

## Reports for Job pb\_359\_8-20000



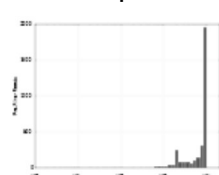
SMRT Cells: 1 Movies: 1

### Overview

#### Job Metric

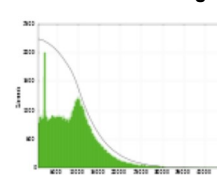
Job Metric	Value
Polished Contigs	1
Adapter Dimers (0-10bp)	0.02%
Short Inserts (11-100bp)	0.0%
Number of Bases	1,266,330,556
Number of Reads	98,352
N50 Read Length	18,030
Mean Read Length	12,875
Mean Read Score	0.86
Mapped Reads	90,004
Mapped Read Length of Insert	7,774
Average Reference Length	5,838,736
Average Reference Bases Called	100.0%
Average Reference Consensus Concordance	100.0%
Average Reference Coverage	169.61

#### Adapters



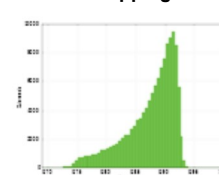
Observed Insert Length Distribution Histogram

#### Subread Filtering



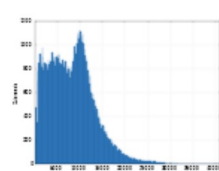
Subread Filtering

#### Mapping



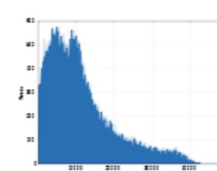
Mapped Subread Concordance

#### Mapping



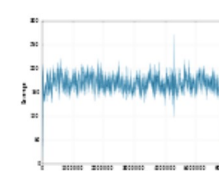
Mapped Subread Length

#### Mapping



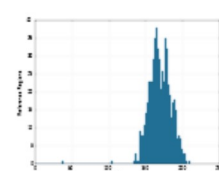
Mapped Polymerase Read Length

#### Coverage



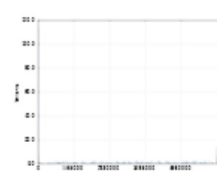
Coverage Across Reference

#### Coverage



Depth of Coverage

#### Corrections



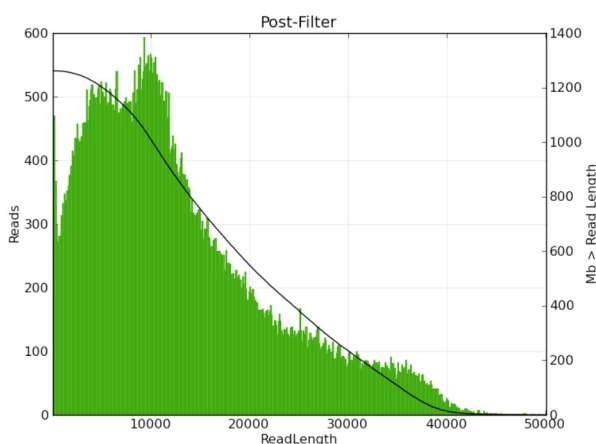
Corrections Across Contigs

### Filtering

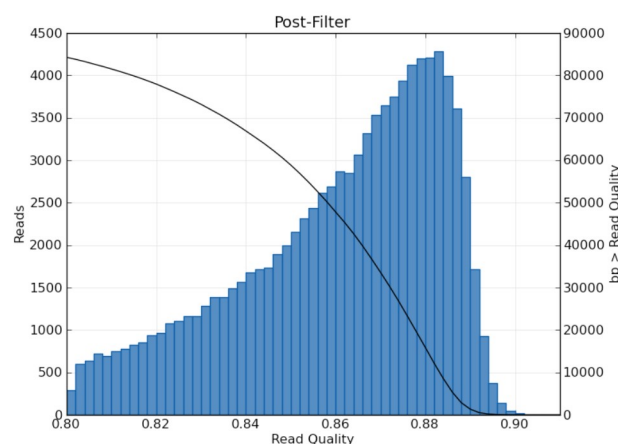
#### Filtering

Metrics	Pre-Filter	Post-Filter
Polymerase Read Bases	1377999157	1266330556
Polymerase Reads	150292	98352
Polymerase Read N50	17487	18030
Polymerase Read Length	9168	12875
Polymerase Read Quality	0.621	0.859

#### Polymerase Read Length

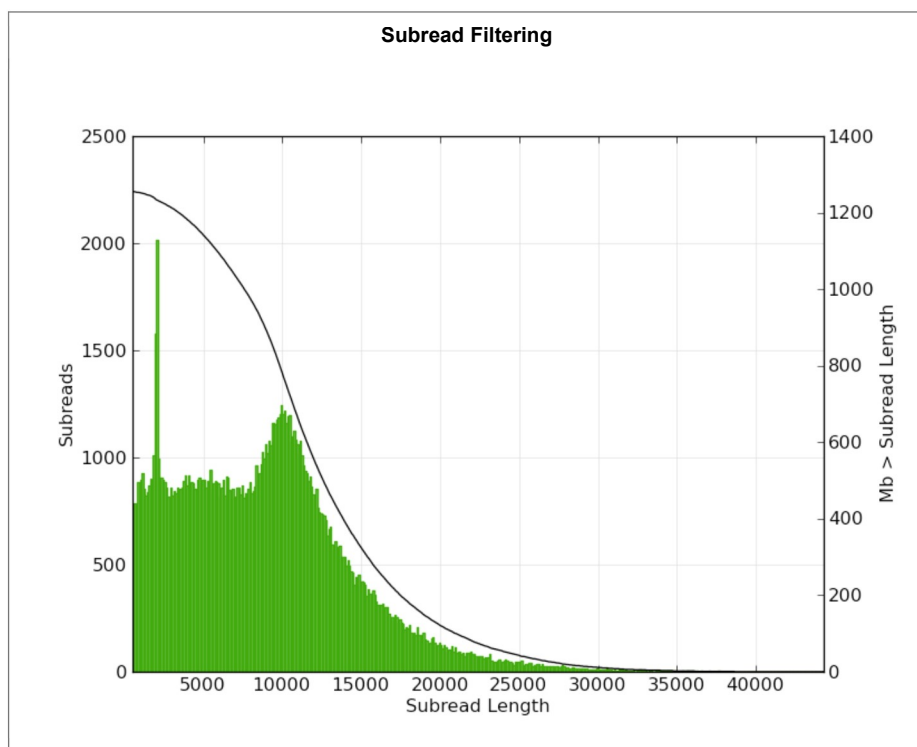


#### Polymerase Read Quality



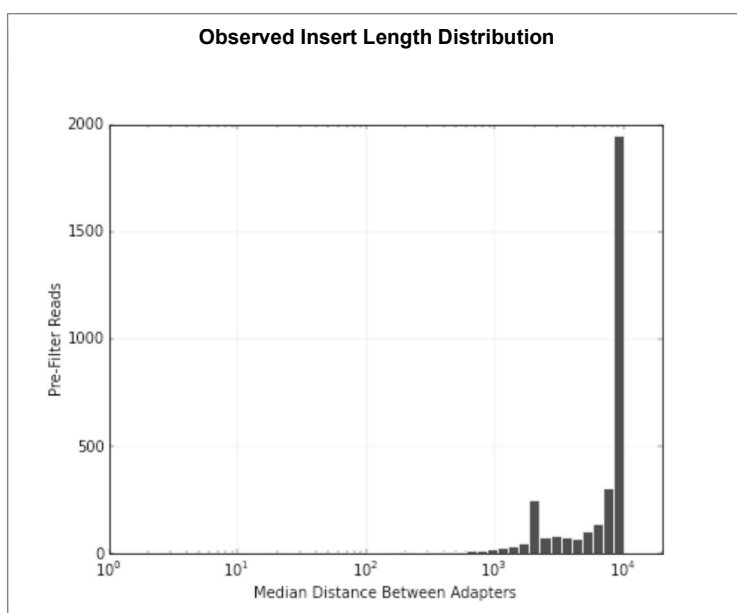
### Subread Filtering

Mean Subread length	8,800	N50	11,384
Total Number of Bases	1,262,901,012	Number of Reads	143,503



#### Adapters

Adapter Dimers (0-10bp) 0.02%  
Short Inserts (11-100bp) 0.0%



#### Loading

SMRT Cell ID	Productive ZMWs	ZMW Loading For Productivity 0	ZMW Loading For Productivity 1	ZMW Loading For Productivity 2
m160814_192830_42237_c101088372550000001823265803091782	150,292	20.69%	70.98%	8.33%

#### Mapping

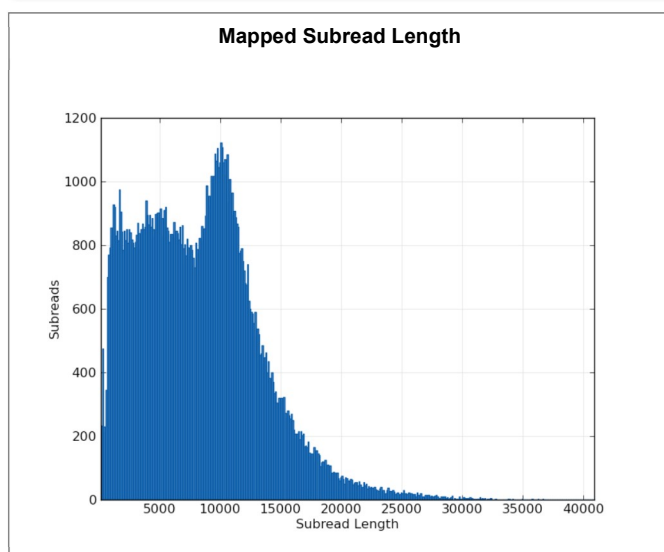
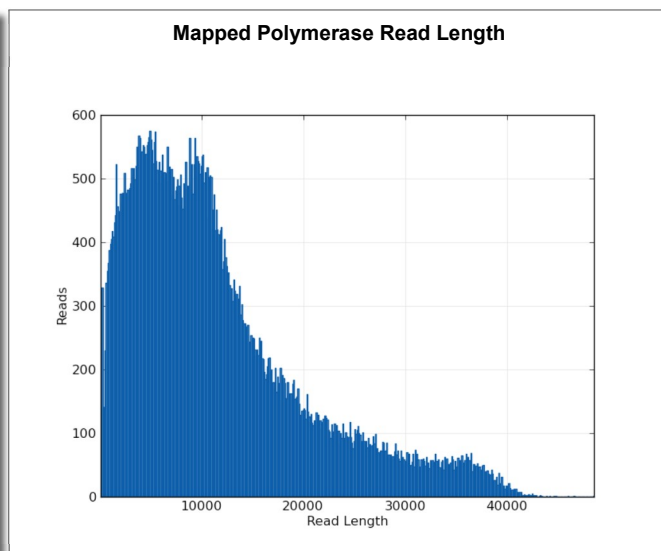
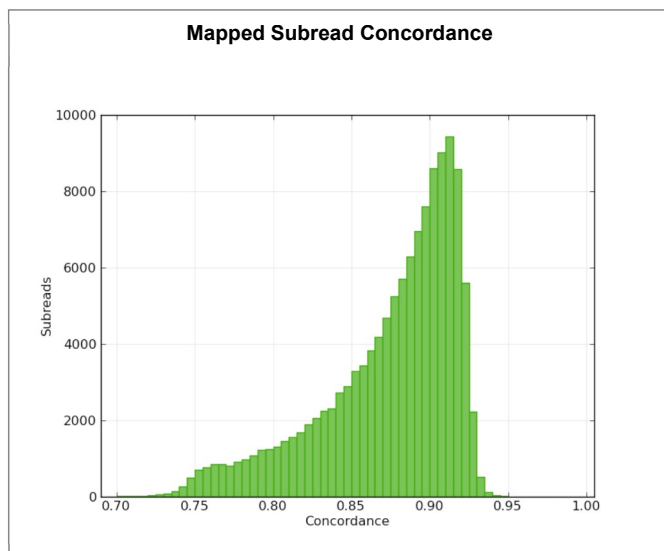
Mapped Subread Length N50 (bp) 10,660 Mapped Polymerase Read Length 95% (bp) 30,670  
Mapped Subread Length Mean (bp) 8,082 Mapped Polymerase Read Length Max (bp) 48,384

#### Mapping Stats Summary

Movie	Mapped Read	Mapped Polymerase Read Length	Mapped Polymerase Read Length N50	Mapped Subreads	Mapped Subread Bases	Mapped Subread Length	Mean Mapped Subread Concordance
All Movies	90,004	11,465	16102	126,298	1020701602	8,082	0.869
m160814_192830_42237_c101088372550000001823265803091782_s1_p0	90,004	11,465	16102	126,298	1020701602	8,082	0.869

#### Coverage

Mean Coverage 169.61  
Missing Bases (%) 0.0

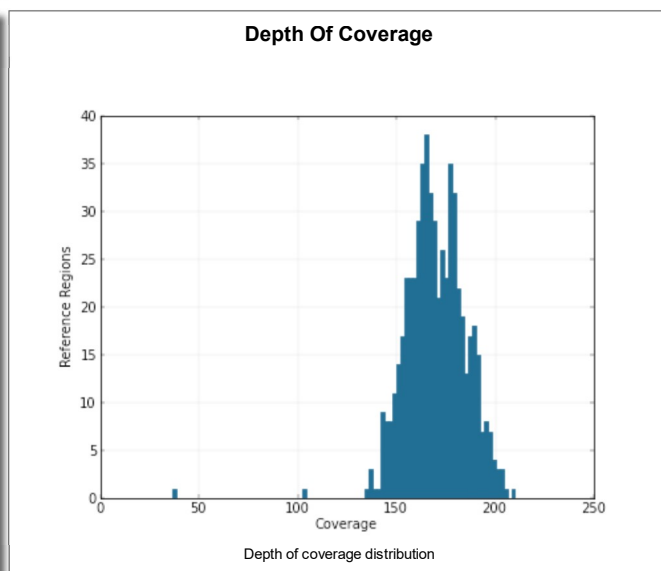
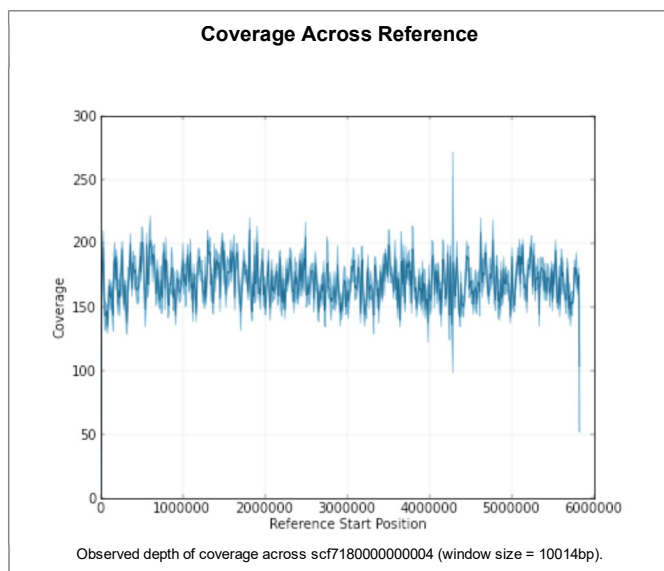


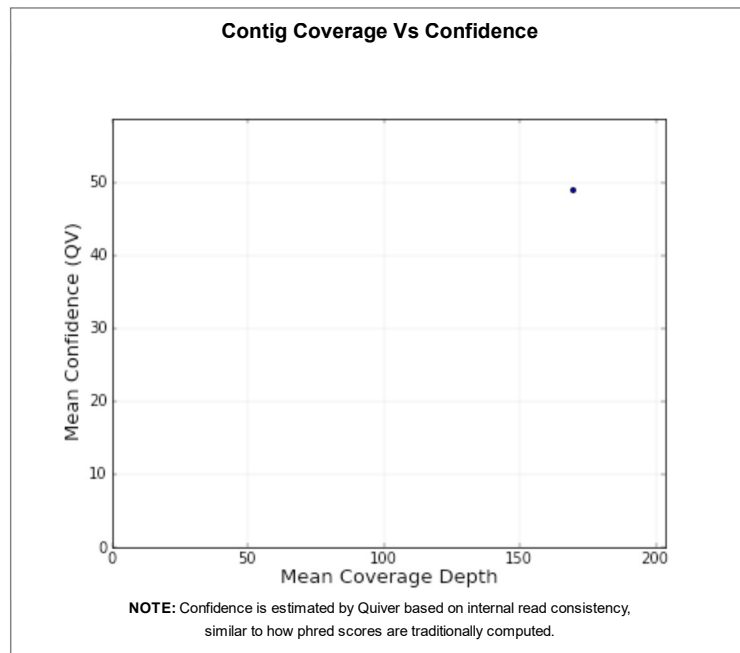
### Pre-Assembler Report

Polymerase Read Bases	1,262,901,012	Length Cutoff	20,000
Seed Bases	124,542,175	Pre-Assembled bases	83,817,299
Pre-Assembled Yield	.673	Pre-Assembled Reads	6,616
Pre-Assembled Reads Length	12,668	Pre-Assembled N50	20,409

### Polished Assembly

Polished Contigs	1	Max Contig Length	5,839,016
N50 Contig Length	5,839,016	Sum of Contig Lengths	5,839,016



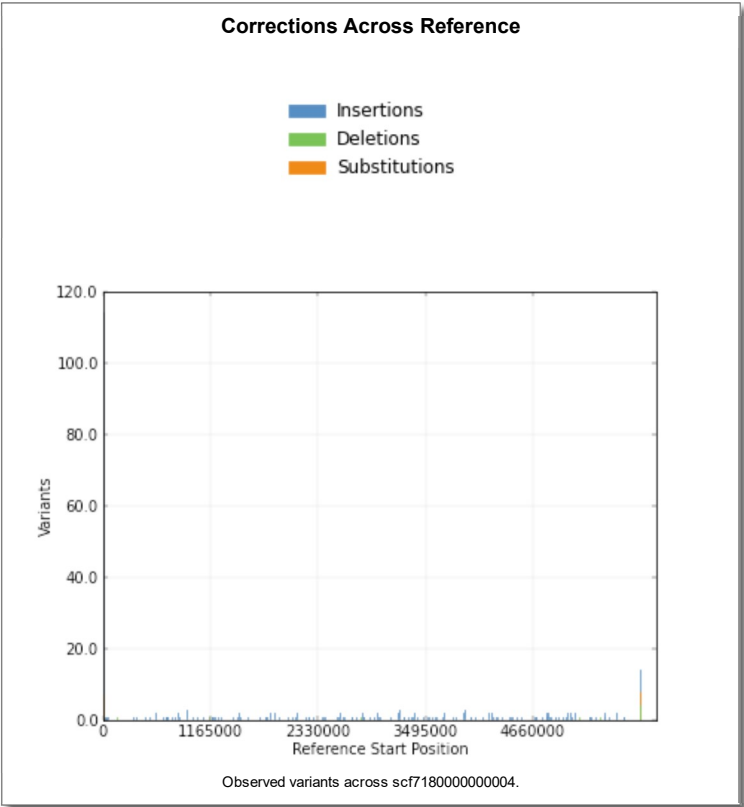


### Top Corrections

Sequence	Position	Correction	Type	Coverage	Confidence	Genotype
scf7180000000004	2,557,026	2557026_2557027insG	INS	100	53	haploid
scf7180000000004	3,191,068	3191068_3191069insG	INS	100	53	haploid
scf7180000000004	1,708,867	1708867_1708868insG	INS	100	52	haploid
scf7180000000004	1,859,457	1859457_1859458insG	INS	100	52	haploid
scf7180000000004	2,198,511	2198511_2198512insC	INS	100	52	haploid
scf7180000000004	3,401,525	3401525_3401526insG	INS	100	52	haploid
scf7180000000004	3,514,570	3514570_3514571insC	INS	100	52	haploid
scf7180000000004	3,820,578	3820578_3820579insC	INS	100	52	haploid
scf7180000000004	4,694,301	4694301_4694302insA	INS	100	52	haploid
scf7180000000004	3,423	3423_3424insG	INS	13	51	haploid
scf7180000000004	4,123	4123_4124insC	INS	15	51	haploid
scf7180000000004	4,156	4156_4157insA	INS	15	51	haploid
scf7180000000004	4,260	4260_4261insG	INS	19	51	haploid
scf7180000000004	4,551	4551_4552insTG	INS	22	51	haploid
scf7180000000004	4,552	4552A>G	SUB	22	51	haploid
scf7180000000004	4,844	4844_4845insC	INS	26	51	haploid
scf7180000000004	806,988	806988_806989insC	INS	100	51	haploid
scf7180000000004	807,192	807192_807193insC	INS	100	51	haploid
scf7180000000004	837,397	837397_837398insC	INS	100	51	haploid
scf7180000000004	1,270,706	1270706_1270707insA	INS	100	51	haploid
scf7180000000004	1,573,346	1573346_1573347insG	INS	100	51	haploid
scf7180000000004	2,544,310	2544310_2544311insG	INS	100	51	haploid
scf7180000000004	3,535,442	3535442_3535443insA	INS	100	51	haploid
scf7180000000004	3,902,053	3902053_3902054insC	INS	100	51	haploid
scf7180000000004	4,036,041	4036041_4036042insC	INS	100	51	haploid
scf7180000000004	4,174,716	4174716_4174717insC	INS	100	51	haploid
scf7180000000004	4,215,864	4215864_4215865insG	INS	100	51	haploid
scf7180000000004	4,258,876	4258876_4258877insC	INS	100	51	haploid
scf7180000000004	4,426,395	4426395_4426396insC	INS	100	51	haploid
scf7180000000004	4,907,454	4907454_4907455insT	INS	100	51	haploid
scf7180000000004	4,991,139	4991139_4991140insC	INS	100	51	haploid
scf7180000000004	5,114,268	5114268_5114269insA	INS	100	51	haploid
scf7180000000004	5,293,802	5293802_5293803insC	INS	100	51	haploid
scf7180000000004	5,436,194	5436194_5436195insC	INS	100	51	haploid
scf7180000000004	5,447,502	5447502_5447503insG	INS	100	51	haploid
scf7180000000004	3,872	3872_3873insC	INS	14	50	haploid
scf7180000000004	4,046	4046_4047insTCGTCT	INS	15	50	haploid
scf7180000000004	4,368	4368_4369insG	INS	20	50	haploid
scf7180000000004	4,487	4487_4488insC	INS	22	50	haploid
scf7180000000004	4,492	4492_4493insTATGAAAAACAC	INS	22	50	haploid
scf7180000000004	4,599	4599_4600insATT	INS	22	50	haploid
scf7180000000004	4,607	4607_4608insGGAGGATGCTACCA	INS	22	50	haploid
scf7180000000004	5,312	5312_5313insC	INS	34	50	haploid
scf7180000000004	5,359	5359_5360insC	INS	34	50	haploid
scf7180000000004	5,502	5502_5503insAA	INS	35	50	haploid
scf7180000000004	7,298	7298_7299insGC	INS	60	50	haploid
scf7180000000004	7,706	7706_7707insA	INS	62	50	haploid
scf7180000000004	30,812	30812_30813insA	INS	100	50	haploid
scf7180000000004	58,033	58033_58034insG	INS	100	50	haploid
scf7180000000004	155,827	155827delA	DEL	100	50	haploid
scf7180000000004	322,029	322029_322030insC	INS	100	50	haploid
scf7180000000004	361,564	361564_361565insC	INS	100	50	haploid
scf7180000000004	645,371	645371_645372insC	INS	100	50	haploid
scf7180000000004	905,000	905000_905001insG	INS	100	50	haploid
scf7180000000004	1,081,323	1081323_1081324insC	INS	100	50	haploid
scf7180000000004	1,187,044	1187044_1187045insT	INS	100	50	haploid
scf7180000000004	1,201,973	1201973_1201974insG	INS	100	50	haploid
scf7180000000004	1,467,655	1467655_1467656insC	INS	100	50	haploid
scf7180000000004	1,807,168	1807168_1807169insG	INS	100	50	haploid
scf7180000000004	2,084,120	2084120_2084121insC	INS	100	50	haploid
scf7180000000004	2,091,076	2091076_2091077insG	INS	100	50	haploid
scf7180000000004	2,419,306	2419306_2419307insC	INS	100	50	haploid
scf7180000000004	2,740,046	2740046_2740047insG	INS	100	50	haploid
scf7180000000004	2,810,137	2810137_2810138insA	INS	100	50	haploid
scf7180000000004	2,811,684	2811684_2811685insA	INS	100	50	haploid
scf7180000000004	2,899,350	2899350_2899351insG	INS	100	50	haploid

Corrections

Consensus Calling Results				
Reference	Reference Length	Bases Called	Consensus Concordance	Coverage
scf7180000000004	5,838,736	100.0%	99.9960%	169.61



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