

# MAPPING STATS

Library	Read Length	Mapping	Species	Raw fragments	Complexity	Unique	Unique Splices	Multi	Multi Splices	Fraction mapped
2025-06-20-LHG250529L01_exp250527_MS8_YPD	<b>2x150</b>	STAR-2.5.3a	<b>Candida</b>	25,501,531	0.62	4,137,327	124,343	104,384	5,690	0.09
2025-06-20-LHG250529L01_exp250527_MS8_YPD	<b>2x150</b>	STAR-2.5.3a	<b>sacCer3</b>	25,501,531	0.47	29,337,264	1,005,422	2,751,239	120,391	0.65
2025-06-20-LHG250529L02_exp250527_MS8_SCGE	<b>2x150</b>	STAR-2.5.3a	<b>Candida</b>	28,174,824	0.58	6,783,746	205,184	87,755	10,893	0.13
2025-06-20-LHG250529L02_exp250527_MS8_SCGE	<b>2x150</b>	STAR-2.5.3a	<b>sacCer3</b>	28,174,824	0.50	31,067,818	831,100	1,988,698	96,316	0.60
2025-06-20-LHG250529L03_exp250528_MS8_YPD	<b>2x150</b>	STAR-2.5.3a	<b>Candida</b>	26,080,249	0.62	4,340,357	123,983	56,766	5,692	0.09
2025-06-20-LHG250529L03_exp250528_MS8_YPD	<b>2x150</b>	STAR-2.5.3a	<b>sacCer3</b>	26,080,249	0.47	29,442,543	988,829	2,512,362	109,120	0.63
2025-06-20-LHG250529L04_exp250528_MS8_SCGE	<b>2x150</b>	STAR-2.5.3a	<b>Candida</b>	22,885,122	0.61	5,910,961	169,539	68,143	8,779	0.13
2025-06-20-LHG250529L04_exp250528_MS8_SCGE	<b>2x150</b>	STAR-2.5.3a	<b>sacCer3</b>	22,885,122	0.53	25,235,443	650,167	1,566,961	62,117	0.60

#	Exonic:	Intergenic:	Intronic:
2025-06-20-LHG250529L01_exp250527_MS8_YPD.sacCer3	0.93	0.06	0.00
2025-06-20-LHG250529L02_exp250527_MS8_SCGE.sacCer3	0.92	0.08	0.00
2025-06-20-LHG250529L03_exp250528_MS8_YPD.sacCer3	0.93	0.07	0.00
2025-06-20-LHG250529L04_exp250528_MS8_SCGE.sacCer3	0.91	0.08	0.00

# COVERAGE

## Coverage of genes; >1000bp, sacCer3

