

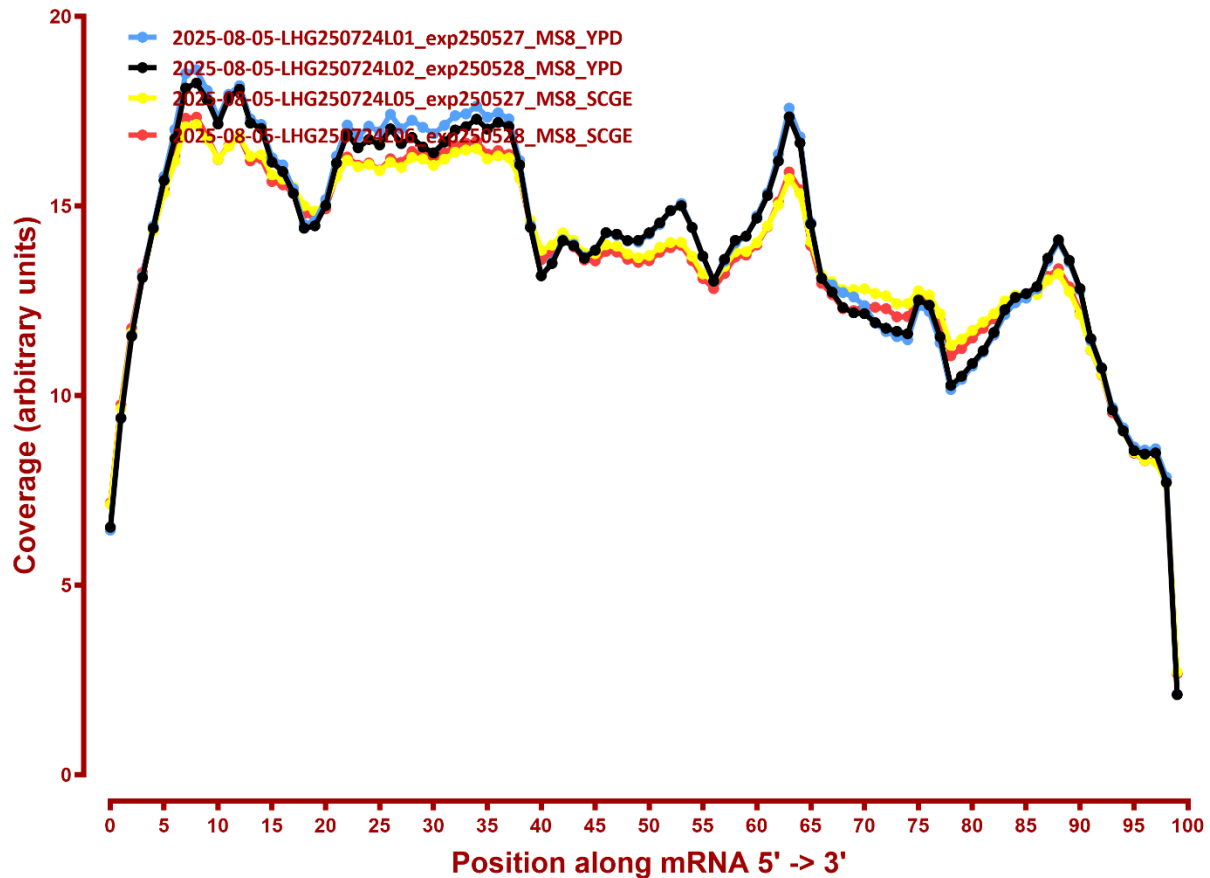
MAPPING STATS

Library	Read Length	Mapping	Species	Raw fragments	Complexity	Unique	Unique Splices	Multi	Multi Splices	Fraction mapped
2025-08-05-LHG250724L01_exp250527_MS8_YPD	2x150	STAR-2.5.3a	Candida	27,727,032	0.54	4,021,460	76,130	58,347	5,291	0.08
2025-08-05-LHG250724L01_exp250527_MS8_YPD	2x150	STAR-2.5.3a	sacCer3	27,727,032	0.38	28,292,744	814,586	9,792,652	529,524	0.71
2025-08-05-LHG250724L02_exp250528_MS8_YPD	2x150	STAR-2.5.3a	Candida	27,185,611	0.54	4,135,859	78,859	76,502	6,080	0.08
2025-08-05-LHG250724L02_exp250528_MS8_YPD	2x150	STAR-2.5.3a	sacCer3	27,185,611	0.39	27,613,210	796,876	9,234,436	500,802	0.70
2025-08-05-LHG250724L05_exp250527_MS8_SCGE	2x150	STAR-2.5.3a	Candida	27,671,713	0.52	5,993,936	114,692	93,176	9,178	0.11
2025-08-05-LHG250724L05_exp250527_MS8_SCGE	2x150	STAR-2.5.3a	sacCer3	27,671,713	0.43	27,264,050	593,234	5,671,966	327,994	0.61
2025-08-05-LHG250724L06_exp250528_MS8_SCGE	2x150	STAR-2.5.3a	Candida	24,739,462	0.51	5,885,020	116,912	76,282	11,362	0.12
2025-08-05-LHG250724L06_exp250528_MS8_SCGE	2x150	STAR-2.5.3a	sacCer3	24,739,462	0.42	24,655,462	587,460	5,134,273	319,967	0.62
2025-08-05-LHG_250724L03_exp250213_MS8_SCD	2x150	STAR-2.5.3a	Candida	25,982,935	0.51	5,638,553	107,583	98,958	9,638	0.11
2025-08-05-LHG_250724L03_exp250213_MS8_SCD	2x150	STAR-2.5.3a	sacCer3	25,982,935	0.39	29,248,227	775,423	6,226,910	322,138	0.70
2025-08-05-LHG_250724L04_exp250222_MS8_SCD	2x150	STAR-2.5.3a	Candida	23,983,746	0.53	5,192,333	96,607	78,243	9,333	0.11
2025-08-05-LHG_250724L04_exp250222_MS8_SCD	2x150	STAR-2.5.3a	sacCer3	23,983,746	0.40	25,100,712	724,990	6,815,549	364,807	0.69

#	Exonic:	Intergenic:	Intronic:
2025-08-05-LHG250724L01_exp250527_MS8_YPD	0.93	0.07	0.00
2025-08-05-LHG250724L02_exp250528_MS8_YPD	0.93	0.07	0.00
2025-08-05-LHG250724L05_exp250527_MS8_SCGE	0.91	0.08	0.00
2025-08-05-LHG250724L06_exp250528_MS8_SCGE	0.91	0.08	0.00
2025-08-05-LHG_250724L03_exp250213_MS8_SCD	0.93	0.07	0.00
2025-08-05-LHG_250724L04_exp250222_MS8_SCD	0.93	0.07	0.00

COVERAGE

Coverage of genes; >1000bp, sacCer3



Coverage of genes; >1000bp, sacCer3

