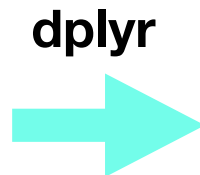


Sample (chr)	Count (int)
WT_1000_00	37
WT_1000_01	38
WT_1000_02	43
GFP_1000_00	33
GFP_1000_01	40
GFP_1000_02	46



Genotype (fctr)	Dilution (int)	Tech_rep (fctr)	Count (int)	True_count (int)
WT	1000	00	37	37000
WT	1000	01	38	38000
WT	1000	02	43	43000
GFP	1000	00	33	33000
GFP	1000	01	40	40000
GFP	1000	02	46	46000

df %>%

i

```
separate(Sample, into = c("Genotype", "Dilution", "Tech_rep",
                           sep = "_", convert = TRUE) %>%
```

ii

```
mutate_at(vars(Genotype, Tech_rep) as.factor) %>%
```

iii

```
mutate(True_count = Count * Dilution)
```