean number of patients
 404 discharged to community undiagnosed. For screening every 3 days and 7-day contact tracing, we considered two different
 405 test sensitivity scenarios: time-invariant perfect test sensitivity (perfect sens) and time-varying imperfect test sensitivity.
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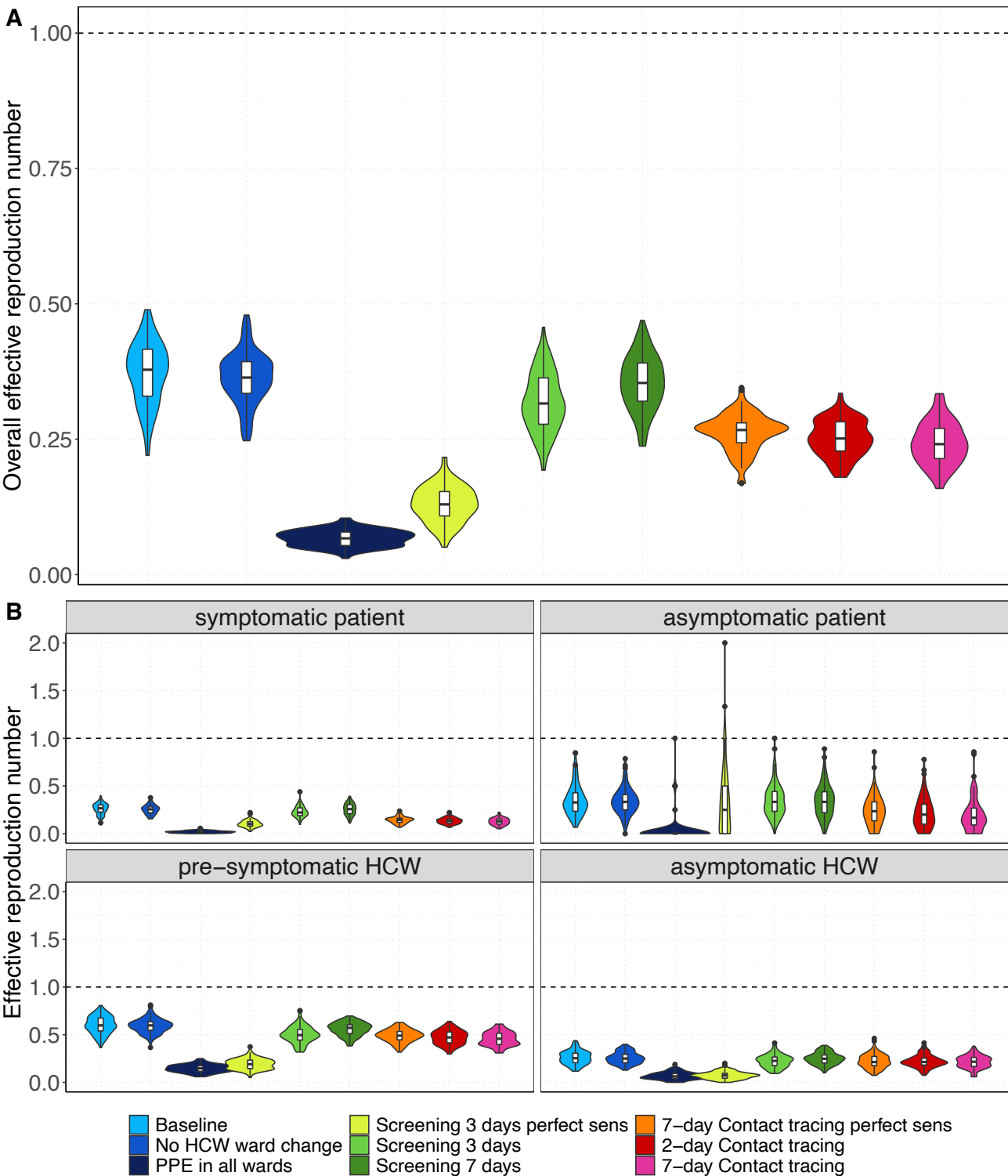
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409 **Figure S16. Daily percentage of absent HCWs during the hospital epidemic for each simulation scenario assuming**
 410 **equal reproduction numbers for symptomatic and asymptomatic individuals $R_S=1.95$ and $R_A=1.95$.** The 7-day
 411 moving average of the mean percentage (over 100 simulation runs) of HCWs absent from work due to symptom onset or
 412 a detected SARS-CoV-2 infection screening or contact tracing is shown. For screening every 3 days and contact tracing 7
 413 days prior to symptom onset of SARS-CoV-2 infected HCWs, we considered two different test sensitivity scenarios: time-
 414 invariant perfect test sensitivity (perfect sens) and imperfect test sensitivity from time since infection.

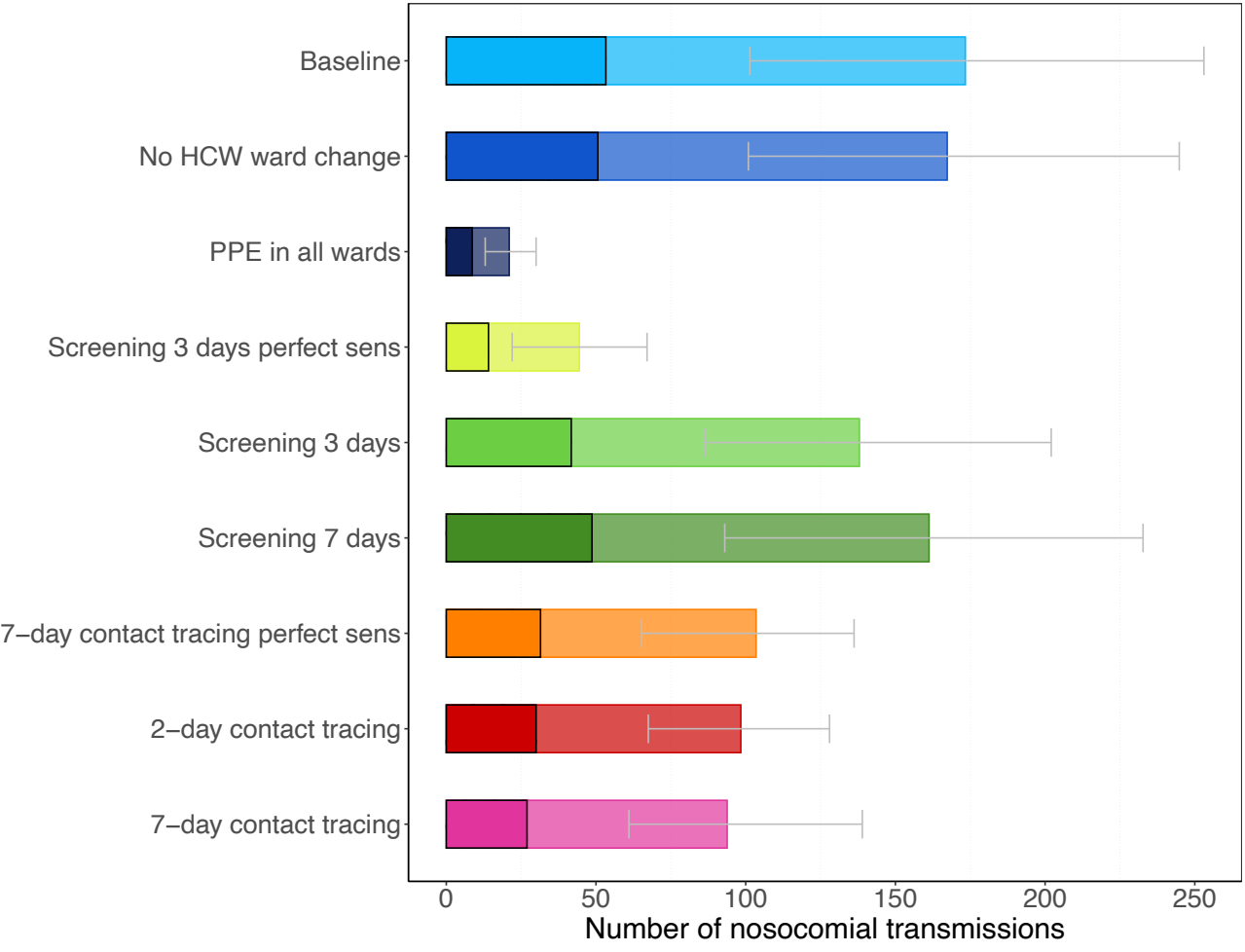


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417 **Figure S17. Effective reproduction numbers for each simulation scenario assuming reproduction numbers of the**
 418 **wild-type SARS-CoV-2 variant.** Results shown are based on $R_S=1.25$ and $R_A=0.5$. (A) For each simulation scenario,
 419 violin and boxplots of the overall reproduction numbers (for pre-/symptomatic and asymptomatic patients and HCWs
 420 combined) are shown (over 100 simulations). (B) For each simulation scenario, violin and boxplots of the reproduction
 421 numbers for pre-/symptomatic and asymptomatic individuals are shown (over 100 simulations). Note that since HCWs are
 422 assumed to immediately self-isolate upon symptom onset, the reproduction number is assigned to the pre-symptomatic
 423 state. The horizontal dashed line represents a reproduction number of 1. For screening every three days and contact tracing
 424 seven days prior to symptom onset of SARS-CoV-2 infected HCWs, we considered two different test sensitivity scenarios:
 425 time-invariant perfect test sensitivity (perfect sens) and imperfect test sensitivity varying from time since infection.

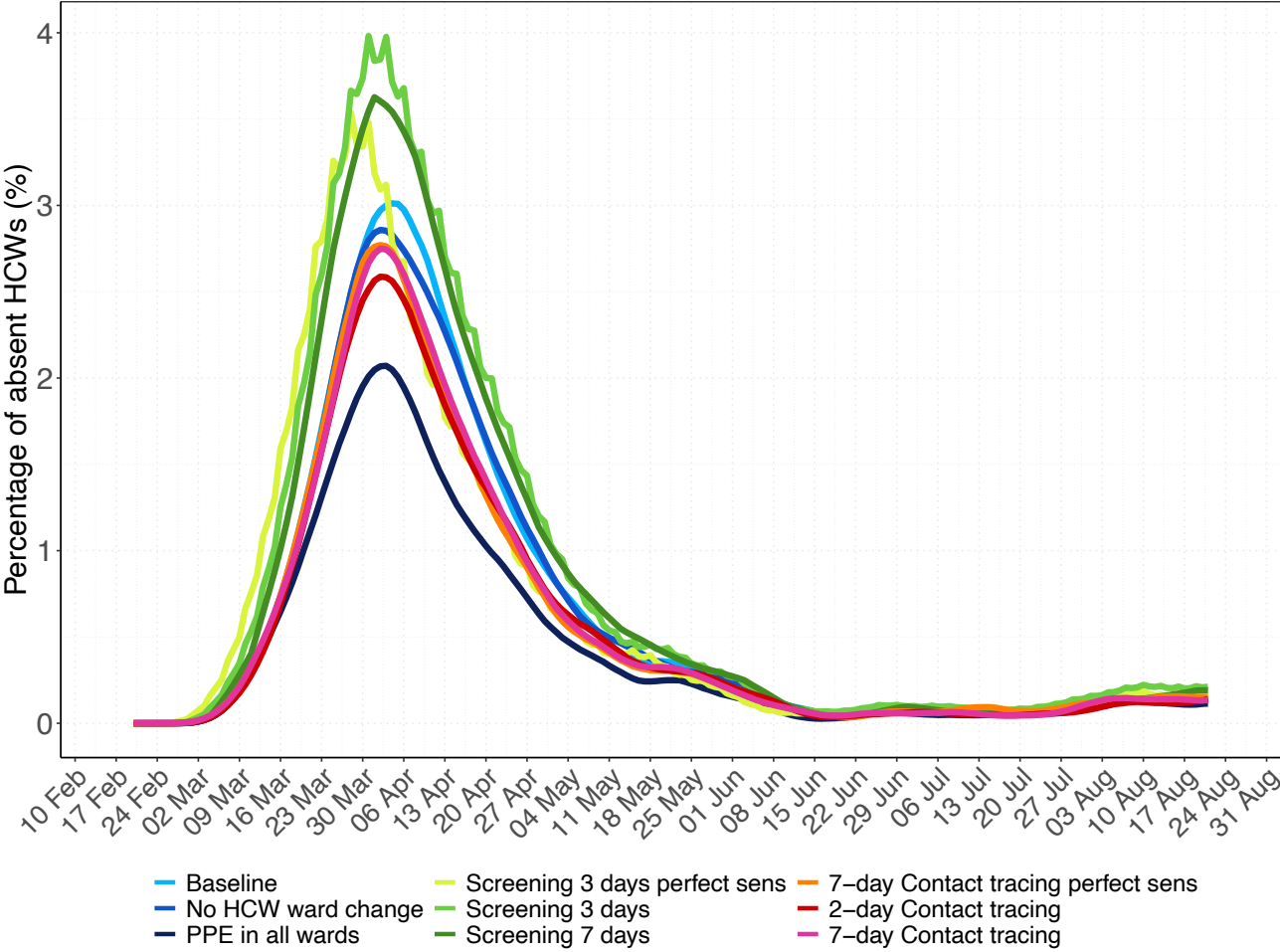


428 **Figure S18. Number of nosocomial transmissions of the SARS-CoV-2 variant for each simulation scenario assuming**
 429 **reproduction numbers of the wild-type SARS-CoV-2 variant.** Results shown are based on $R_S=1.25$ and $R_A=0.5$. The
 430 full rectangular bar height represents the mean total number of nosocomial transmissions during the whole study period
 431 (over 100 simulation runs). The grey error bars represent the corresponding 95% uncertainty intervals. Patients that acquire
 432 a SARS-CoV-2 nosocomial infection may be diagnosed in the hospital (due to symptom onset during hospital stay or due
 433 to detection by an intervention) or discharged to the community in a pre-symptomatic or asymptomatic state. The
 434 rectangular bars with the black border represent the mean number of individuals (patients and HCWs) infected with SARS-
 435 CoV-2 and diagnosed in the hospital. The lighter rectangular bars represent the remaining mean number of patients
 436 discharged to community undiagnosed. For screening every 3 days and 7-day contact tracing, we considered two different
 437 test sensitivity scenarios: time-invariant perfect test sensitivity (perfect sens) and time-varying imperfect test sensitivity.
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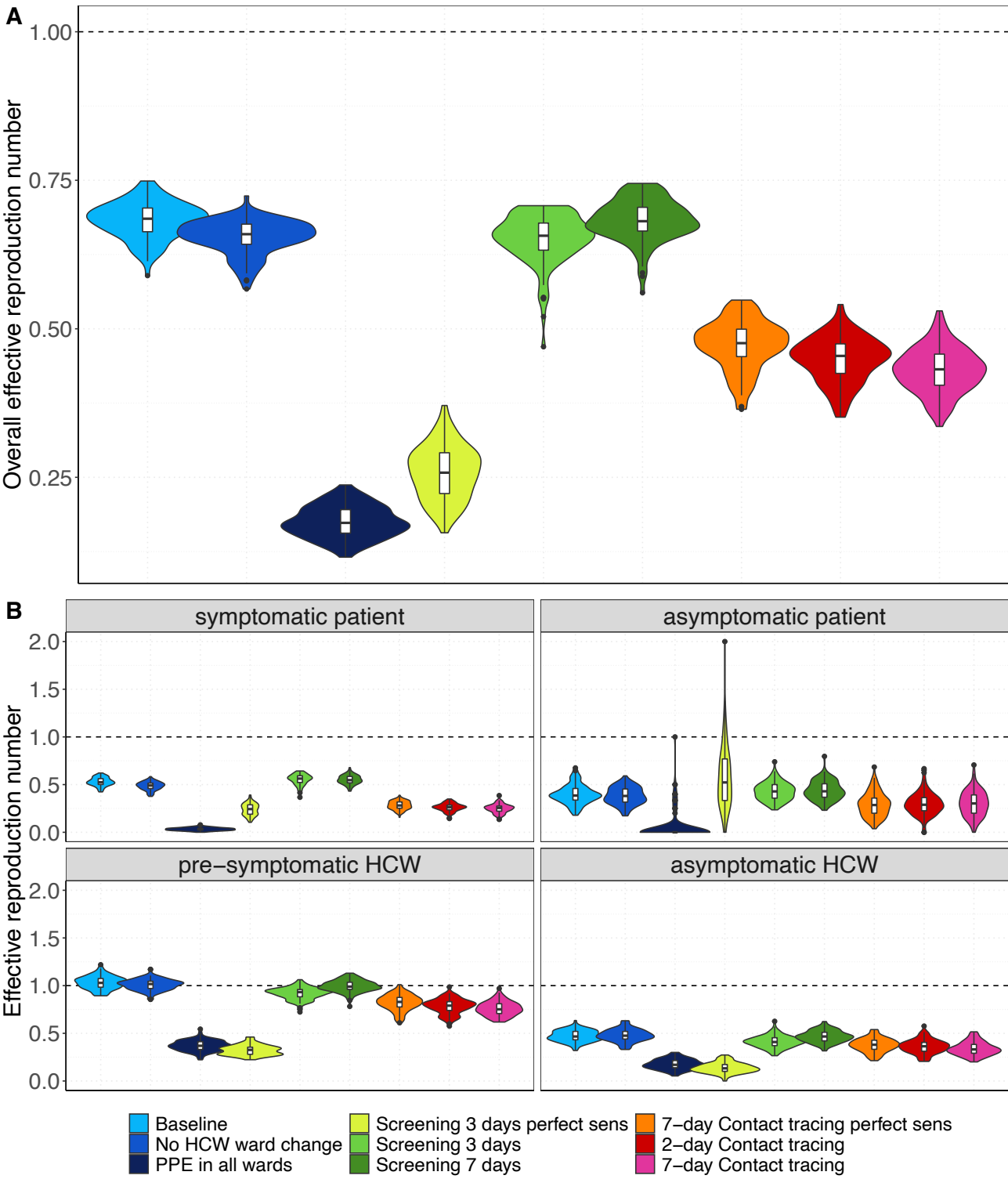
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442 **Figure S19. Daily percentage of absent HCWs during the hospital epidemic for each simulation scenario assuming**
 443 **reproduction numbers of the wild-type SARS-CoV-2 variant.** Results shown are based on $R_S=1.25$ and $R_A=0.5$. The 7-
 444 day moving average of the mean percentage (over 100 simulation runs) of HCWs absent from work due to symptom onset
 445 or a detected SARS-CoV-2 infection screening or contact tracing is shown. For screening every 3 days and contact tracing
 446 7 days prior to symptom onset of SARS-CoV-2 infected HCWs, we considered two different test sensitivity scenarios:
 447 time-invariant perfect test sensitivity (perfect sens) and imperfect test sensitivity from time since infection.



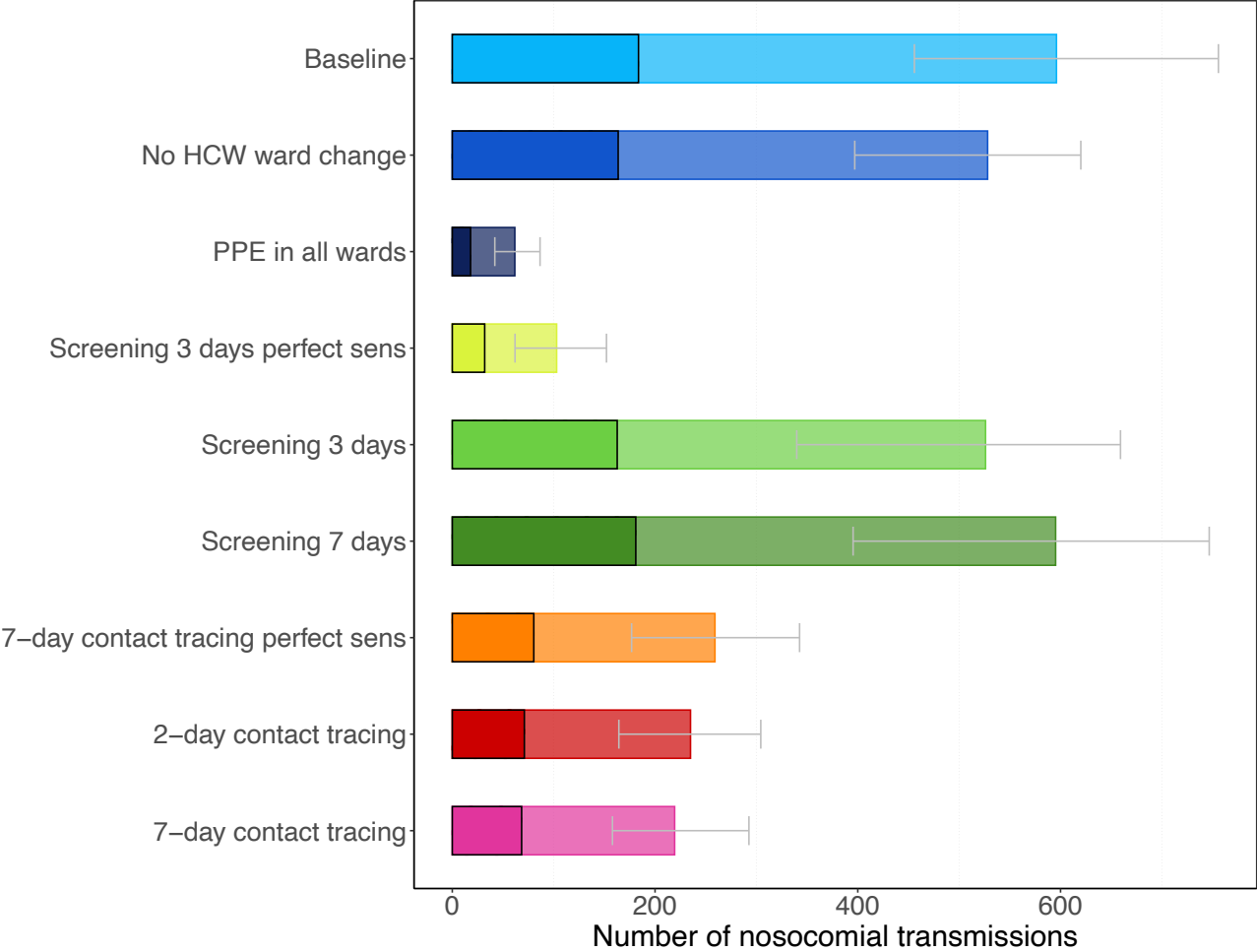
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450 **Figure S20. Effective reproduction numbers for the nosocomial spread of the SARS-CoV-2 variant for each**
 451 **simulation scenario assuming higher contact rates between HCWs.** Results shown are based on $R_S=1.95$ and $R_A=0.8$
 452 (reproduction numbers for the SARS-CoV-2 variant with 56% higher transmissibility with respect to the wild-type SARS-
 453 CoV-2 variant). (A) For each simulation scenario, violin and boxplots of the overall reproduction numbers (for pre-
 454 symptomatic and asymptomatic patients and HCWs combined) are shown (over 100 simulations). (B) For each simulation
 455 scenario, violin and boxplots of the reproduction numbers for pre-/symptomatic and asymptomatic individuals are shown
 456 (over 100 simulations). Note that since HCWs are assumed to immediately self-isolate upon symptom onset, the
 457 reproduction number is assigned to the pre-symptomatic state. The horizontal dashed line represents a reproduction number
 458 of 1. For screening every three days and contact tracing seven days prior to symptom onset of SARS-CoV-2 infected
 459 HCWs, we considered two different test sensitivity scenarios: time-invariant perfect test sensitivity (perfect sens) and
 460 imperfect test sensitivity varying from time since infection.



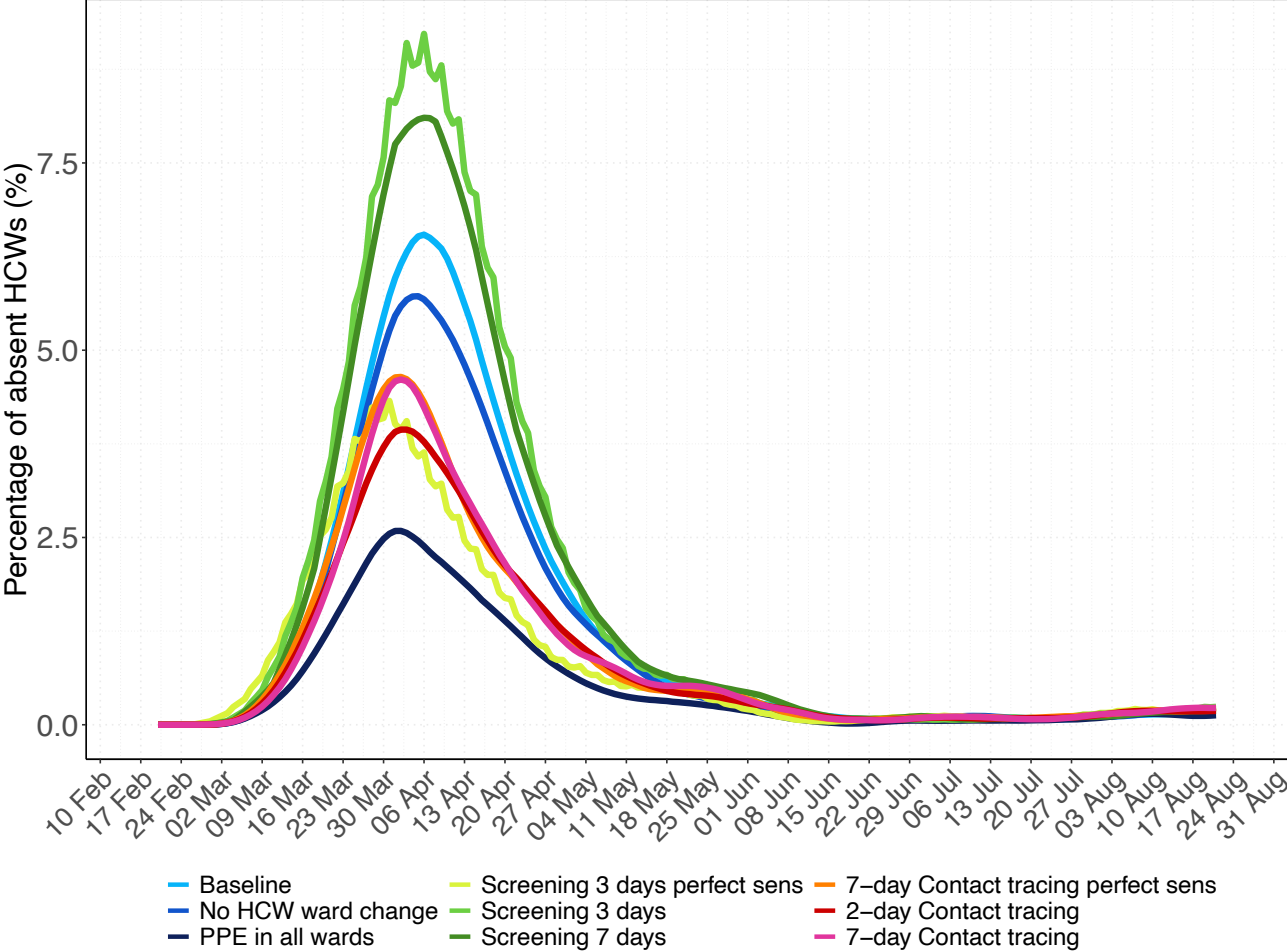
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463 **Figure S21. Number of nosocomial transmissions of the SARS-CoV-2 variant for each simulation scenario assuming**
 464 **higher contact rates between HCWs.** Results shown are based on $R_S=1.95$ and $R_A=0.8$ (reproduction numbers for the
 465 SARS-CoV-2 variant with 56% higher transmissibility with respect to the wild-type SARS-CoV-2 variant). The full
 466 rectangular bar height represents the mean total number of nosocomial transmissions during the whole study period (over
 467 100 simulation runs). The grey error bars represent the corresponding 95% uncertainty intervals. Patients that acquire a
 468 SARS-CoV-2 nosocomial infection may be diagnosed in the hospital (due to symptom onset during hospital stay or due to
 469 detection by an intervention) or discharged to the community in a pre-symptomatic or asymptomatic state. The rectangular
 470 bars with the black border represent the mean number of individuals (patients and HCWs) infected with SARS-CoV-2 and
 471 diagnosed in the hospital. The lighter rectangular bars represent the remaining mean number of patients discharged to
 472 community undiagnosed. For screening every 3 days and 7-day contact tracing, we considered two different test sensitivity
 473 scenarios: time-invariant perfect test sensitivity (perfect sens) and time-varying imperfect test sensitivity.
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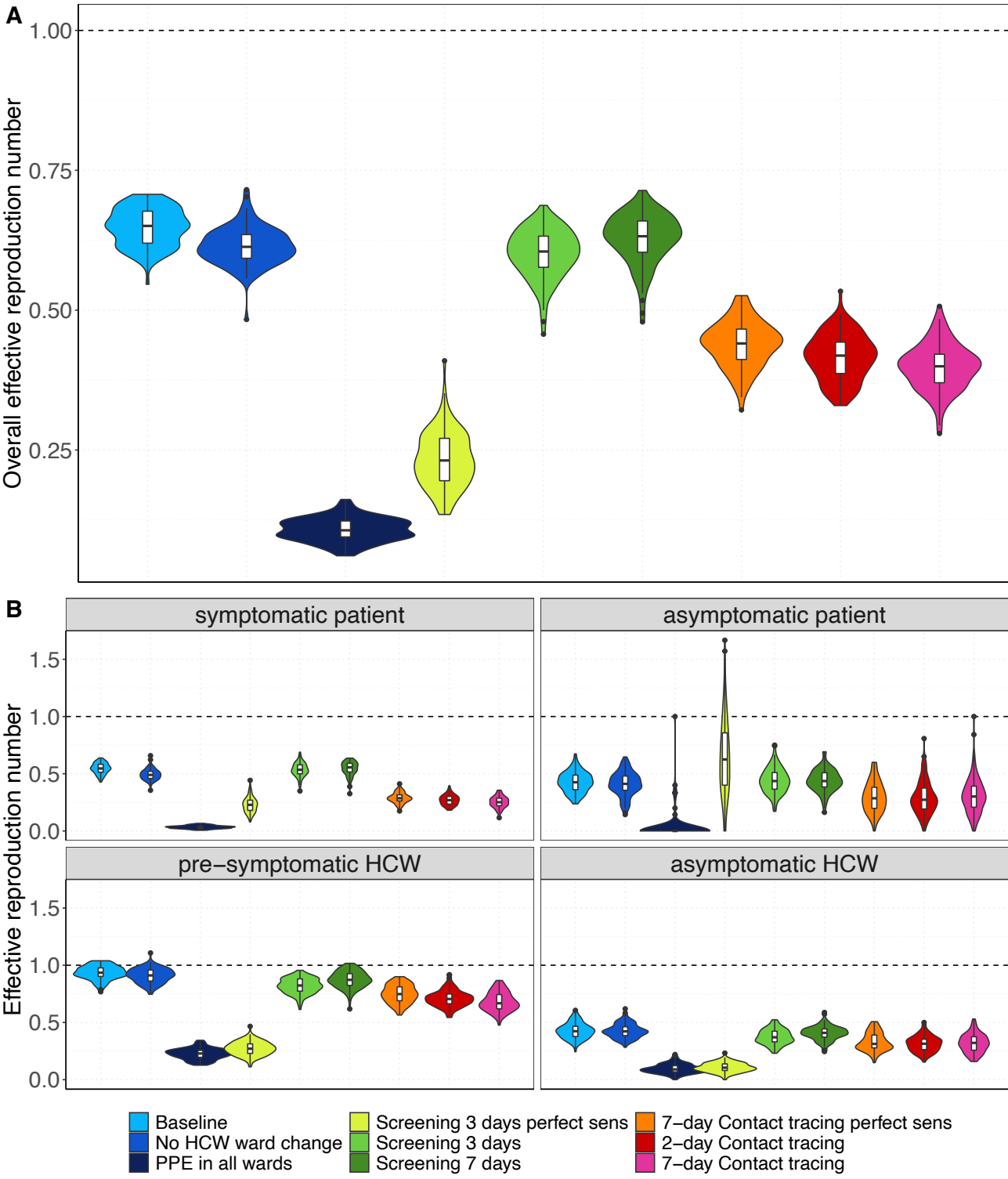
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479 **Figure S22. Daily percentage of absent HCWs during the hospital epidemic for each simulation scenario assuming**
 480 **higher contact rates between HCWs.** Results shown are based on $R_S=1.95$ and $R_A=0.8$ (reproduction numbers for the
 481 SARS-CoV-2 variant with 56% higher transmissibility with respect to the wild-type SARS-CoV-2 variant). The 7-day
 482 moving average of the mean percentage (over 100 simulation runs) of HCWs absent from work due to symptom onset or
 483 a detected SARS-CoV-2 infection screening or contact tracing is shown. For screening every 3 days and contact tracing 7
 484 days prior to symptom onset of SARS-CoV-2 infected HCWs, we considered two different test sensitivity scenarios: time-
 485 invariant perfect test sensitivity (perfect sens) and imperfect test sensitivity from time since infection.



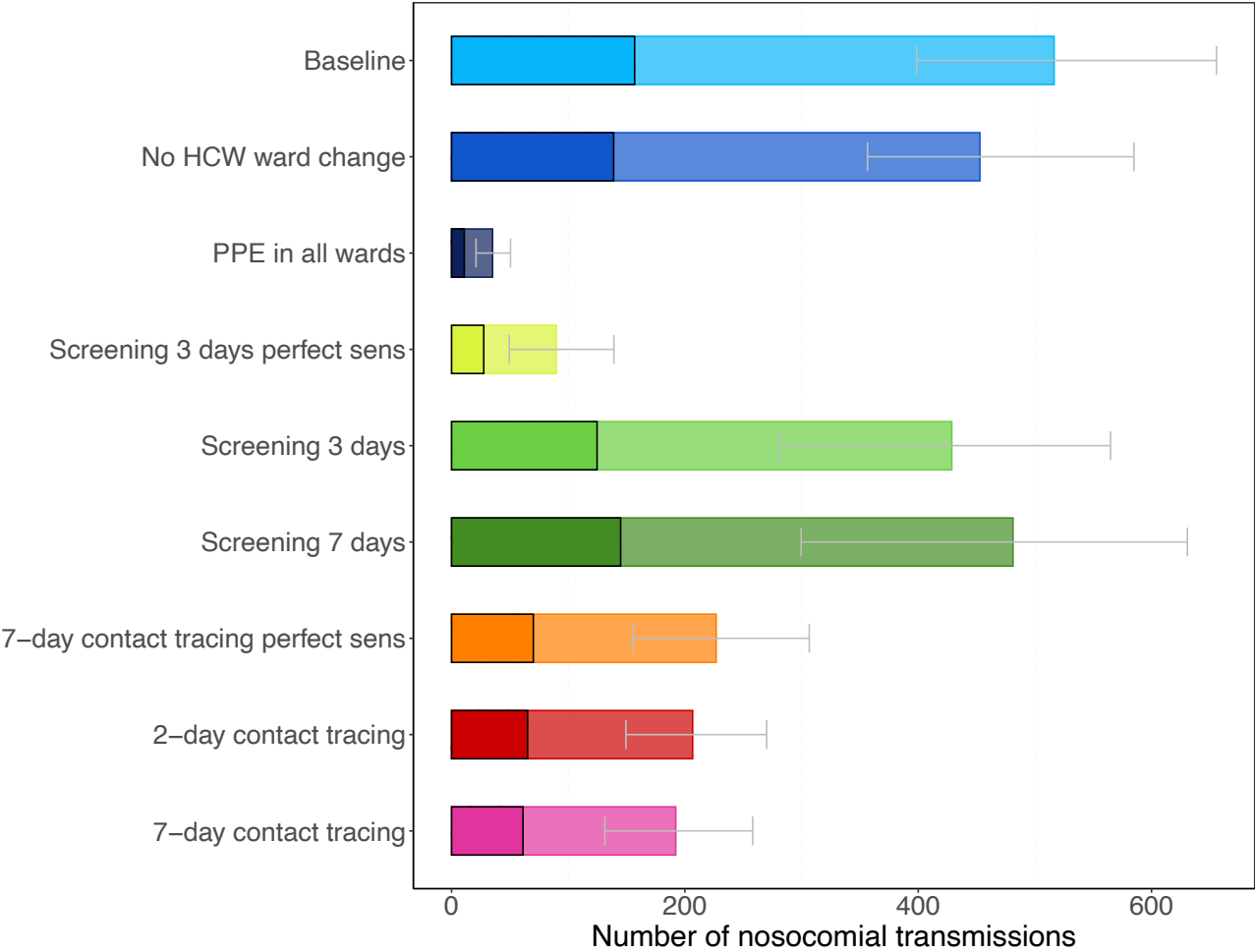
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487 **Figure S23. Effective reproduction numbers for the nosocomial spread of the SARS-CoV-2 variant for the high test**
 488 **sensitivity scenario.** Results shown are based on $R_S=1.95$ and $R_A=0.8$ (reproduction numbers for the SARS-CoV-2 variant
 489 with 56% higher transmissibility with respect to the wild-type SARS-CoV-2 variant). (A) For each simulation scenario,
 490 violin and boxplots of the overall reproduction numbers (for pre-/symptomatic and asymptomatic patients and HCWs
 491 combined) are shown (over 100 simulations). (B) For each simulation scenario, violin and boxplots of the reproduction
 492 numbers for pre-/symptomatic and asymptomatic individuals are shown (over 100 simulations). Note that since HCWs are
 493 assumed to immediately self-isolate upon symptom onset, the reproduction number is assigned to the pre-symptomatic
 494 state. The horizontal dashed line represents a reproduction number of 1. For screening every three days and contact tracing
 495 seven days prior to symptom onset of SARS-CoV-2 infected HCWs, we considered two different test sensitivity scenarios:
 496 time-invariant perfect test sensitivity (perfect sens) and imperfect test sensitivity varying from time since infection.



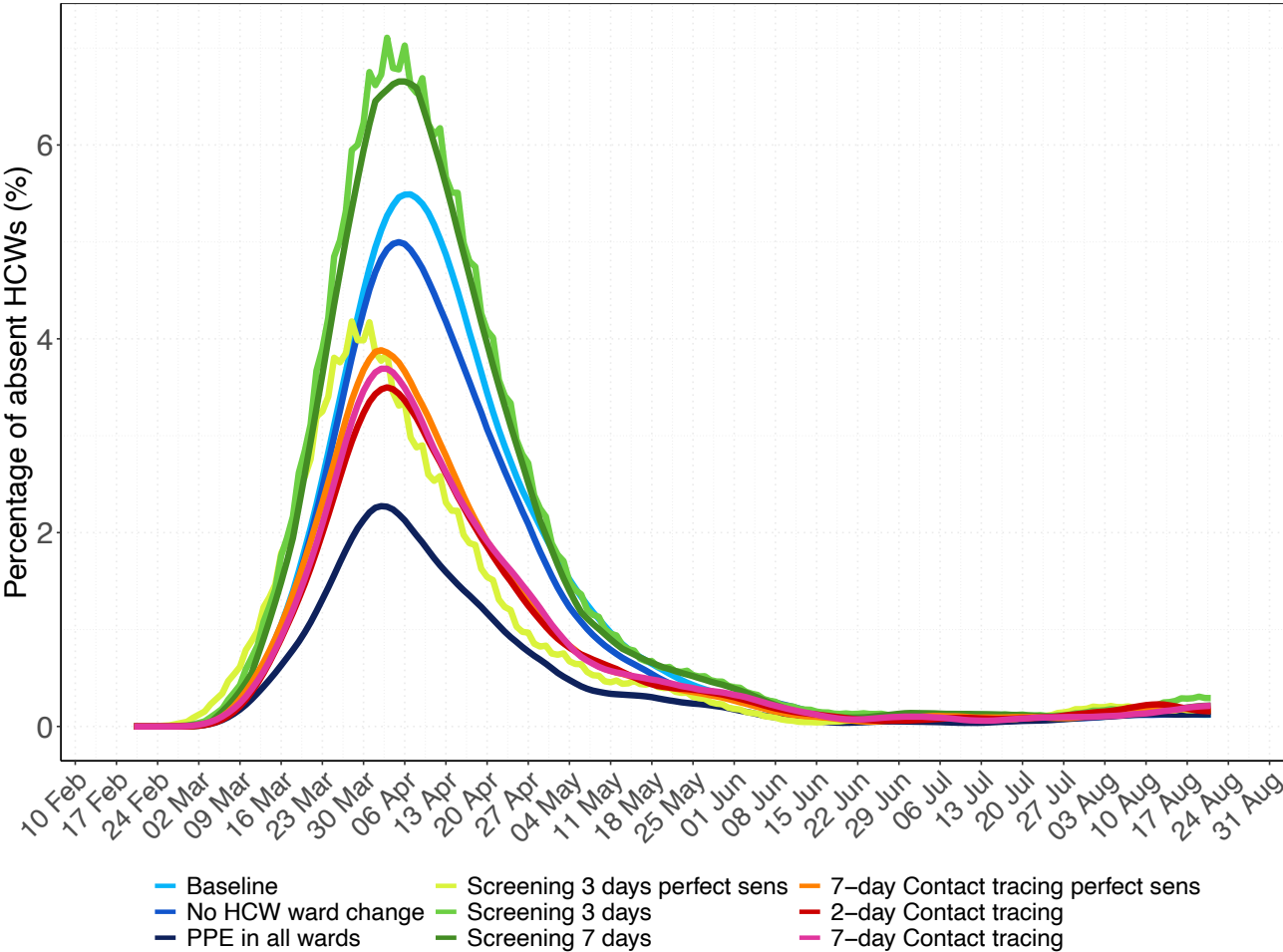
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499 **Figure S24. Number of nosocomial transmissions of the SARS-CoV-2 variant for each simulation scenario for the**
 500 **high test sensitivity scenario.** Results shown are based on $R_S=1.95$ and $R_A=0.8$ (reproduction numbers for the SARS-
 501 CoV-2 variant with 56% higher transmissibility with respect to the wild-type SARS-CoV-2 variant). The full rectangular
 502 bar height represents the mean total number of nosocomial transmissions during the whole study period (over 100
 503 simulation runs). The grey error bars represent the corresponding 95% uncertainty intervals. Patients that acquire a SARS-
 504 CoV-2 nosocomial infection may be diagnosed in the hospital (due to symptom onset during hospital stay or due to
 505 detection by an intervention) or discharged to the community in a pre-symptomatic or asymptomatic state. The rectangular
 506 bars with the black border represent the mean number of individuals (patients and HCWs) infected with SARS-CoV-2 and
 507 diagnosed in the hospital. The lighter rectangular bars represent the remaining mean number of patients discharged to
 508 community undiagnosed. For screening every 3 days and 7-day contact tracing, we considered two different test sensitivity
 509 scenarios: time-invariant perfect test sensitivity (perfect sens) and time-varying imperfect test sensitivity.
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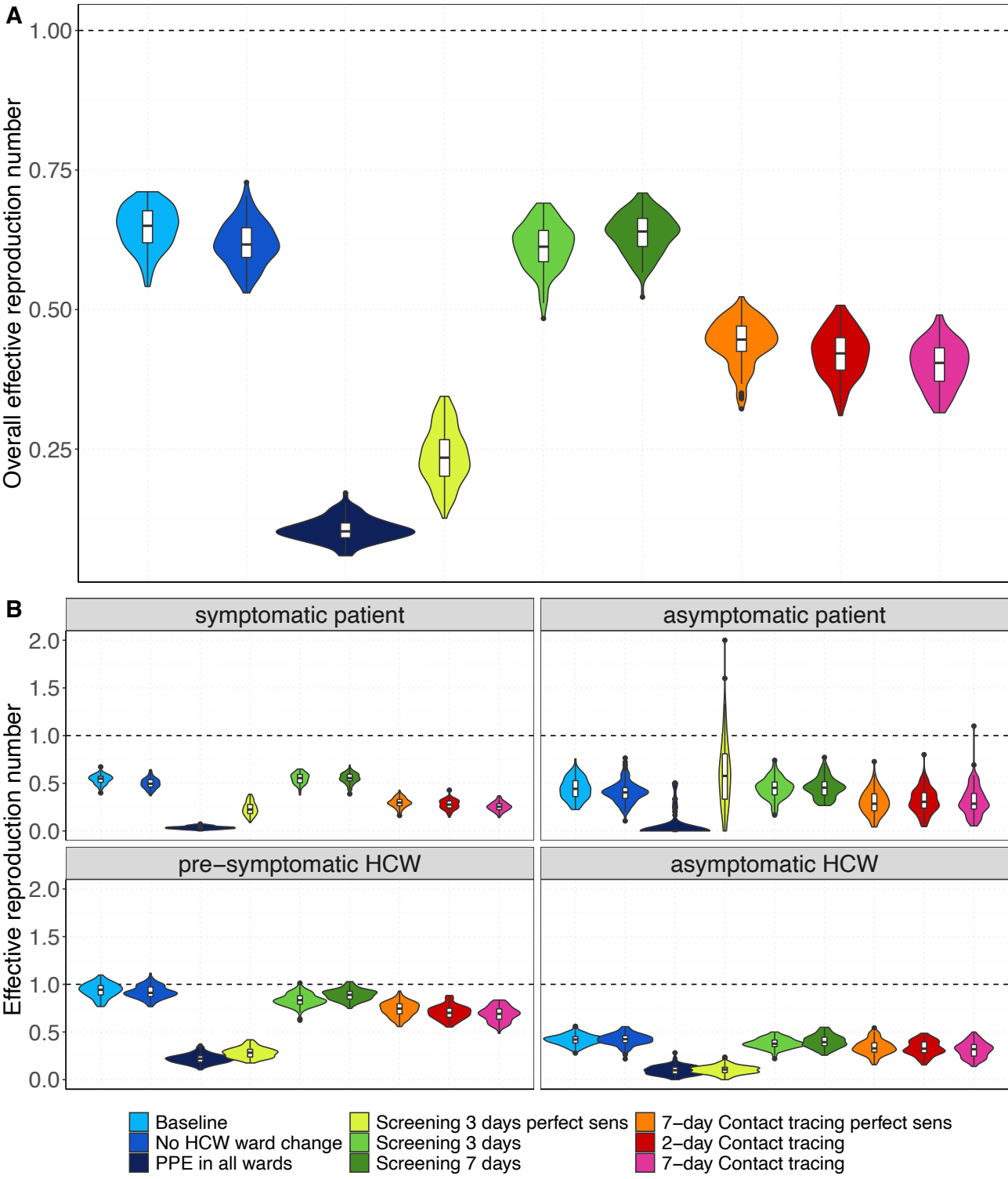
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515 **Figure S25. Daily percentage of absent HCWs during the hospital epidemic for each simulation scenario for the**
 516 **high test sensitivity scenario.** Results shown are based on $R_S=1.95$ and $R_A=0.8$ (reproduction numbers for the SARS-
 517 CoV-2 variant with 56% higher transmissibility with respect to the wild-type SARS-CoV-2 variant). The 7-day moving
 518 average of the mean percentage (over 100 simulation runs) of HCWs absent from work due to symptom onset or a detected
 519 SARS-CoV-2 infection screening or contact tracing is shown. For screening every 3 days and contact tracing 7 days prior
 520 to symptom onset of SARS-CoV-2 infected HCWs, we considered two different test sensitivity scenarios: time-invariant
 521 perfect test sensitivity (perfect sens) and imperfect test sensitivity from time since infection.



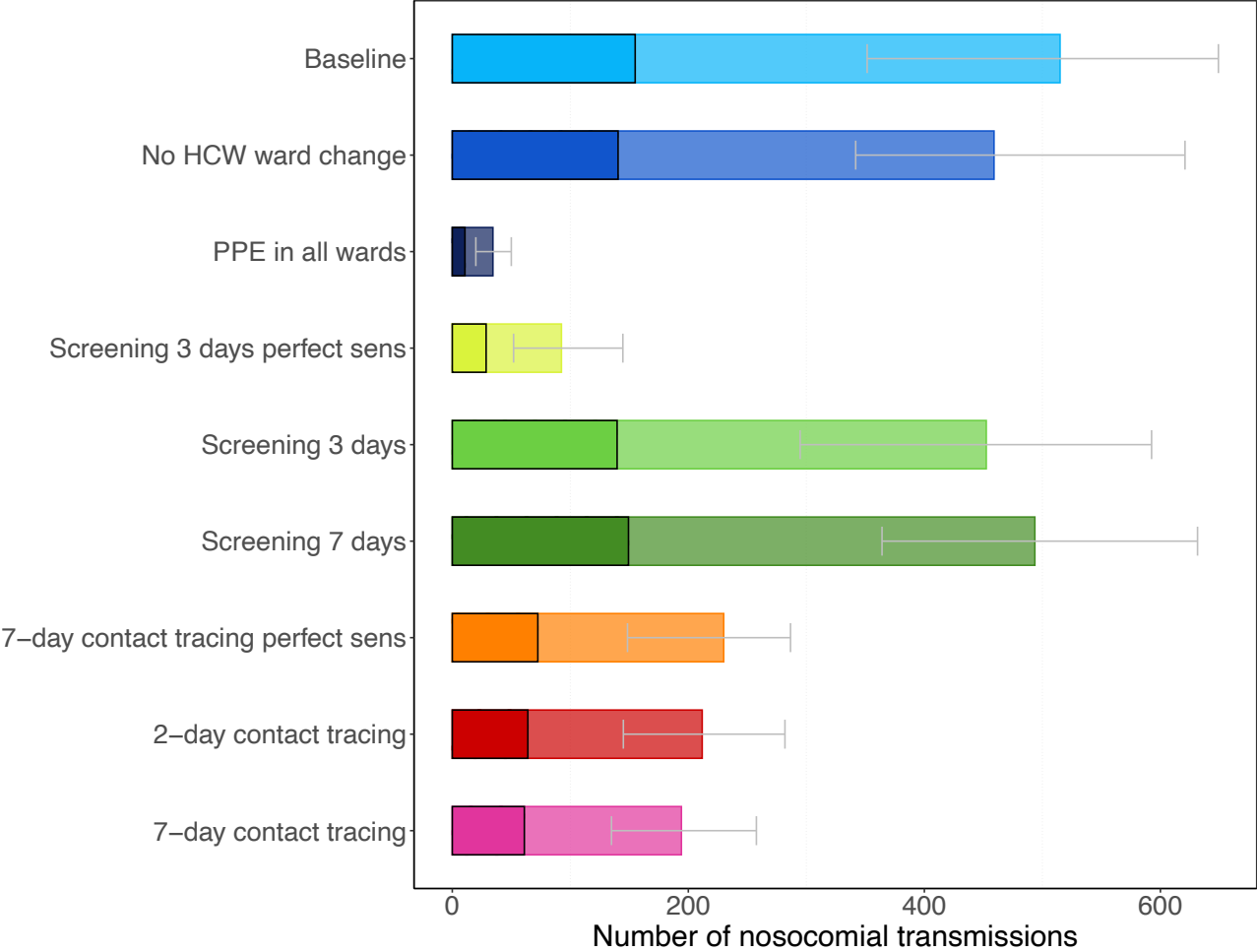
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523 **Figure S26. Effective reproduction numbers for the nosocomial spread of the SARS-CoV-2 variant for the low test**
 524 **sensitivity scenario.** Results shown are based on $R_S=1.95$ and $R_A=0.8$ (reproduction numbers for the SARS-CoV-2 variant
 525 with 56% higher transmissibility with respect to the wild-type SARS-CoV-2 variant). (A) For each simulation scenario,
 526 violin and boxplots of the overall reproduction numbers (for pre-/symptomatic and asymptomatic patients and HCWs
 527 combined) are shown (over 100 simulations). (B) For each simulation scenario, violin and boxplots of the reproduction
 528 numbers for pre-/symptomatic and asymptomatic individuals are shown (over 100 simulations). Note that since HCWs are
 529 assumed to immediately self-isolate upon symptom onset, the reproduction number is assigned to the pre-symptomatic
 530 state. The horizontal dashed line represents a reproduction number of 1. For screening every three days and contact tracing
 531 seven days prior to symptom onset of SARS-CoV-2 infected HCWs, we considered two different test sensitivity scenarios:
 532 time-invariant perfect test sensitivity (perfect sens) and imperfect test sensitivity varying from time since infection.



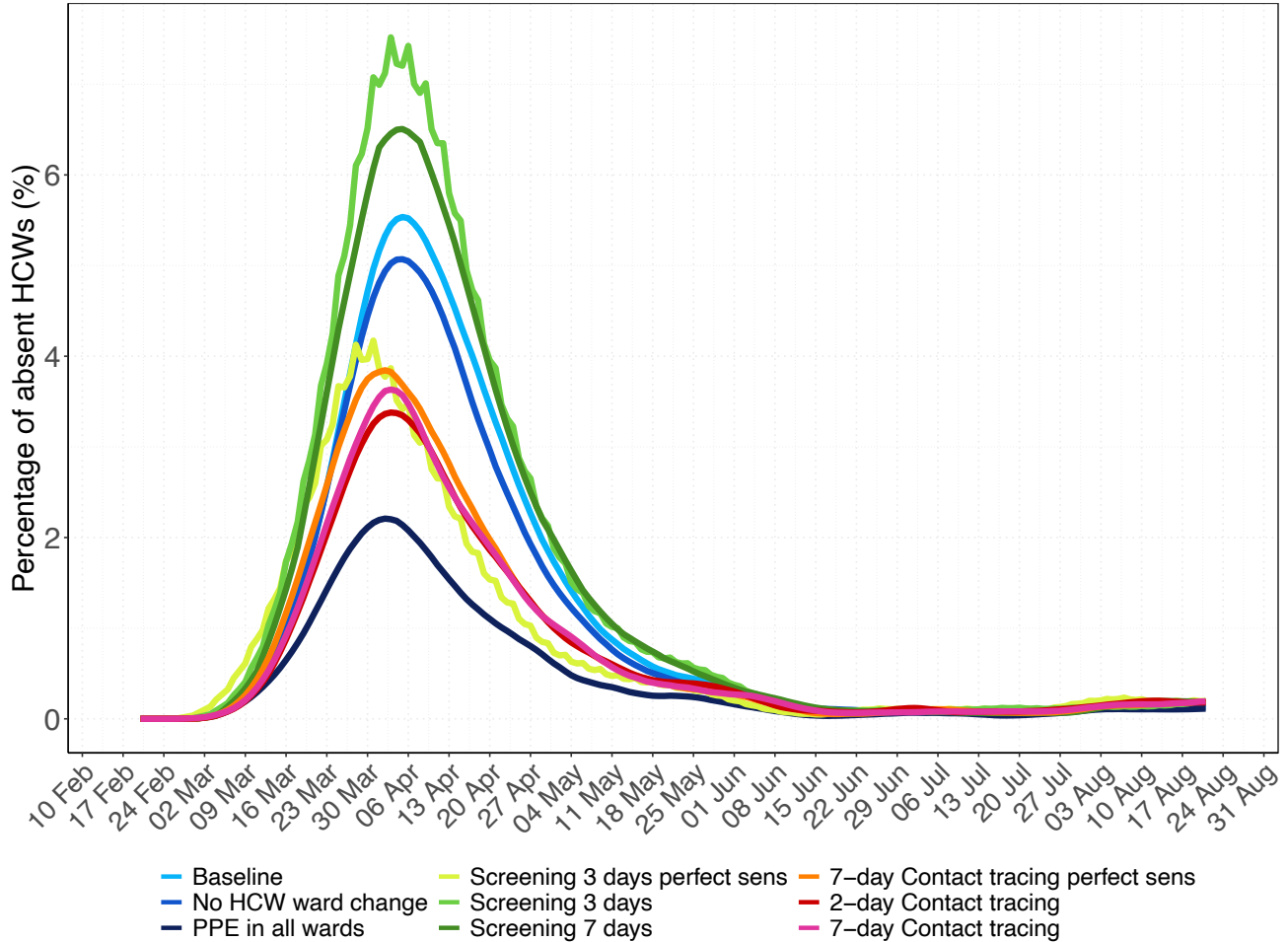
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535 **Figure S27. Number of nosocomial transmissions of the SARS-CoV-2 variant for each simulation scenario for the**
 536 **low test sensitivity scenario.** Results shown are based on $R_S=1.95$ and $R_A=0.8$ (reproduction numbers for the SARS-CoV-
 537 2 variant with 56% higher transmissibility with respect to the wild-type SARS-CoV-2 variant). The full rectangular bar
 538 height represents the mean total number of nosocomial transmissions during the whole study period (over 100 simulation
 539 runs). The grey error bars represent the corresponding 95% uncertainty intervals. Patients that acquire a SARS-CoV-2
 540 nosocomial infection may be diagnosed in the hospital (due to symptom onset during hospital stay or due to detection by
 541 an intervention) or discharged to the community in a pre-symptomatic or asymptomatic state. The rectangular bars with
 542 the black border represent the mean number of individuals (patients and HCWs) infected with SARS-CoV-2 and diagnosed
 543 in the hospital. The lighter rectangular bars represent the remaining mean number of patients discharged to community
 544 undiagnosed. For screening every 3 days and 7-day contact tracing, we considered two different test sensitivity scenarios:
 545 time-invariant perfect test sensitivity (perfect sens) and time-varying imperfect test sensitivity.
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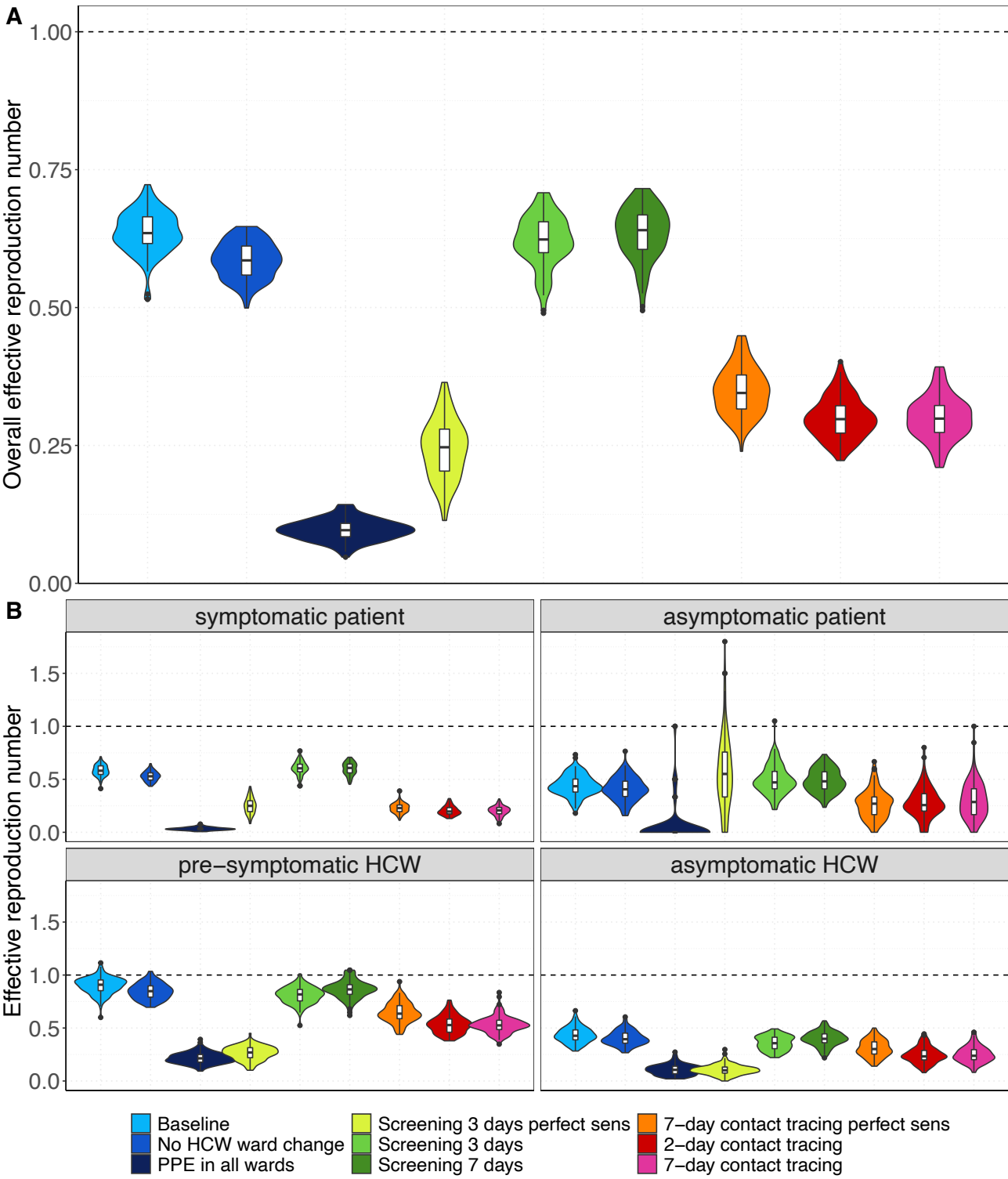


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548 **Figure S28. Daily percentage of absent HCWs during the hospital epidemic for each simulation scenario for the low**
 549 **test sensitivity scenario.** Results shown are based on $R_S=1.95$ and $R_A=0.8$ (reproduction numbers for the SARS-CoV-2
 550 variant with 56% higher transmissibility with respect to the wild-type SARS-CoV-2 variant). The 7-day moving average
 551 of the mean percentage (over 100 simulation runs) of HCWs absent from work due to symptom onset or a detected SARS-
 552 CoV-2 infection screening or contact tracing is shown. For screening every 3 days and contact tracing 7 days prior to
 553 symptom onset of SARS-CoV-2 infected HCWs, we considered two different test sensitivity scenarios: time-invariant
 554 perfect test sensitivity (perfect sens) and imperfect test sensitivity from time since infection.

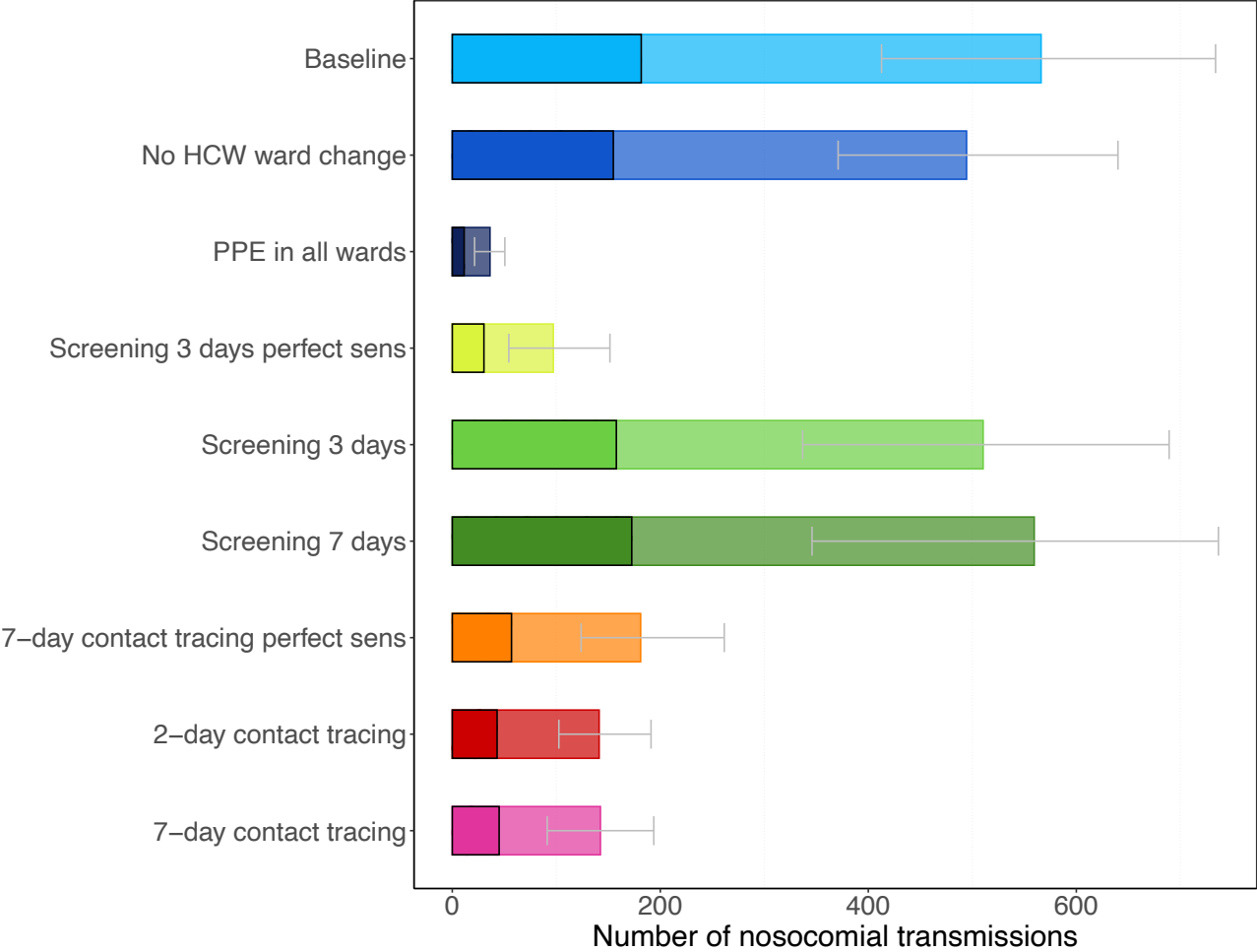


577 **Figure S29. Effective reproduction numbers for the nosocomial spread of the SARS-CoV-2 variant for the recovery**
 578 **time sensitivity scenario.** Results shown are based on $R_S=1.95$ and $R_A=0.8$ (reproduction numbers for the SARS-CoV-2
 579 variant with 56% higher transmissibility with respect to the wild-type SARS-CoV-2 variant). (A) For each simulation
 580 scenario, violin and boxplots of the overall reproduction numbers (for pre-/symptomatic and asymptomatic patients and
 581 HCWs combined) are shown (over 100 simulations). (B) For each simulation scenario, violin and boxplots of the
 582 reproduction numbers for pre-/symptomatic and asymptomatic individuals are shown (over 100 simulations). Note that
 583 since HCWs are assumed to immediately self-isolate upon symptom onset, the reproduction number is assigned to the pre-
 584 symptomatic state. The horizontal dashed line represents a reproduction number of 1. For screening every three days and
 585 contact tracing seven days prior to symptom onset of SARS-CoV-2 infected HCWs, we considered two different test
 586 sensitivity scenarios: time-invariant perfect test sensitivity (perfect sens) and imperfect test sensitivity varying from time
 587 since infection.



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589 **Figure S30. Number of nosocomial transmissions of the SARS-CoV-2 variant for each simulation scenario for the**
 590 **recovery time sensitivity scenario.** Results shown are based on $R_S=1.95$ and $R_A=0.8$ (reproduction numbers for the SARS-
 591 CoV-2 variant with 56% higher transmissibility with respect to the wild-type SARS-CoV-2 variant). The full rectangular
 592 bar height represents the mean total number of nosocomial transmissions during the whole study period (over 100
 593 simulation runs). The grey error bars represent the corresponding 95% uncertainty intervals. Patients that acquire a SARS-
 594 CoV-2 nosocomial infection may be diagnosed in the hospital (due to symptom onset during hospital stay or due to
 595 detection by an intervention) or discharged to the community in a pre-symptomatic or asymptomatic state. The rectangular
 596 bars with the black border represent the mean number of individuals (patients and HCWs) infected with SARS-CoV-2 and
 597 diagnosed in the hospital. The lighter rectangular bars represent the remaining mean number of patients discharged to
 598 community undiagnosed. For screening every 3 days and 7-day contact tracing, we considered two different test sensitivity
 599 scenarios: time-invariant perfect test sensitivity (perfect sens) and time-varying imperfect test sensitivity.
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618 **Figure S31. Daily percentage of absent HCWs during the hospital epidemic for each simulation scenario for the**
 619 **recovery time sensitivity scenario.** Results shown are based on $R_S=1.95$ and $R_A=0.8$ (reproduction numbers for the SARS-
 620 CoV-2 variant with 56% higher transmissibility with respect to the wild-type SARS-CoV-2 variant). The 7-day moving
 621 average of the mean percentage (over 100 simulation runs) of HCWs absent from work due to symptom onset or a detected
 622 SARS-CoV-2 infection screening or contact tracing is shown. For screening every 3 days and contact tracing 7 days prior
 623 to symptom onset of SARS-CoV-2 infected HCWs, we considered two different test sensitivity scenarios: time-invariant
 624 perfect test sensitivity (perfect sens) and imperfect test sensitivity from time since infection.
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