ILMN Run 16

40-AU Package Assessment Report

Structural package conformance, receipt disposition, and cohort QC context

35	0	40/40	5
STANDARD PASS	VALIDATED NO-CALL	STRUCTURE CONFORMANT	REVIEW-REQUIRED

Prepared 2026-09-08 | pclu19074-ilmn16-40au-20260907t144637z | customer-facing evidence summary

01 / Executive summary

Package readiness at a glance

All 40 Inflection package structures pass producer integrity checks. The audit confirmed 35,620 declared artifacts at their recorded byte sizes, with no missing paths, size mismatches, or recorded VCF/CRAM identity exceptions. Thirty-five AUs are standard PASS; five carry component failures requiring disposition before customer release.

What was verified

Every package_manifest.json and component-status index was read. Every manifest-declared path was checked for presence and recorded byte size. Artifact counts, package status, packaged sample identifiers, and producer VCF identity, CRAM identity, reference-validation and index-validation evidence were evaluated across all 40 AUs.

Receipt disposition

Seven FAIL receipts affect five AUs: CASE11-P/PMS2 and CASE17/CFH each have a caller failure plus a propagated VCF-statistics failure; the three CASE2-P libraries each have a short-read Ganon failure. These are five failed components plus two downstream receipts, not seven independent caller failures. No NO_CALL receipts were reported.

Packaging transformations

Each package carries transformation receipts. Primary SNV dot filters are normalized to PASS; mitochondrial and ExpansionHunter FILTER updates preserve the exact original value in IFX_ORIGINAL_FILTER; CNV review tags are projected to FILTER with preserved provenance.

Recommended disposition

Accept structural conformance for all 40 packages. Thirty-five AUs are standard PASS; no validated NO_CALL packages were reported. Review CASE11-P/PMS2 and CASE17/CFH caller failures and their propagated statistics failures, and explicitly disposition the three CASE2-P short-read Ganon QC failures before external release of those five AUs. Failed QC is not a negative screening result.

Cohort payload: 5.09 TiB declared across 35,620 artifacts. Full payload rehashing was not repeated; producer integrity is PASS.

02 / Package disposition

AU package assessment (1-12 of 40)

Analysis unit	External ID	Integrity	Missing	Size mismatch	Delivery state	Declared	GiB	Component disposition
BUCCAL1-cs550zzb54046g	BUCCAL1	PASS	0	0	PASS	894	121.9	None
BUCCAL10-zmxrxmmgv2nzs7	BUCCAL10	PASS	0	0	PASS	890	125.6	None
BUCCAL2-ykhg3rmacynq62	BUCCAL2	PASS	0	0	PASS	892	103.9	None
BUCCAL3-q5vxnnc1adv0wm	BUCCAL3	PASS	0	0	PASS	890	167.6	None
CASE1-F-v36b748bjs4ge9	CASE1-F	PASS	0	0	PASS	894	101.6	None
CASE1-M-93pjsz1jmt4gkt	CASE1-M	PASS	0	0	PASS	892	161.4	None
CASE1-P-26c2b48xgyckzj	CASE1-P	PASS	0	0	PASS	892	129.0	None
CASE10-F-bqnw1gvbj2xafr	CASE10-F	PASS	0	0	PASS	894	176.8	None
CASE10-M-66gk205q8k03x0	CASE10-M	PASS	0	0	PASS	894	134.3	None
CASE10-P-6kgec106s58wrp	CASE10-P	PASS	0	0	PASS	890	125.1	None
CASE11-M-1k42tk60e8hx0r	CASE11-M	PASS	0	0	PASS	892	128.3	None
CASE11-P-aycjnkav6wac3c	CASE11-P	PASS	0	0	WITH FAILURES	882	130.9	segdup:PMS2: FAIL (CALLER_NONZERO_EXIT); vcf_statistics: FAIL (UPSTREAM_COMPONENT_FAILURES)

Amber denotes a validated no-call. Rose denotes a failed or required not-configured component; structural integrity is separate.

02 / Package disposition

AU package assessment (13-24 of 40)

Analysis unit	External ID	Integrity	Missing	Size mismatch	Delivery state	Declared	GiB	Component disposition
CASE12-M-rfbf6r14f4bt2t	CASE12-M	PASS	0	0	PASS	890	115.0	None
CASE12-P-zqxx8bcdj503z4	CASE12-P	PASS	0	0	PASS	892	102.0	None
CASE13-F-6eymrvm8g093xp	CASE13-F	PASS	0	0	PASS	894	129.4	None
CASE13-M-zs51eec1k9wq9x	CASE13-M	PASS	0	0	PASS	890	136.5	None
CASE13-P-ztgcenrafaks0b	CASE13-P	PASS	0	0	PASS	892	137.1	None
CASE14-F-08eb1y7ap5t2bz	CASE14-F	PASS	0	0	PASS	892	134.7	None
CASE14-M-bfbfbw1w4qn5hj	CASE14-M	PASS	0	0	PASS	890	115.1	None
CASE14-P-ssn5kdyqxd3yx2	CASE14-P	PASS	0	0	PASS	892	120.5	None
CASE15-P-k2f1ea2wwqyay8	CASE15-P	PASS	0	0	PASS	890	129.7	None
CASE16-M-pvpjsb10r2nr0r	CASE16-M	PASS	0	0	PASS	890	162.7	None
CASE16-P-22nw4bwm9fhf3h	CASE16-P	PASS	0	0	PASS	892	140.3	None
CASE17-f1d2tcphbav8y5	CASE17	PASS	0	0	WITH FAILURES	884	121.8	segdup:CFH: FAIL (CALLER_NONZERO_EXIT); vcf_statistics: FAIL (UPSTREAM_COMPONENT_FAILURES)

Amber denotes a validated no-call. Rose denotes a failed or required not-configured component; structural integrity is separate.

02 / Package disposition

AU package assessment (25-36 of 40)

Analysis unit	External ID	Integrity	Missing	Size mismatch	Delivery state	Declared	GiB	Component disposition
CASE18-r5x6cqknvtpq25	CASE18	PASS	0	0	PASS	890	93.9	None
CASE19-M-1kjc1w9bz5c2zs	CASE19-M	PASS	0	0	PASS	890	127.3	None
CASE19-P-ca146f2dmp7ezp	CASE19-P	PASS	0	0	PASS	890	145.6	None
CASE2-P-3cqp5nkm8gsy1e	CASE2-P	PASS	0	0	WITH FAILURES	884	138.5	ganon2_sr: FAIL (CALLER_NONZERO_EXIT)
CASE2-P-cc0yhpat7j34d4	CASE2-P	PASS	0	0	WITH FAILURES	884	133.8	ganon2_sr: FAIL (CALLER_NONZERO_EXIT)
CASE2-P-kbsyn18esya2wp	CASE2-P	PASS	0	0	WITH FAILURES	884	129.2	ganon2_sr: FAIL (CALLER_NONZERO_EXIT)
CASE5-F-g5n7t0xds4hh9k	CASE5-F	PASS	0	0	PASS	892	173.0	None
CASE5-M-45a79np6t5vtkw	CASE5-M	PASS	0	0	PASS	892	137.6	None
CASE5-P-y2wjwxq561hydb	CASE5-P	PASS	0	0	PASS	890	104.1	None
CASE6-P-99kkh6v67wkyvp	CASE6-P	PASS	0	0	PASS	892	142.8	None
CASE7-F-ac5prpd5an1g3x	CASE7-F	PASS	0	0	PASS	892	127.8	None
CASE7-M-wb9ztse8nxyrg2	CASE7-M	PASS	0	0	PASS	890	132.7	None

Amber denotes a validated no-call. Rose denotes a failed or required not-configured component; structural integrity is separate.

02 / Package disposition

AU package assessment (37-40 of 40)

Analysis unit	External ID	Integrity	Missing	Size mismatch	Delivery state	Declared	GiB	Component disposition
CASE7-P-9fnp4ga78w7wtd	CASE7-P	PASS	0	0	PASS	892	108.0	None
CASE8-P-9d7ewk8cjvc011	CASE8-P	PASS	0	0	PASS	892	120.1	None
CASE9-M-665f6n08gx63e1	CASE9-M	PASS	0	0	PASS	890	120.6	None
CASE9-P-3chmntjfgqhs34	CASE9-P	PASS	0	0	PASS	892	127.4	None

Amber denotes a validated no-call. Rose denotes a failed or required not-configured component; structural integrity is separate.

03 / Sequencing and identity QC

Coverage, alignment, contamination, and sex fields (1-12 of 40)

Analysis unit	SR med cov	SR insert	LR med cov	LR aligned bases/read	LR pri+supp aligned %	RSR med cov	SR contam %	Requested sex	Observed	Peddy
BUCCAL1-cs550zzb54046g	42	445	9	6433.2	79.7670	0	0.3000	NOT_AVAILABLE	XY	male
BUCCAL10-zmxrxmmgv2nzs7	45	420	8	2099.4	81.6412	0	0.2500	NOT_AVAILABLE	XY	male
BUCCAL2-ykhg3rmacynq62	44	450	10	6578.4	92.5145	0	0.3500	NOT_AVAILABLE	XX	female
BUCCAL3-q5vxnnc1adv0wm	31	435	11	5883.4	59.6517	0	0.3500	NOT_AVAILABLE	XX	female
CASE1-F-v36b748bjs4ge9	48	383	5	3368.4	87.7680	0	0.3000	NOT_AVAILABLE	XY	male
CASE1-M-93pjsz1jmt4gkt	71	297	13	6177.6	95.1308	0	0.1500	NOT_AVAILABLE	XX	female
CASE1-P-26c2b48xgyckzj	59	374	19	8364.3	95.0374	0	0.2500	NOT_AVAILABLE	XY	male
CASE10-F-bqnw1gvbj2xafr	19	346	5	2503.9	35.9477	0	0.2000	NOT_AVAILABLE	XY	male
CASE10-M-66gk205q8k03x0	48	383	18	5197.5	87.4709	0	0.2000	NOT_AVAILABLE	XX	female
CASE10-P-6kgec106s58wrp	36	408	14	7735.5	94.8510	0	0.4000	NOT_AVAILABLE	XX	female
CASE11-M-1k42tk60e8hx0r	41	371	16	6912.8	93.5548	0	0.2500	NOT_AVAILABLE	XX	female
CASE11-P-aycjnkav6wac3c	32	376	9	5040.6	92.2372	0	0.3500	NOT_AVAILABLE	XX	female

Values are descriptive cohort QC context, not package thresholds. N/A means unavailable or not configured.

03 / Sequencing and identity QC

Coverage, alignment, contamination, and sex fields (13-24 of 40)

Analysis unit	SR med cov	SR insert	LR med cov	LR aligned bases/read	LR pri+supp aligned %	RSR med cov	SR contam %	Requested sex	Observed	Peddy
CASE12-M-rfbf6r14f4bt2t	60	319	7	2728.7	89.0192	0	0.1500	NOT_AVAILABLE	XX	female
CASE12-P-zqxx8bcdj503z4	42	391	10	5568.8	93.1350	0	0.2500	NOT_AVAILABLE	XY	male
CASE13-F-6eymrvm8g093xp	61	325	5	3312.3	89.1720	0	0.2000	NOT_AVAILABLE	XY	male
CASE13-M-zs51eec1k9wq9x	39	367	24	8891.2	96.0823	0	0.2000	NOT_AVAILABLE	XX	female
CASE13-P-ztgcenrafaks0b	30	439	12	5478.2	89.3466	0	0.4000	NOT_AVAILABLE	XY	male
CASE14-F-08eb1y7ap5t2bz	32	306	2	1363.6	60.8810	0	0.2000	NOT_AVAILABLE	XY	male
CASE14-M-bfbfbw1w4qn5hj	37	418	8	3823.0	91.0009	0	0.3500	NOT_AVAILABLE	XX	female
CASE14-P-ssn5kdyqxd3yx2	32	436	10	5915.7	92.6095	0	0.5000	NOT_AVAILABLE	XY	male
CASE15-P-k2f1ea2wwqyay8	36	449	14	5866.7	94.1167	0	0.4000	NOT_AVAILABLE	XX	female
CASE16-M-pvpjsb10r2nr0r	15	345	11	4332.2	83.5498	0	0.3500	NOT_AVAILABLE	XX	female
CASE16-P-22nw4bwm9fhf3h	42	430	22	7415.2	95.7294	0	1.0500	NOT_AVAILABLE	XY	male
CASE17-f1d2tcphbav8y5	34	343	10	5480.8	93.9760	0	0.1500	NOT_AVAILABLE	XY	male

Values are descriptive cohort QC context, not package thresholds. N/A means unavailable or not configured.

03 / Sequencing and identity QC

Coverage, alignment, contamination, and sex fields (25-36 of 40)

Analysis unit	SR med cov	SR insert	LR med cov	LR aligned bases/read	LR pri+supp aligned %	RSR med cov	SR contam %	Requested sex	Observed	Peddy
CASE18-r5x6cqknvtpq25	50	430	7	3952.4	92.0183	0	0.3000	NOT_AVAILABLE	XX	female
CASE19-M-1kjc1w9bz5c2zs	32	433	8	4559.8	88.5149	0	0.4000	NOT_AVAILABLE	XX	female
CASE19-P-ca146f2dmp7ezp	32	434	15	6729.8	94.6238	0	0.4500	NOT_AVAILABLE	XX	female
CASE2-P-3cqp5nkm8gsy1e	35	436	14	6012.9	85.3640	0	0.3500	NOT_AVAILABLE	XY	male
CASE2-P-cc0yhpat7j34d4	29	455	11	6386.8	85.6884	0	0.3500	NOT_AVAILABLE	XY	male
CASE2-P-kbsyn18esya2wp	31	448	9	5924.3	85.3622	0	0.3000	NOT_AVAILABLE	XY	male
CASE5-F-g5n7t0xds4hh9k	36	341	7	2141.8	52.9412	0	0.2500	NOT_AVAILABLE	XY	male
CASE5-M-45a79np6t5vtkw	64	361	16	8277.4	94.6853	0	0.2500	NOT_AVAILABLE	XX	female
CASE5-P-y2wjwxq561hydb	50	412	12	8391.2	95.2464	0	0.3000	NOT_AVAILABLE	XX	female
CASE6-P-99kkh6v67wkyvp	39	448	22	10741.5	95.4273	0	0.6000	NOT_AVAILABLE	XY	male
CASE7-F-ac5prpd5an1g3x	43	369	6	1717.2	70.2996	0	0.3000	NOT_AVAILABLE	XY	male
CASE7-M-wb9ztse8nxyrg2	45	404	10	2401.4	84.1603	0	0.3000	NOT_AVAILABLE	XX	female

Values are descriptive cohort QC context, not package thresholds. N/A means unavailable or not configured.

03 / Sequencing and identity QC

Coverage, alignment, contamination, and sex fields (37-40 of 40)

Analysis unit	SR med cov	SR insert	LR med cov	LR aligned bases/read	LR pri+supp aligned %	RSR med cov	SR contam %	Requested sex	Observed	Peddy
CASE7-P-9fnp4ga78w7wtd	37	425	10	7895.0	94.4484	0	0.3500	NOT_AVAILABLE	XY	male
CASE8-P-9d7ewk8cjvc011	34	444	10	7418.0	93.5250	0	0.4000	NOT_AVAILABLE	XY	male
CASE9-M-665f6n08gx63e1	45	425	8	3121.6	83.9341	0	0.4500	NOT_AVAILABLE	XX	female
CASE9-P-3chmntjfgqhs34	30	450	10	6434.7	92.9400	0	0.7000	NOT_AVAILABLE	XY	male

Values are descriptive cohort QC context, not package thresholds. N/A means unavailable or not configured.

04 / Configured truth-set and taxonomy context

Configured truth-set metrics and taxonomy screen (1-12 of 40)

Analysis unit	GIAB SNPts F1	GIAB SNPtv F1	Sniffles2 Truvari F1	LongReadSV Truvari F1	SR classified %	Top SR taxon	Top taxon %
BUCCAL1-cs550zzb54046g	N/A	N/A	N/A	N/A	71.8922	Klebsiella sp. K5-306	17.4286
BUCCAL10-zmxrxmmgv2nzs7	N/A	N/A	N/A	N/A	58.8634	Streptococcus sp. M334	0.9976
BUCCAL2-ykhg3rmacynq62	N/A	N/A	N/A	N/A	66.3656	Streptococcus sp. K0074	1.4814
BUCCAL3-q5vxnnc1adv0wm	N/A	N/A	N/A	N/A	54.9899	Haemophilus_D	5.0914
CASE1-F-v36b748bjs4ge9	N/A	N/A	N/A	N/A	62.1699	Magnoliaceae	3.6031
CASE1-M-93pjsz1jmt4gkt	N/A	N/A	N/A	N/A	67.3323	Hominidae	1.2703
CASE1-P-26c2b48xgyckzj	N/A	N/A	N/A	N/A	68.3463	Theaceae	2.3210
CASE10-F-bqnw1gvbj2xafr	N/A	N/A	N/A	N/A	58.0481	Rothia sp. HMSC069C03	5.0223
CASE10-M-66gk205q8k03x0	N/A	N/A	N/A	N/A	67.4123	Rothia sp. HMSC069C03	2.5886
CASE10-P-6kgec106s58wrp	N/A	N/A	N/A	N/A	50.9077	Hominidae	1.1446
CASE11-M-1k42tk60e8hx0r	N/A	N/A	N/A	N/A	65.9834	Sus scrofa	6.9107
CASE11-P-aycjnkav6wac3c	N/A	N/A	N/A	N/A	59.2686	Streptococcus sp. KHUD_015	2.6571

N/A means the benchmark was not configured. Taxonomy values are screening context, not a clinical interpretation.

04 / Configured truth-set and taxonomy context

Configured truth-set metrics and taxonomy screen (13-24 of 40)

Analysis unit	GIAB SNPts F1	GIAB SNPtv F1	Sniffles2 Truvari F1	LongReadSV Truvari F1	SR classified %	Top SR taxon	Top taxon %
CASE12-M-rfbf6r14f4bt2t	N/A	N/A	N/A	N/A	65.7121	Hominidae	1.5501
CASE12-P-zqxx8bcdj503z4	N/A	N/A	N/A	N/A	73.3026	Magnoliaceae	2.1927
CASE13-F-6eymrvm8g093xp	N/A	N/A	N/A	N/A	65.9634	Hominidae	1.5748
CASE13-M-zs51eec1k9wq9x	N/A	N/A	N/A	N/A	69.1293	Hominidae	1.7876
CASE13-P-ztgcenrafaks0b	N/A	N/A	N/A	N/A	68.6210	Veillonella sp. 3310	4.3575
CASE14-F-08eb1y7ap5t2bz	N/A	N/A	N/A	N/A	54.8230	Rothia sp. HMSC069C03	5.6883
CASE14-M-bfbfbw1w4qn5hj	N/A	N/A	N/A	N/A	69.5890	Streptococcus	1.6683
CASE14-P-ssn5kdyqxd3yx2	N/A	N/A	N/A	N/A	69.7990	Magnoliaceae	2.2836
CASE15-P-k2f1ea2wwqyay8	N/A	N/A	N/A	N/A	73.6244	Hominidae	1.4867
CASE16-M-pvpjsb10r2nr0r	N/A	N/A	N/A	N/A	54.3347	Magnoliaceae	4.9271
CASE16-P-22nw4bwm9fhf3h	N/A	N/A	N/A	N/A	71.0960	Hominidae	1.2919
CASE17-f1d2tcphbav8y5	N/A	N/A	N/A	N/A	69.3871	Hominidae	1.5640

N/A means the benchmark was not configured. Taxonomy values are screening context, not a clinical interpretation.

04 / Configured truth-set and taxonomy context

Configured truth-set metrics and taxonomy screen (25-36 of 40)

Analysis unit	GIAB SNPts F1	GIAB SNPtv F1	Sniffles2 Truvari F1	LongReadSV Truvari F1	SR classified %	Top SR taxon	Top taxon %
CASE18-r5x6cqknvtpq25	N/A	N/A	N/A	N/A	75.0450	Hominidae	1.4275
CASE19-M-1kjc1w9bz5c2zs	N/A	N/A	N/A	N/A	62.0345	Streptococcus sp. 20925_1_24	2.8687
CASE19-P-ca146f2dmp7ezp	N/A	N/A	N/A	N/A	58.4001	Aeolidiidae	12.8414
CASE2-P-3cqp5nkm8gsy1e	N/A	N/A	N/A	N/A	FAIL	FAIL	FAIL
CASE2-P-cc0yhpat7j34d4	N/A	N/A	N/A	N/A	FAIL	FAIL	FAIL
CASE2-P-kbsyn18esya2wp	N/A	N/A	N/A	N/A	FAIL	FAIL	FAIL
CASE5-F-g5n7t0xds4hh9k	N/A	N/A	N/A	N/A	68.8269	Rothia sp. HMSC069C03	22.1737
CASE5-M-45a79np6t5vtkw	N/A	N/A	N/A	N/A	70.8459	Hominidae	1.5226
CASE5-P-y2wjwxq561hydb	N/A	N/A	N/A	N/A	71.7864	Hominidae	1.7276
CASE6-P-99kkh6v67wkyvp	N/A	N/A	N/A	N/A	71.1454	Hominidae	1.4893
CASE7-F-ac5prpd5an1g3x	N/A	N/A	N/A	N/A	59.3557	Streptococcus sp. 20925_1_24	11.3961
CASE7-M-wb9ztse8nxyrg2	N/A	N/A	N/A	N/A	57.5104	Streptococcus sp. 20925_1_24	3.8232

N/A means the benchmark was not configured. Taxonomy values are screening context, not a clinical interpretation.

04 / Configured truth-set and taxonomy context

Configured truth-set metrics and taxonomy screen (37-40 of 40)

Analysis unit	GIAB SNPts F1	GIAB SNPtv F1	Sniffles2 Truvari F1	LongReadSV Truvari F1	SR classified %	Top SR taxon	Top taxon %
CASE7-P-9fnp4ga78w7wtd	N/A	N/A	N/A	N/A	69.1423	Ictaluridae	1.9044
CASE8-P-9d7ewk8cjvc011	N/A	N/A	N/A	N/A	66.0844	Magnoliaceae	2.4383
CASE9-M-665f6n08gx63e1	N/A	N/A	N/A	N/A	58.8546	Streptococcus sp. M334	7.8396
CASE9-P-3chmntjfgqhs34	N/A	N/A	N/A	N/A	63.6728	Hominidae	1.7581

N/A means the benchmark was not configured. Taxonomy values are screening context, not a clinical interpretation.

05 / Packaging transformation evidence

Customer-facing transformations are explicit and traceable

206,023,173	296	57	18
SNV records: . to PASS	Mito FILTER values to PASS	ExpansionHunter LowDepth to PASS	CNV review tags projected to FILTER

Original values remain recoverable

For mitochondrial and ExpansionHunter FILTER normalization, the exact original FILTER string is retained in INFO/IFX_ORIGINAL_FILTER. CNV review-tag projection uses the same provenance field and percent-encoded original value. Package manifests link delivered artifacts to transformation receipts and digests.

Sample identity is package-wide

All packaged VCF identity evidence resolved to the package external sample ID. All packaged CRAM identity evidence resolved to the same ID, with reference and index validation reported as SUCCESS. No recorded VCF or CRAM identity exceptions were found. These are producer evidence checks, not a new full-file identity scan.

Zero-length artifacts are isolated to native experimental evidence

The manifests declare 2,038 zero-length files, all under experimental/tiddit/ native evidence. No zero-length files were found outside experimental/. These are declared native intermediates, not missing primary result files.

Optional truth-set components remain explicit

Optional RTG/Truvari evaluations not configured for an AU are represented as NOT_CONFIGURED in the package manifest rather than inferred as failures or omitted silently. No configured truth-set F1 metrics were available for this 40-AU cohort; Section 04 retains those columns as N/A.

06 / Interpretation guide

Definitions, caveats, and release disposition

Package integrity

PASS means the producer completed its package integrity contract: required controls and declared artifacts were incorporated, safe relative paths were enforced, and the manifest records each artifact's byte size and SHA-256 digest. This assessment independently rechecked path presence and recorded byte size; it did not rehash the entire 5.09 TiB payload.

Receipt states

PASS indicates a completed validated component. NO_CALL is an explicit validated scientific terminal state. FAIL records a component or validation failure. NOT_CONFIGURED records a component deliberately excluded by configuration or policy. These states are not interchangeable with a missing file. FAIL never means a negative scientific result.

Cohort QC context

Coverage, alignment, contamination, sex-inference, benchmark, and taxonomy fields are descriptive context from final DayOA/MultiQC evidence, not additional package-integrity criteria. N/A denotes unavailable or not-configured metrics. Section 04 explicitly marks the three failed Ganon screens as FAIL, not zero or negative.

Release disposition

Accept structural conformance for all 40 packages. Thirty-five AUs are standard PASS; no validated NO_CALL packages were reported. Review CASE11-P/PMS2 and CASE17/CFH caller failures and their propagated statistics failures, and explicitly disposition the three CASE2-P short-read Ganon QC failures before external release of those five AUs. Failed QC is not a negative screening result.

Evidence boundary

Evidence was read on 2026-09-08 from the completed FSx capsule through public DYEC headnode inspection. This report does not assert S3 export. Delivery batch: pclu19074-ilmn16-40au-20260907t144637z. Run source: DayOA 16.0.88 with the approved Ganon report-scope repair; not a rerun on 16.0.88.5.