TSAR: Clinical EDA 3

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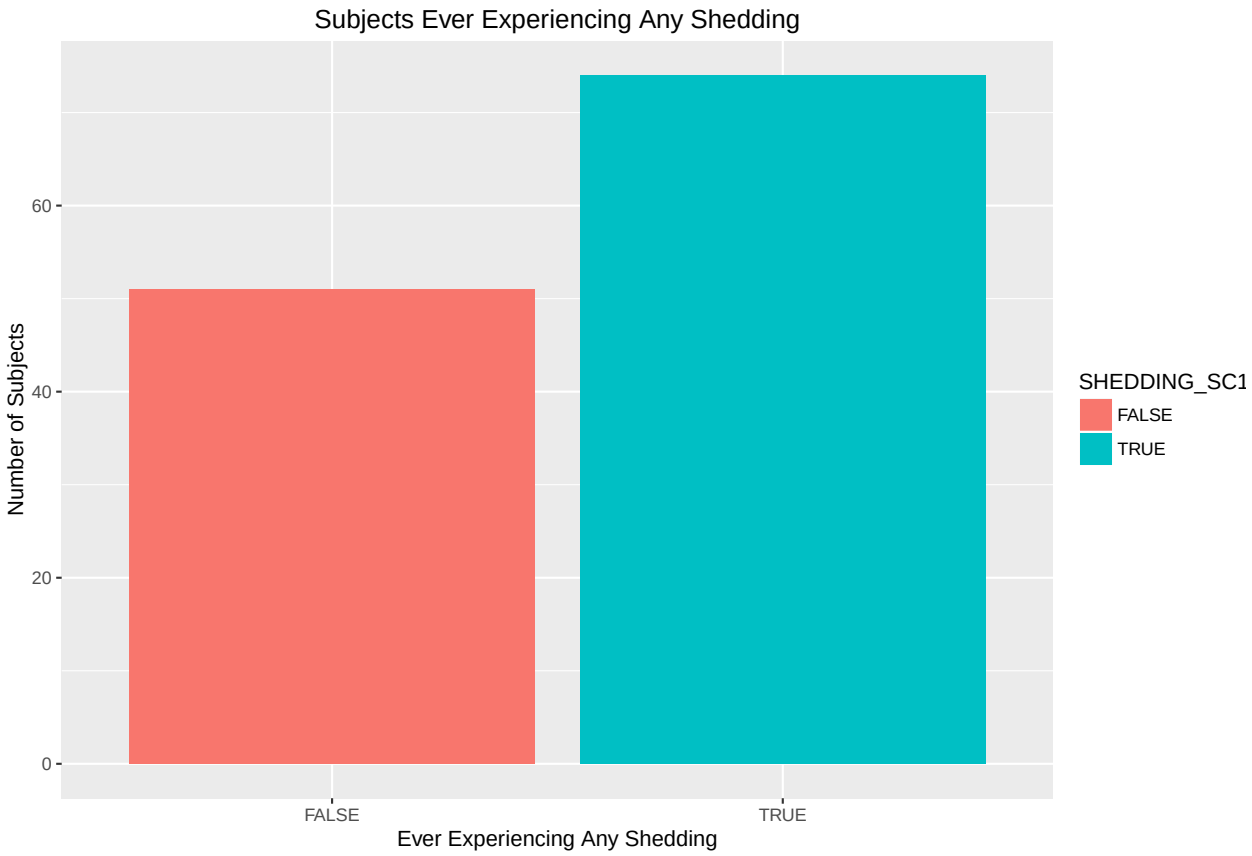
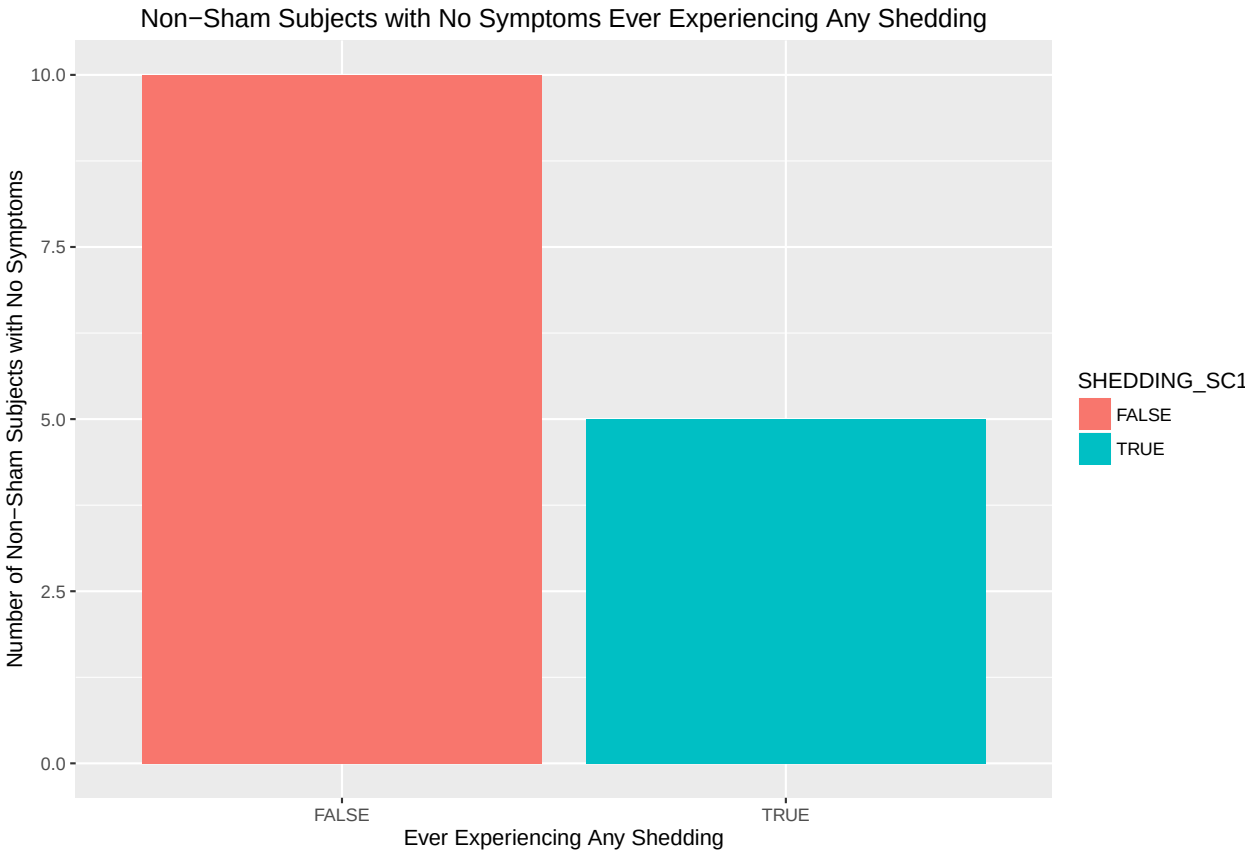
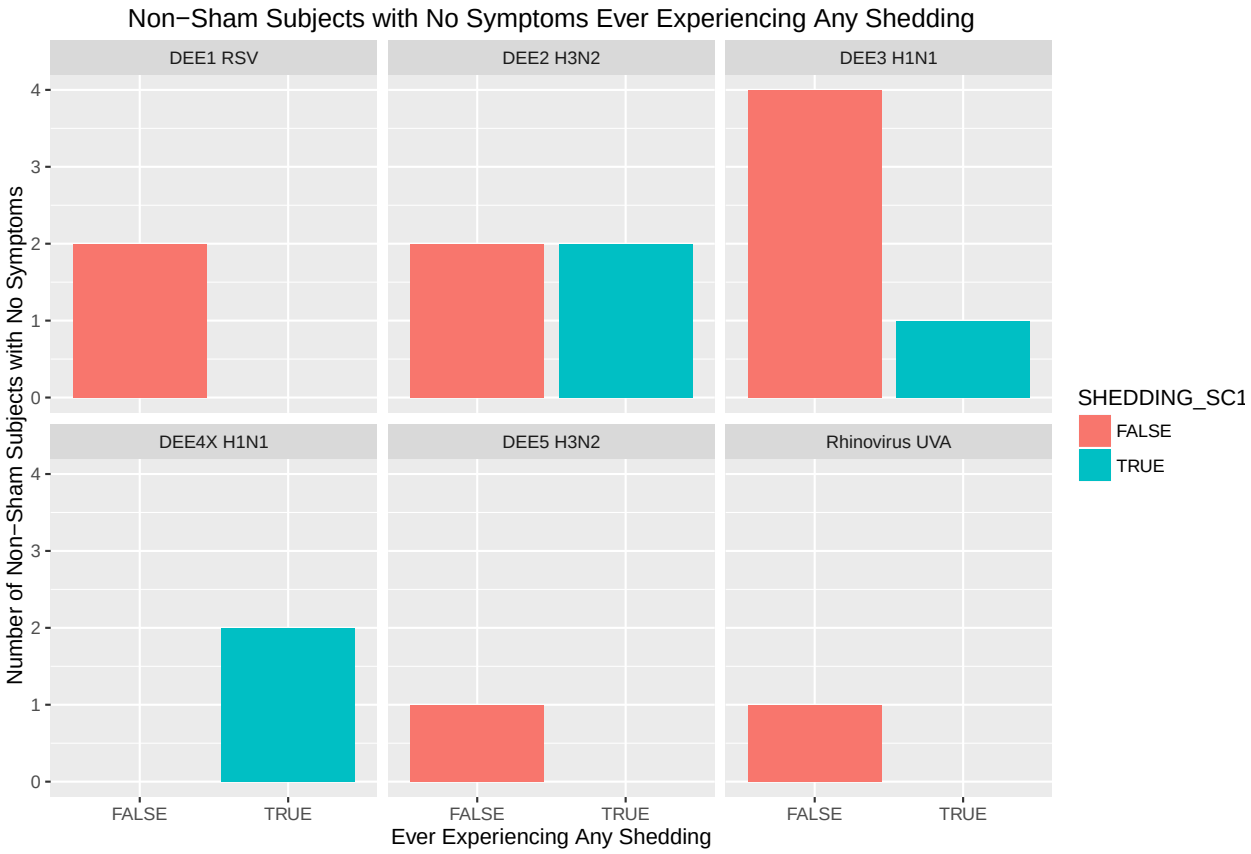
Shedding

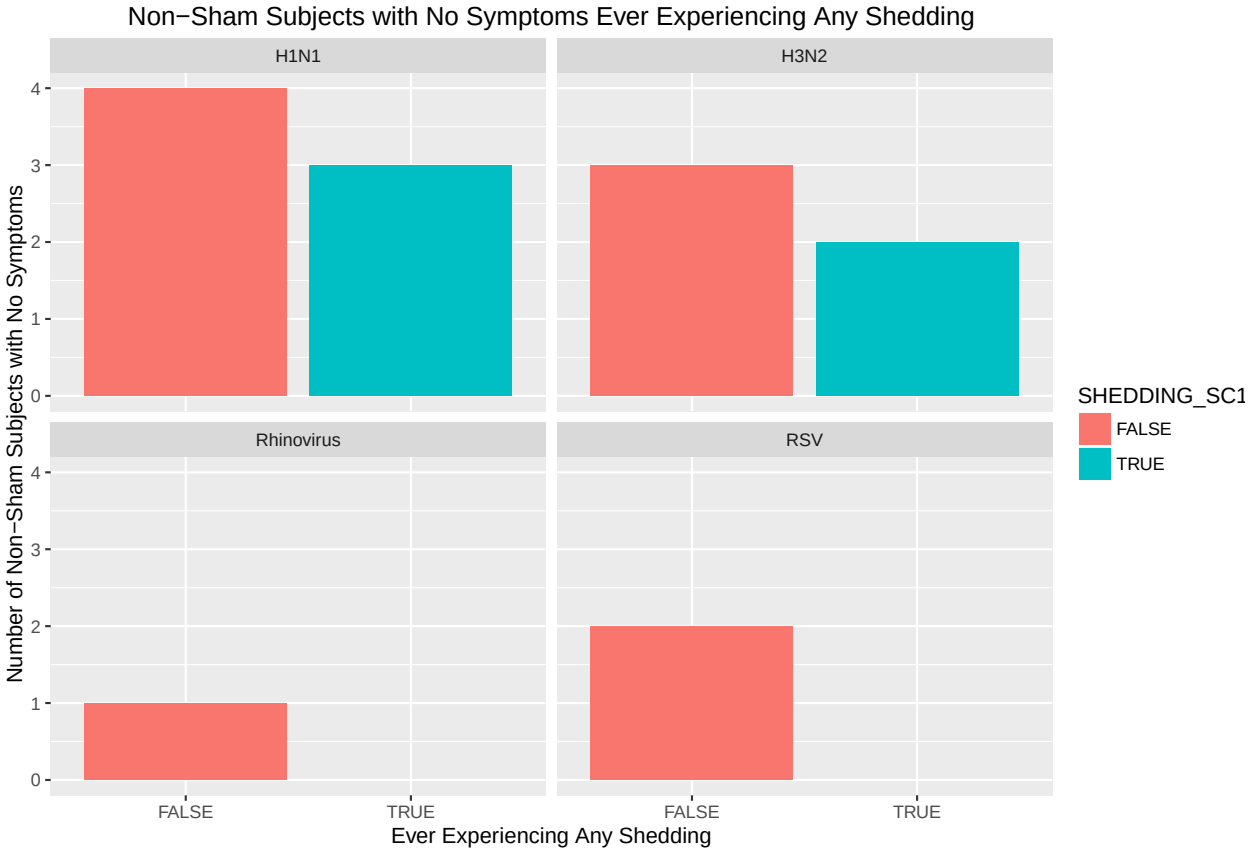



Subjects Ever Experiencing Any Shedding
DEE1 RSV
DEE2 H3N2
DEE3 H1N1
DEE4X H1N1
DEE5 H3N2
Rhinovirus Duke
Rhinovirus UVA
Number of Subjects
0
5
10
FALSE
TRUE
Ever Experiencing Any Shedding
SHEDDING_SC1
FALSE
TRUE
Subjects Ever Experiencing Any Shedding
H1N1
H3N2
Rhinovirus
RSV
Number of Subjects
0
5
10
15
20
FALSE
TRUE
Ever Experiencing Any Shedding
SHEDDING_SC1
FALSE
TRUE

Shedding without Symptoms




Non−Sham Subjects with No Symptoms Ever Experiencing Any Shedding
DEE1 RSV
DEE2 H3N2
DEE3 H1N1
DEE4X H1N1
DEE5 H3N2
Rhinovirus UVA
Number of Non−Sham Subjects with No Symptoms
0
1
2
3
4
FALSE
TRUE
Ever Experiencing Any Shedding
SHEDDING_SC1
FALSE
TRUE


Non−Sham Subjects with No Symptoms Ever Experiencing Any Shedding
H1N1
H3N2
Rhinovirus
RSV
Number of Non−Sham Subjects with No Symptoms
0
1
2
3
4
FALSE
TRUE
Ever Experiencing Any Shedding
SHEDDING_SC1
FALSE
TRUE

```
no_symptoms_and_any_shedding %>%
  dplyr::mutate(SHAM = SHAM > 0) %>%
  dplyr::filter(SHEDDING_SC1 == FALSE, SHAM==FALSE) %>%
  dplyr::select(VIRUS,STUDYID,SUBJECTID,SUM_SCORE,LOGSYMPTSCORE_SC3) %>%
  dplyr::arrange(VIRUS) %>%
  pander(split.cells = 50, split.table = Inf)
```

VIRUS	STUDYID	SUBJECTID	SUM_SCORE	LOGSYMPTSCORE_SC3
H1N1	DEE3 H1N1	3014	0	0
H1N1	DEE3 H1N1	3016	0	0
H1N1	DEE3 H1N1	3022	0	0
H1N1	DEE3 H1N1	3024	0	0
H3N2	DEE5 H3N2	5013	0	0
H3N2	DEE2 H3N2	flu003	0	0
H3N2	DEE2 H3N2	flu017	0	0
Rhinovirus	Rhinovirus UVA	13	0	0
RSV	DEE1 RSV	RSV004	0	0
RSV	DEE1 RSV	RSV019	0	0

```
no_symptoms_and_any_shedding %>%
  dplyr::mutate(SHAM = SHAM > 0) %>%
  dplyr::filter(SHEDDING_SC1 == FALSE, SHAM==FALSE) %>%
  dim()
```

[1] 10 7

LOGSYMPTSCORE_SC3 Remains Constant Per-Subject Across Time

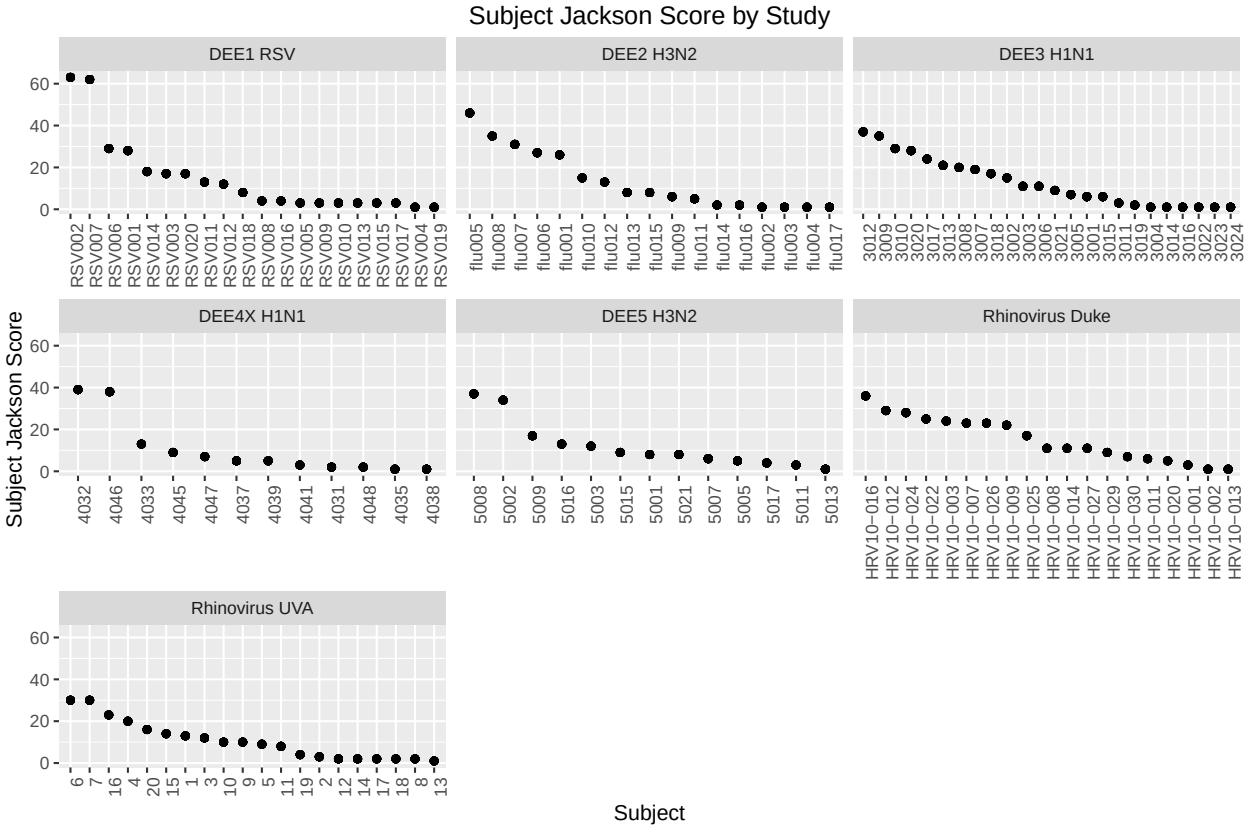
```
#check sd's are 0

train_clinicl_df %>%
  dplyr::group_by(SUBJECTID) %>%
  dplyr::mutate(JACKSON_SCORE = 10^LOGSYMPTSCORE_SC3) %>%
  dplyr::summarise(jackson_mean=mean(JACKSON_SCORE),
                   jackson_sd=sd(JACKSON_SCORE),
                   log_mean=mean(LOGSYMPTSCORE_SC3),
                   log_sd=sd(LOGSYMPTSCORE_SC3)) %>%
  dplyr::arrange(desc(jackson_sd)) %>%
  pander(split.cells = 50, split.table = Inf)
```

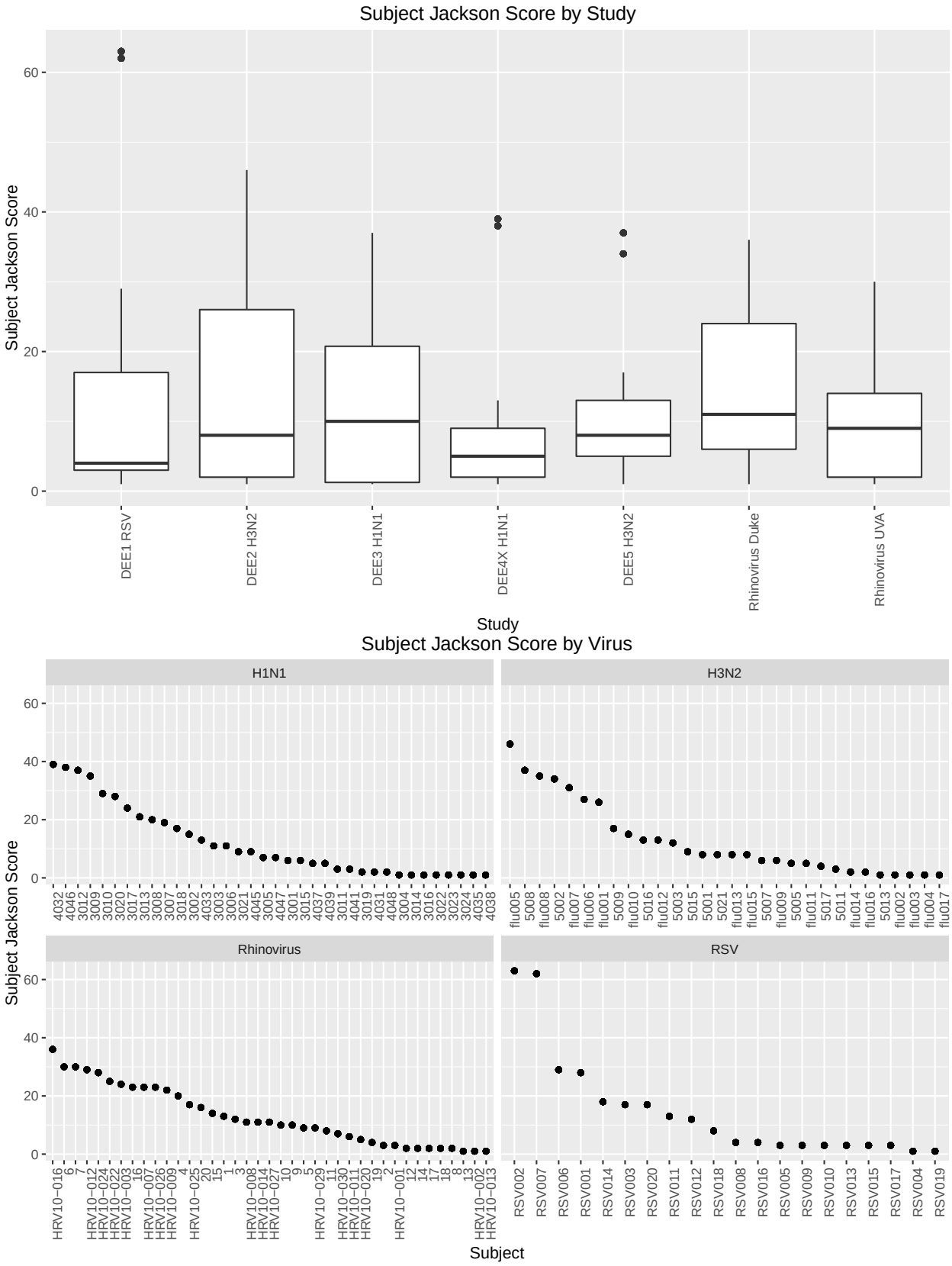
SUBJECTID	jackson_mean	jackson_sd	log_mean	log_sd
1	13	0	1.1139434	0
10	10	0	1.0000000	0
11	8	0	0.9030900	0
12	2	0	0.3010300	0
13	1	0	0.0000000	0
14	2	0	0.3010300	0

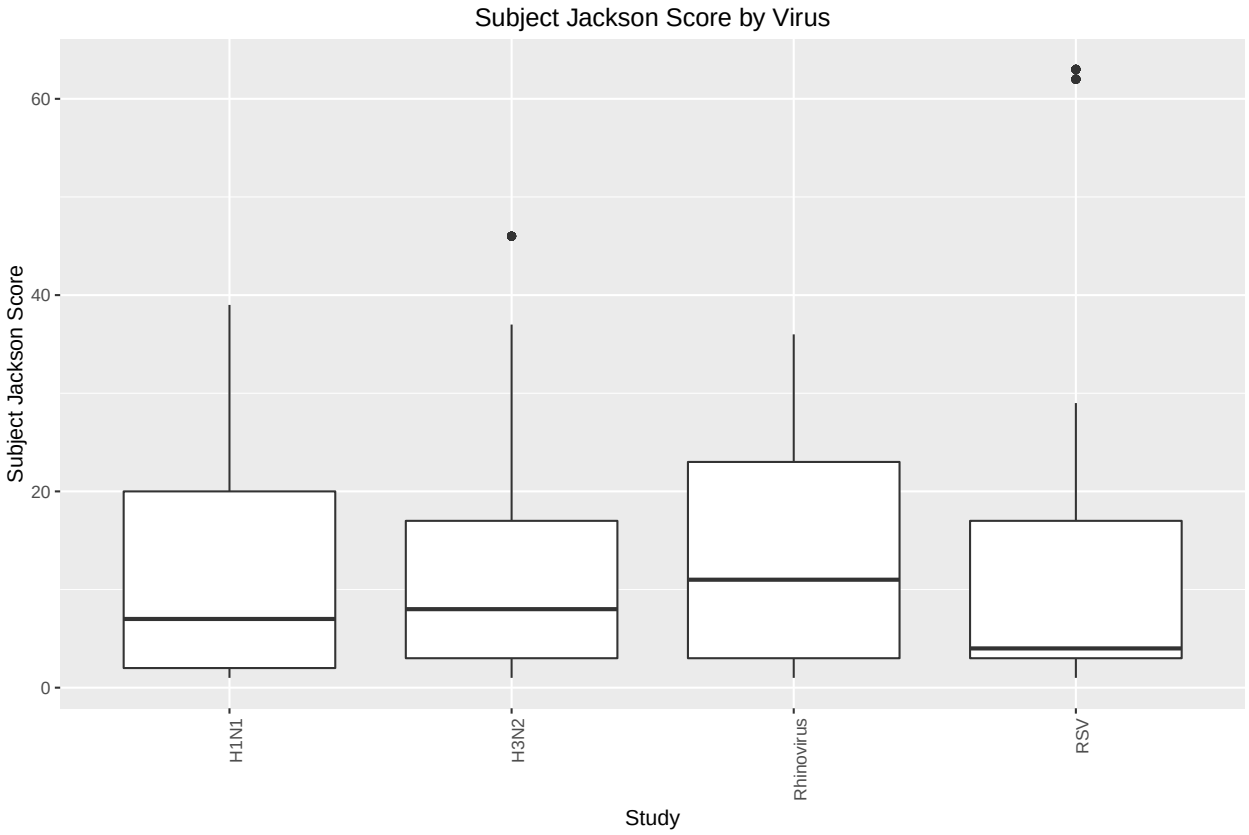
SUBJECTID	jackson_mean	jackson_sd	log_mean	log_sd
15	14	0	1.1461280	0
16	23	0	1.3617278	0
17	2	0	0.3010300	0
18	2	0	0.3010300	0
19	4	0	0.6020600	0
2	3	0	0.4771213	0
20	16	0	1.2041200	0
3	12	0	1.0791812	0
3001	6	0	0.7781513	0
3002	15	0	1.1760913	0
3003	11	0	1.0413927	0
3004	1	0	0.0000000	0
3005	7	0	0.8450980	0
3006	11	0	1.0413927	0
3007	19	0	1.2787536	0
3008	20	0	1.3010300	0
3009	35	0	1.5440680	0
3010	29	0	1.4623980	0
3011	3	0	0.4771213	0
3012	37	0	1.5682017	0
3013	21	0	1.3222193	0
3014	1	0	0.0000000	0
3015	6	0	0.7781513	0
3016	1	0	0.0000000	0
3017	24	0	1.3802112	0
3018	17	0	1.2304489	0
3019	2	0	0.3010300	0
3020	28	0	1.4471580	0
3021	9	0	0.9542425	0
3022	1	0	0.0000000	0
3023	1	0	0.0000000	0
3024	1	0	0.0000000	0
4	20	0	1.3010300	0
4031	2	0	0.3010300	0
4032	39	0	1.5910646	0
4033	13	0	1.1139434	0
4035	1	0	0.0000000	0
4037	5	0	0.6989700	0
4038	1	0	0.0000000	0
4039	5	0	0.6989700	0
4041	3	0	0.4771213	0
4045	9	0	0.9542425	0
4046	38	0	1.5797836	0
4047	7	0	0.8450980	0
4048	2	0	0.3010300	0
5	9	0	0.9542425	0
5001	8	0	0.9030900	0
5002	34	0	1.5314789	0
5003	12	0	1.0791812	0
5005	5	0	0.6989700	0
5007	6	0	0.7781513	0
5008	37	0	1.5682017	0

SUBJECTID	jackson_mean	jackson_sd	log_mean	log_sd
5009	17	0	1.2304489	0
5011	3	0	0.4771213	0
5013	1	0	0.0000000	0
5015	9	0	0.9542425	0
5016	13	0	1.1139434	0
5017	4	0	0.6020600	0
5021	8	0	0.9030900	0
6	30	0	1.4771213	0
7	30	0	1.4771213	0
8	2	0	0.3010300	0
9	10	0	1.0000000	0
flu001	26	0	1.4149733	0
flu002	1	0	0.0000000	0
flu003	1	0	0.0000000	0
flu004	1	0	0.0000000	0
flu005	46	0	1.6627578	0
flu006	27	0	1.4313638	0
flu007	31	0	1.4913617	0
flu008	35	0	1.5440680	0
flu009	6	0	0.7781513	0
flu010	15	0	1.1760913	0
flu011	5	0	0.6989700	0
flu012	13	0	1.1139434	0
flu013	8	0	0.9030900	0
flu014	2	0	0.3010300	0
flu015	8	0	0.9030900	0
flu016	2	0	0.3010300	0
flu017	1	0	0.0000000	0
HRV10-001	3	0	0.4771213	0
HRV10-002	1	0	0.0000000	0
HRV10-003	24	0	1.3802112	0
HRV10-007	23	0	1.3617278	0
HRV10-008	11	0	1.0413927	0
HRV10-009	22	0	1.3424227	0
HRV10-011	6	0	0.7781513	0
HRV10-012	29	0	1.4623980	0
HRV10-013	1	0	0.0000000	0
HRV10-014	11	0	1.0413927	0
HRV10-016	36	0	1.5563025	0
HRV10-020	5	0	0.6989700	0
HRV10-022	25	0	1.3979400	0
HRV10-024	28	0	1.4471580	0
HRV10-025	17	0	1.2304489	0
HRV10-026	23	0	1.3617278	0
HRV10-027	11	0	1.0413927	0
HRV10-029	9	0	0.9542425	0
HRV10-030	7	0	0.8450980	0
RSV001	28	0	1.4471580	0
RSV002	63	0	1.7993405	0
RSV003	17	0	1.2304489	0
RSV004	1	0	0.0000000	0
RSV005	3	0	0.4771213	0

SUBJECTID	jackson_mean	jackson_sd	log_mean	log_sd
RSV006	29	0	1.4623980	0
RSV007	62	0	1.7923917	0
RSV008	4	0	0.6020600	0
RSV009	3	0	0.4771213	0
RSV010	3	0	0.4771213	0
RSV011	13	0	1.1139434	0
RSV012	12	0	1.0791812	0
RSV013	3	0	0.4771213	0
RSV014	18	0	1.2552725	0
RSV015	3	0	0.4771213	0
RSV016	4	0	0.6020600	0
RSV017	3	0	0.4771213	0
RSV018	8	0	0.9030900	0
RSV019	1	0	0.0000000	0
RSV020	17	0	1.2304489	0




Subject Jackson Score by Study
Subject Jackson Score
60
40
20
0
DEE1 RSV
DEE2 H3N2
DEE3 H1N1
DEE4X H1N1
DEE5 H3N2
Rhinovirus Duke
Rhinovirus UVA
Study
Subject Jackson Score by Virus
H1N1
H3N2
Rhinovirus
RSV
Subject Jackson Score
Subject


Subject Jackson Score by Virus
Subject Jackson Score
60
40
20
0
H1N1
H3N2
Rhinovirus
RSV
Study