PIPELINES

For tracks and QC:

1. **Align to combined *S. cerevisiae* + *S. pombe* index using STAR 2.5.3a**
2. **Mapping stats and QC metrics for each genome individually**

For quantification:

1. **Align to combined *S. cerevisiae* + *S. pombe* transcriptome index with Bowtie**
2. **Quantification in transcriptome space using eXpress (1.5.1)**

Note on read lengths: the reads as they came to me were 2x150mers. This appears to be longer than the mean fragment length because the rate of end-to-end alignments falls off precipitously from 2x100mers to 2x150mers. This is what this looks like for the G1 sample:

2x50: 84.59%
2x75: 83.73%
2x100: 78.84%
2x150: 42.20%

I have generated TPMs for all samples in all four formats, and given the depth of sequencing (very high), even the 2x150mers are probably fine, but I would work with the 2x100mers.

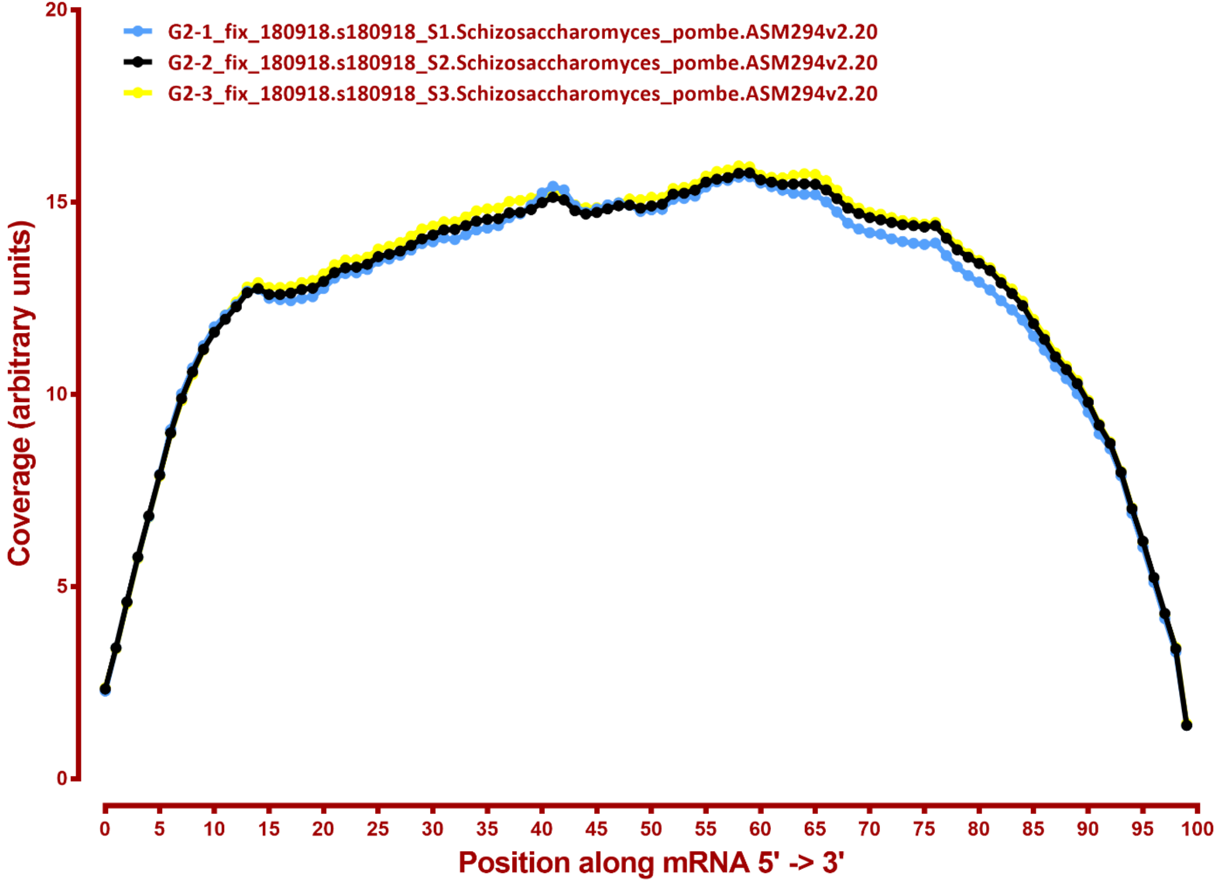
MAPPING STATS

Library	Read Length	Mapping	Species	Raw fragments	Complexity	Unique	Unique Splices	Multi	Multi Splices	Fraction mapped
G2-1_fix_180918.s180918_S1	**2x150**	STAR-2.5.3a	**S_pombe**	67,596,723	0.36	14,412,090	746,368	1,886,752	104,326	0.13
G2-1_fix_180918.s180918_S1	**2x150**	STAR-2.5.3a	**sacCer3**	67,596,723	0.22	55,344,853	1,577,249	19,311,706	1,399,370	0.57
G2-2_fix_180918.s180918_S2	**2x150**	STAR-2.5.3a	**S_pombe**	81,559,408	0.34	16,599,545	858,973	2,214,706	95,894	0.12
G2-2_fix_180918.s180918_S2	**2x150**	STAR-2.5.3a	**sacCer3**	81,559,408	0.19	72,991,877	1,813,673	25,276,739	1,560,407	0.62
G2-3_fix_180918.s180918_S3	**2x150**	STAR-2.5.3a	**S_pombe**	81,761,577	0.33	14,962,619	774,725	1,323,387	55,473	0.10
G2-3_fix_180918.s180918_S3	**2x150**	STAR-2.5.3a	**sacCer3**	81,761,577	0.18	82,555,854	1,904,250	25,464,500	1,510,410	0.68
G2-4_fix_180918.s180918_S4	**2x150**	STAR-2.5.3a	**S_pombe**	84,531,291	0.34	13,292,289	705,613	1,405,949	60,837	0.09
G2-4_fix_180918.s180918_S4	**2x150**	STAR-2.5.3a	**sacCer3**	84,531,291	0.17	86,203,846	1,904,522	28,073,462	1,710,746	0.70
input_fix_180918.s180918_SA	**2x150**	STAR-2.5.3a	**S_pombe**	88,299,105	0.51	2,837	47	11,415	15	0.00
input_fix_180918.s180918_SA	**2x150**	STAR-2.5.3a	**sacCer3**	88,299,105	0.16	105,068,578	2,415,786	25,393,962	1,519,554	0.76
input_live_180918.s180918_SB	**2x150**	STAR-2.5.3a	**S_pombe**	74,344,565	0.36	12,946,044	668,782	915,011	48,051	0.10
input_live_180918.s180918_SB	**2x150**	STAR-2.5.3a	**sacCer3**	74,344,565	0.19	74,197,684	1,761,880	19,212,858	1,227,382	0.65

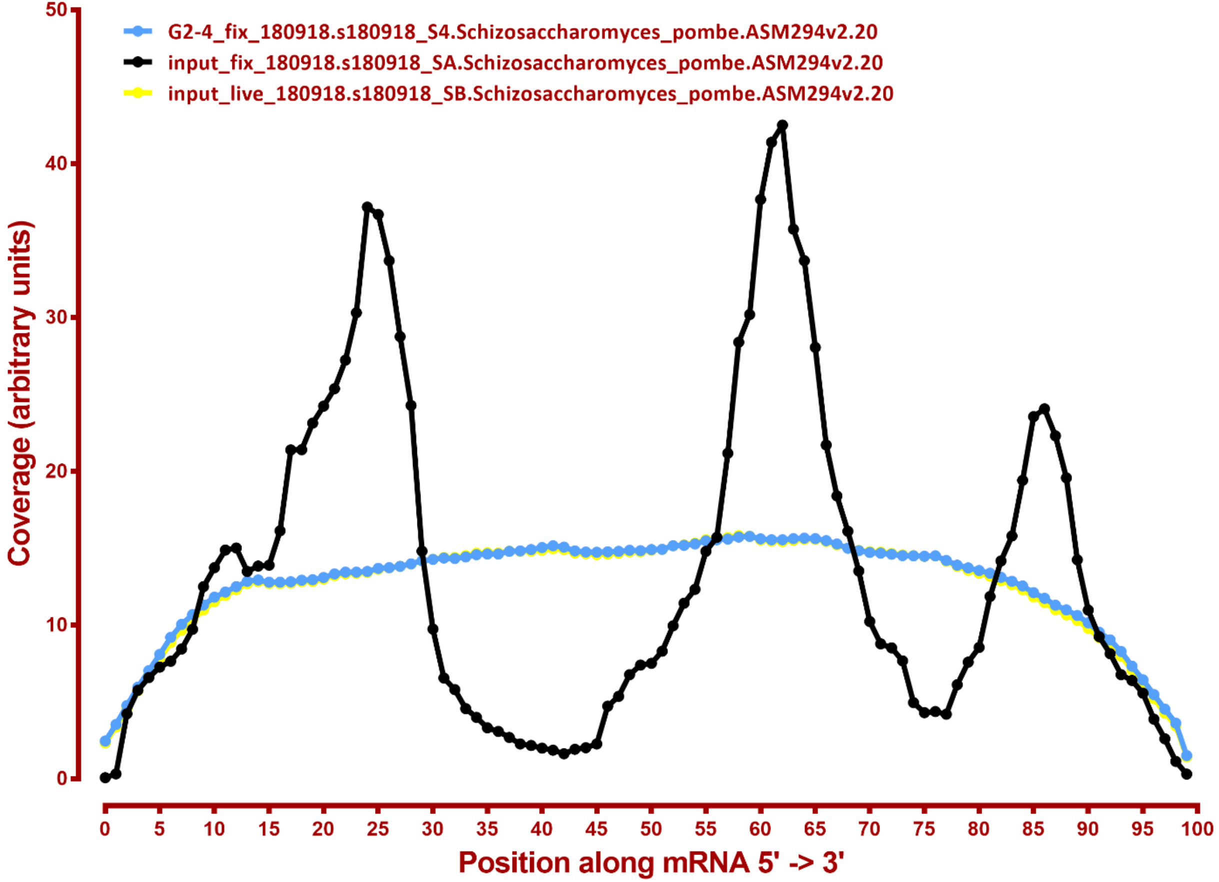
READ DISTRIBUTION

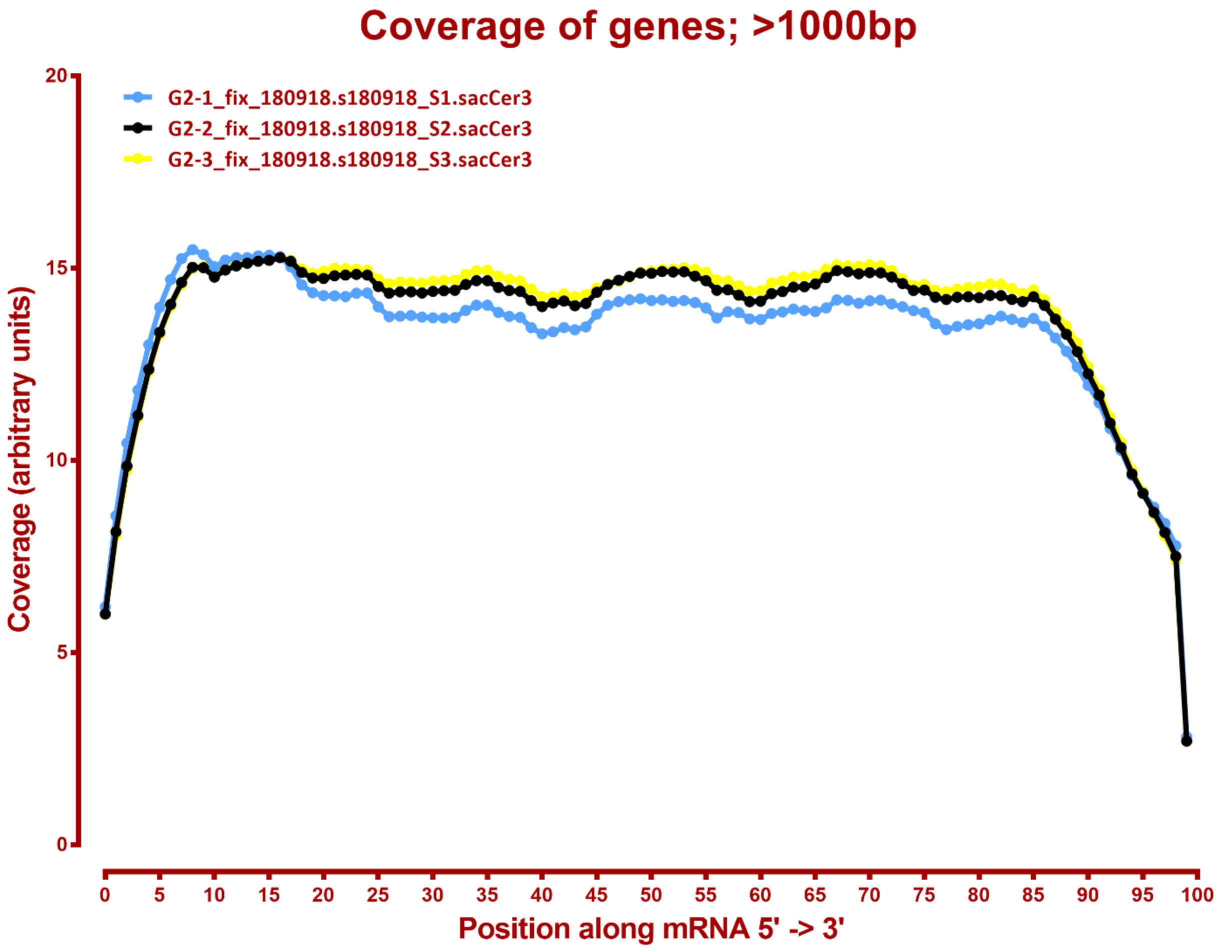
#	Exonic:	Intergenic:	Intronic:
G2-1_fix_180918.s180918_S1.Schizosaccharomyces_pombe.ASM294v2.20	0.98	0.01	0.01
G2-2_fix_180918.s180918_S2.Schizosaccharomyces_pombe.ASM294v2.20	0.98	0.01	0.01
G2-3_fix_180918.s180918_S3.Schizosaccharomyces_pombe.ASM294v2.20	0.98	0.01	0.01
G2-4_fix_180918.s180918_S4.Schizosaccharomyces_pombe.ASM294v2.20	0.98	0.01	0.01
input_fix_180918.s180918_SA.Schizosaccharomyces_pombe.ASM294v2.20	1.00	0.00	0.00
input_live_180918.s180918_SB.Schizosaccharomyces_pombe.ASM294v2.20	0.98	0.01	0.01
G2-1_fix_180918.s180918_S1.sacCer3	0.94	0.06	0.00
G2-2_fix_180918.s180918_S2.sacCer3	0.94	0.06	0.00
G2-3_fix_180918.s180918_S3.sacCer3	0.94	0.06	0.00
G2-4_fix_180918.s180918_S4.sacCer3	0.94	0.06	0.00
input_fix_180918.s180918_SA.sacCer3	0.93	0.07	0.00
input_live_180918.s180918_SB.sacCer3	0.94	0.06	0.00

Coverage of genes; >1000bp

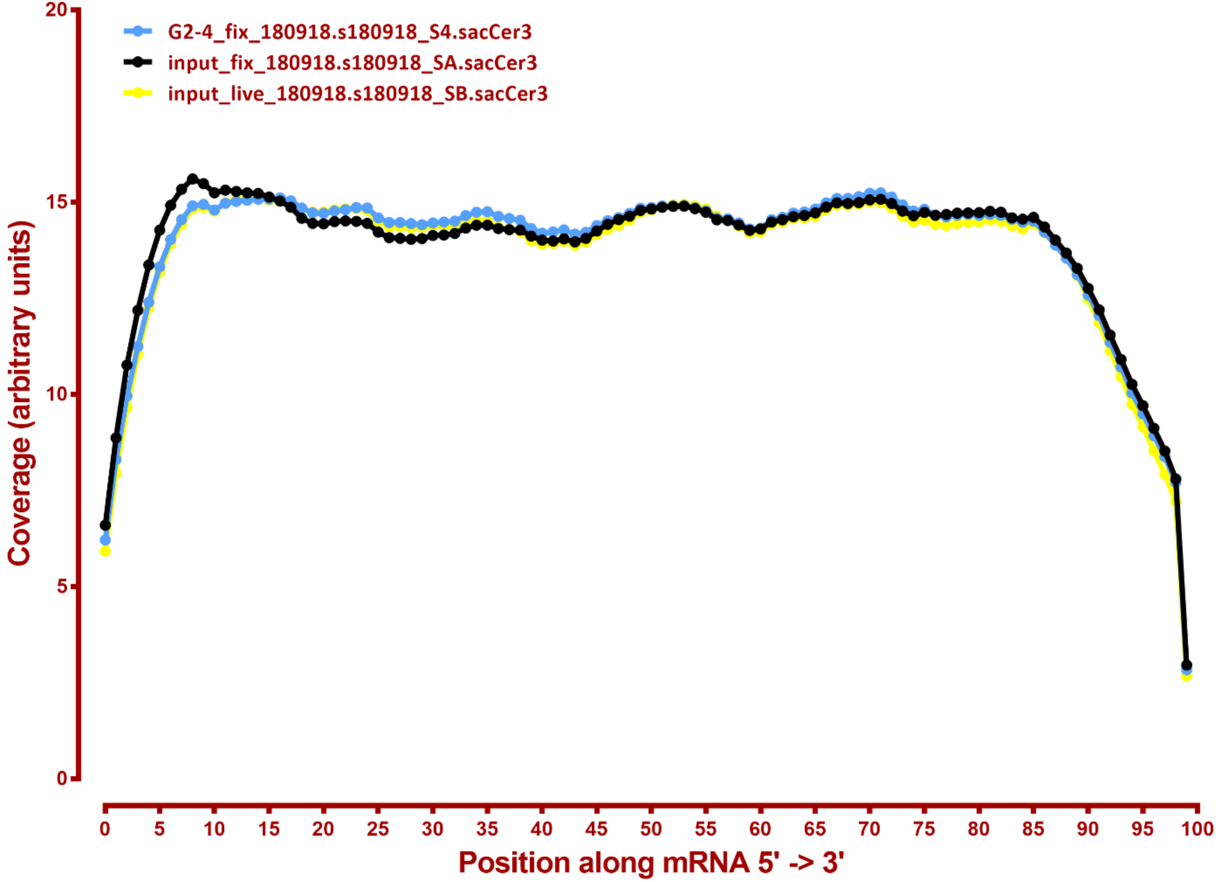


Coverage of genes; >1000bp

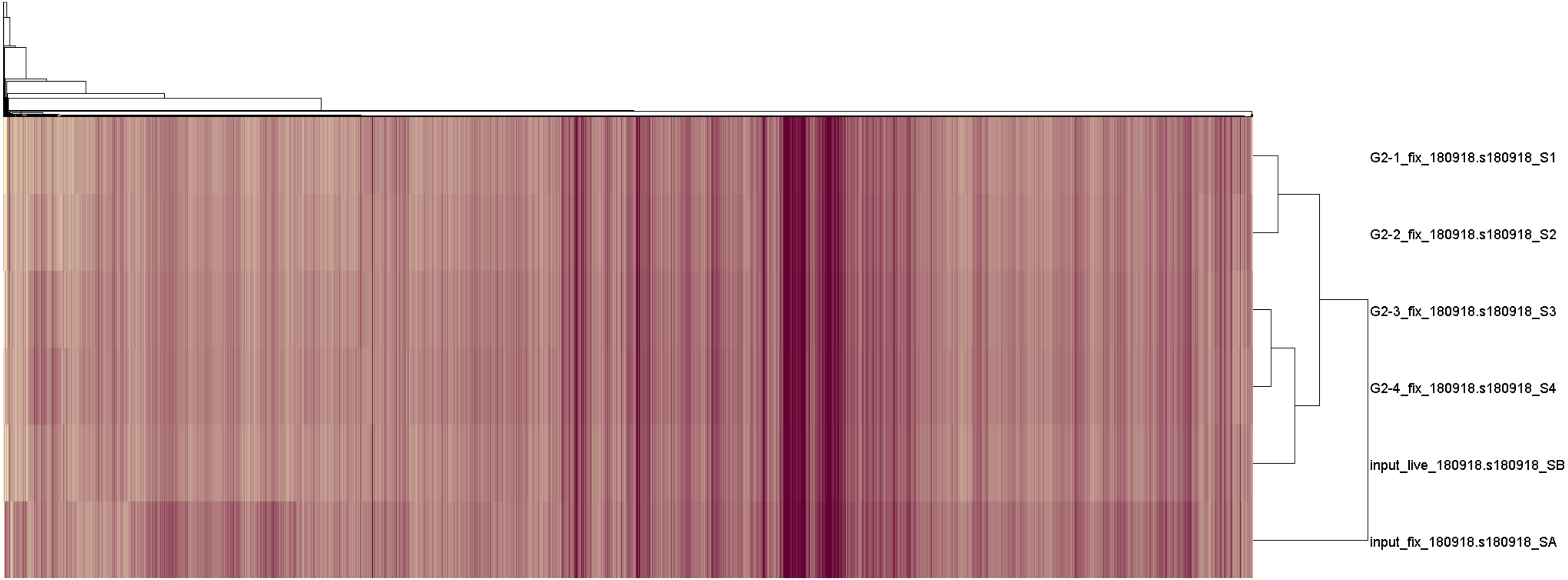



Coverage of genes; >1000bp
G2-1_fix_180918.s180918_S1.sacCer3
G2-2_fix_180918.s180918_S2.sacCer3
G2-3_fix_180918.s180918_S3.sacCer3
Coverage (arbitrary units)
0
5
10
15
20
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
Position along mRNA 5' -> 3'

Coverage of genes; >1000bp



S. cerevisiae genes log2(TPM+1), (TPM > 10 in at least one sample)



S. cerevisiae genes normalized to mean, (TPM > 10 in at least one sample)