

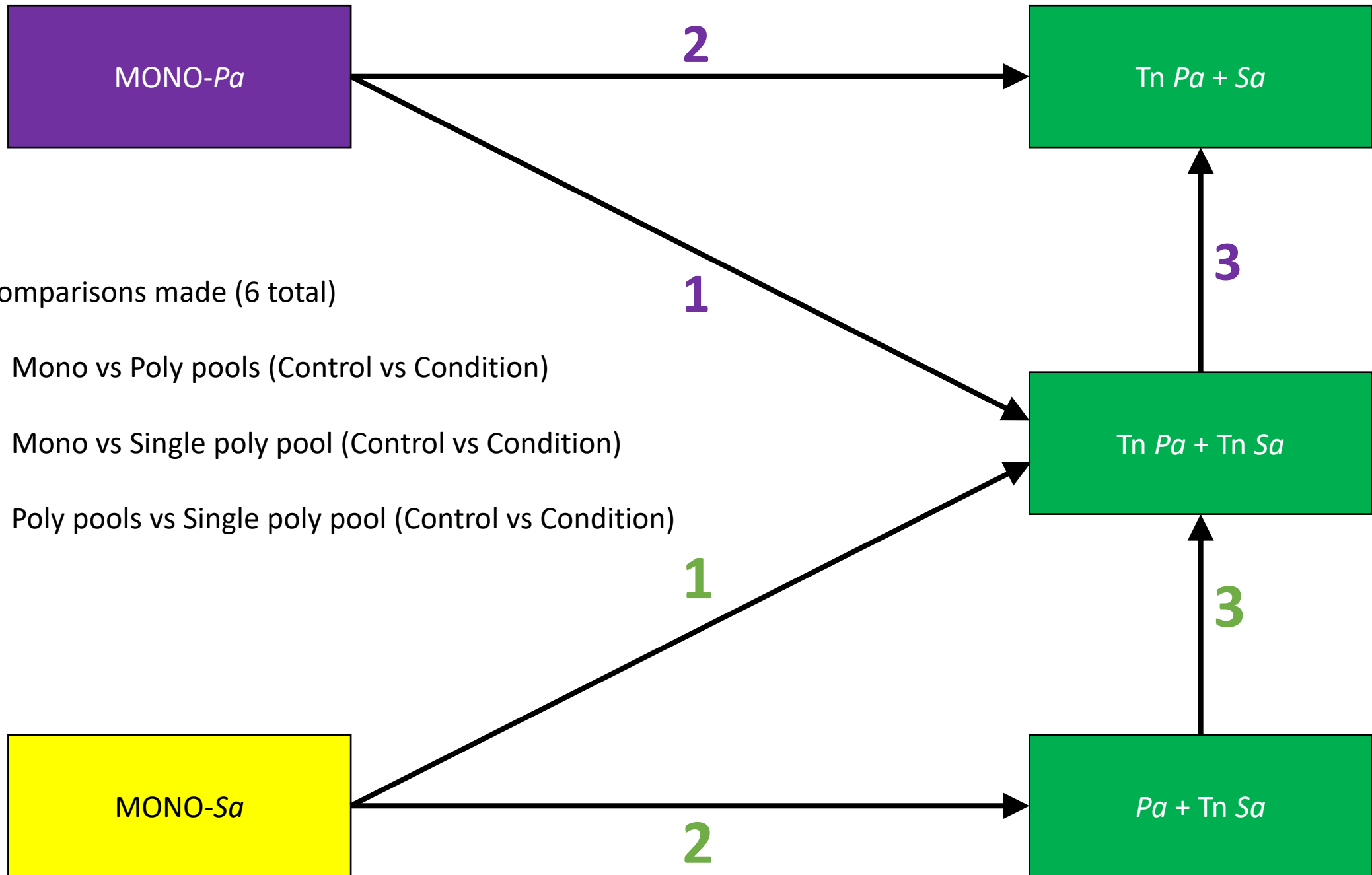
Tnseq stuff

- Reminder
 - 5 conditions (*Sa* USA300LAC, *Pa* LESB58)
 - Mono – Tn *Pa* (Pa)
 - Mono – Tn *Sa* (Sa)
 - Poly – Tn *Pa* + Tn *Sa* (PaSa)
 - Poly – Tn *Pa* + *Sa* (PawtSa)
 - Poly – *Pa* + Tn *Sa* (wtPaSa)
 - 3-day biofilms – HA discs (DMEM-F-G)
 - Pipeline involved tradis (bacteria-tradis), then albatradis for essentiality

Mapping stats

* *Sa* in the *PaSa* is expected to be lower given *Sa* genome is approx. 1/3rd size of *Pa*

ID	Total Reads	USA300 Reads Mapped	USA300 % Mapped	LESB Reads Mapped	LESB % Mapped	USA300 Unique Insertion Sites	USA300 Seq Len/UIS	LESB Unique Insertion Sites	LESB Seq Len/UIS
PA BR1	30826800	104494	0.3	27950715	90.7	8365	343.4	182172	36.2
PA BR3	16086385	74309	0.5	14504825	90.2	4527	634.6	174947	37.7
PA 7	40640027	404005	1.0	37729562	92.8	9608	299.0	151882	43.5
PA 8	21993083	125638	0.6	19069193	86.7	7011	409.8	119208	55.4
SA 6	20791693	18502188	89.0	209719	1.0	356099	8.1	9451	698.5
SA 7	5097355	4645849	91.1	42827	0.8	206504	13.9	8120	813.0
SA BR 2	29462423	27081195	91.9	233411	0.8	396210	7.3	7961	829.3
SA BR 4	9154584	8309199	90.8	55760	0.6	263095	10.9	7009	941.9
PASA 7	32591617	4500228	13.8	25094016	77.0	99730	28.8	94984	69.5
PASA 8	6313128	1245364	19.7	4616011	73.1	38077	75.4	47066	140.3
PASA BR1	25316377	4141925	16.4	19854669	78.4	127522	22.5	66172	99.8
PASA BR 2	16761177	2110288	12.6	12952401	77.3	82043	35.0	48255	136.8
PASAWT BR1	22414879	76336	0.3	20571259	91.8	5210	551.4	62963	104.9
PASAWT BR2	29667095	284332	1.0	27368768	92.3	5679	505.9	58591	112.7
PASAWT BR3	21341773	36981	0.2	20021725	93.8	4745	605.4	16708	395.1
PASAWT BR6	5915264	29887	0.5	5577503	94.3	4798	598.7	52494	125.8
PAWTSa BR1	20809389	19710111	94.7	122908	0.6	253549	11.3	7300	904.4
PAWTSa BR3	26282623	24669837	93.9	363960	1.4	272019	10.6	7036	938.3
PAWTSa BR7	13968414	13118821	93.9	80920	0.6	231877	12.4	4434	1488.9
PAWTSa BR8	9650596	9041893	93.7	52799	0.5	205019	14.0	3886	1698.9



*Comparisons made (6 total)

- 1) Mono vs Poly pools (Control vs Condition)
- 2) Mono vs Single poly pool (Control vs Condition)
- 3) Poly pools vs Single poly pool (Control vs Condition)

Results

- **Gene**
 - location on the genome, duh
- **Essentiality (possible options)**
 - essential
 - non-essential
 - Conditionally essential
 - Essential in control
 - Inconsistent replicates
- **Control**
 - Number of control samples the gene was considered essential in (high = essential, low = not essential)
- **Condition**
 - Number of condition samples the gene was considered essential in (high = essential, low = not essential)
- **Replicates**
 - Number of replicates per group (n=4, means 8 samples)

Gene	Essentiality	Control	Condition	Replicates
ORF159	always non-essential	0	0	4
ORFC109	probably always non-essential	0	1	4
ORFC56	probably always non-essential	0	1	4
ORFC92	probably always non-essential	0	1	4
PALES_00051	conditionally essential	0	4	4
PALES_00061	inconsistent replicates	1	3	4
PALES_00101	always non-essential	0	0	4
PALES_00111	inconsistent replicates	0	2	4
PALES_00121	always non-essential	0	0	4
PALES_00131	always non-essential	0	0	4
PALES_00141	inconsistent replicates	0	3	4
PALES_00161	inconsistent replicates	1	4	4
PALES_00191	conditionally essential	0	4	4
PALES_00201	always essential	4	4	4
PALES_00211	always essential	4	4	4
PALES_00261	probably always non-essential	0	1	4
PALES_00271	inconsistent replicates	0	2	4
PALES_00281	probably always non-essential	0	1	4
PALES_00291	inconsistent replicates	0	2	4
PALES_00311	inconsistent replicates	0	3	4
PALES_00321	probably always essential	3	4	4
PALES_00331	inconsistent replicates	0	2	4

Summary

Control	Condition	# genes predicted essential (control)	# genes predicted essential (condition)	#genes predicted essential (both)
Pa	PaSa	4	428	560
Pa	Pa wtSa	1	155	531
PaSa	Pa wtSa	26	23	1172
Sa	PaSa	13	2	331
Sa	wtPa Sa	44	2	297
PaSa	wtPa Sa	10	3	286