Genotype	Dilution	Tech_rep	Count	True_count
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

nanolyze()
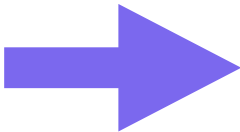
Genotype	Tech_rep_mean	Tech_rep_sd	Tech_rep_se
WT	39667	6506	3756
GFP	39333	3215	1856

```
df %>%
    nanolyze(Genotype,
             name = "Tech_rep",
        param_var = True_count)
```