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Survival and Detectability of Mars-Derived Organic Carbon in Phobos Regolith: A Quantitative Hardness Taxonomy for MMX Sample Analysis

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Abstract

The Martian Moons eXploration (MMX) mission will return ≥ 10 g of Phobos regolith carrying a small admixture of Mars-derived impact ejecta. This paper asks a single, mission-relevant question – what could that returned mass realistically contain in the way of ancient Martian organic matter, and could MMX detect it – in place of an uncited back-of-envelope estimate that assumed, without support, percent-level survival of degraded organics. We build a two-axis mechanical/radiolytic hardness taxonomy across six biosignature classes and show that while ejection shock (< 5 GPa; Hyodo et al., 2019) is non-lethal for every class, 3.8 Gyr of radiolytic exposure on Phobos is lethal for all of them except refractory macromolecular carbon, a conclusion reinforced (with caveats on shared underlying data) by independent planetary-protection risk models (Fujita et al., 2019; Kurosawa et al., 2019). Propagating this through a five-parameter Monte Carlo model ($N = 2 \times 10^6$) – cross-validated by three independent sensitivity measures (Pearson, Spearman, Sobol’), a correlated-parameter robustness check, bootstrap resampling, and six-seed reruns – gives a median refractory-carbon yield of 39.0 ng per 10 g sample (5th–95th percentile: 2.6 ng–0.6 μ g), whose dominant uncertainty (χ_C , bulk organic-carbon content, $\sim 90\%$ of variance) is independently anchored near 4–12 ppm via a Gale Crater back-calculation. Detection probability against real instrumental thresholds ranges from 48.7% (best validated nano-isotope instrumentation) to effectively zero (conventional bulk EA-IRMS) – itself an upper bound, since MMX’s own published curation protocol subdivides the returned sample across sequential analysis phases before any aliquot reaches an instrument (Fukai et al., 2024). We ground this result in the literature it extends: the SHIGAI biosignature framework this taxonomy operationalizes (Hyodo and Usui, 2021), direct hypervelocity-impact experiments on Phobos regolith simulants (Morland et al., 2021), MMX’s published contamination-control budget (Sugahara et al., 2024), and the trace-level (ppb-to-nmol/g) detections already achieved on milligram-scale Ryugu and Bennu returned samples (Oba et al., 2023; Glavin et al., 2025). With MMX now scheduled to launch on 19 October 2026, the conclusion is direct: its realistic organic target is structurally and isotopically diagnostic refractory carbon, not intact biosignatures.

Keywords: Phobos , Mars , MMX , sample return , astrobiology , biosignatures , radiolysis , impact ejecta , organic geochemistry , Monte Carlo

1 Introduction

This paper asks what the Martian Moons eXploration (MMX) mission’s returned Phobos regolith could realistically contain in the way of ancient Martian organic matter, and whether MMX’s own analytical pipeline could detect it. We answer with a two-axis hardness taxonomy across six biosignature classes, a propagated Monte Carlo yield estimate, and explicit detection probabilities against real instrument thresholds – replacing an informal, uncited estimate that this section motivates and Section 8 supersedes.

Dynamical modeling of impact ejecta shows that material launched from the Martian surface at velocities exceeding local escape velocity is delivered, in small but non-negligible quantities, to the surface of Phobos (Ramsley and Head, 2013; Chappaz et al., 2013). Because this ejecta is sourced stochastically across Mars’s geologic history, it has been proposed as a dilute archive of Martian history inaccessible to landed missions (Hyodo et al., 2019). The MMX mission, returning ≥ 10 g of Phobos regolith, is designed in part to exploit this property (Kuramoto et al., 2022).

This has motivated informal claims, including an uncited back-of-envelope calculation that prompted the present analysis, that the returned sample could contain identifiable ancient Martian organic matter or biosignatures, typically via a single chained calculation (mass $\times$ mixing ratio $\times$ source fraction $\times$ survival fractions) that treats organic-mass survival and biosignature survival as interchangeable. They are not: a given mass of carbon can survive transport while losing every property that would make it biologically diagnostic, different biosignature classes have largely uncorrelated survival physics, and even surviving carbon is only detectable above the mass threshold of a specific analytical technique. We address these points in turn, present two complementary but non-equivalent estimates of ejecta antiquity rather than a single over-precise figure, propagate parameter uncertainty through a reproducible Monte Carlo model with an independent empirical anchor for its most influential input, cross-check our radiolytic-survival argument against an unrelated planetary-protection risk assessment while noting where that independence is only partial, and compute explicit detection probabilities against real instrumental thresholds rather than a generic sensitivity claim.

At the time of writing, MMX is no longer a distant prospect: JAXA has set launch for 19 October 2026, with Phobos arrival in 2027, surface sampling around 2029, and Earth return of ≥ 10 g of regolith in 2031 (Kuramoto et al., 2022; Fukai et al., 2024). The question this paper answers – what, quantitatively, is realistic to expect from that returned mass in terms of ancient Martian organics – is therefore immediately actionable rather than speculative.

This work is best understood as a quantitative elaboration of a taxonomy already proposed qualitatively in the field. Hyodo and Usui (2021) introduced the SHIGAI category (Sterilized and Harshly Irradiated Genes, and Ancient Imprints) to describe the class of dead, radiation-processed biosignatures that Phobos sampling could realistically return, explicitly distinguishing this from the search for extant or recently-extinct life pursued by landed Mars missions. Our two-axis mechanical/radiolytic hardness taxonomy (Section 6) can be read as asking, compound class by compound class, which specific biosignature types fall inside the SHIGAI category and by how much – turning a qualitative distinction into six quantified survival curves and a propagated yield estimate.

2 The Mars-to-Phobos Ejecta Pathway

2.1 Mixing ratio

Dynamical transport modeling gives a present-day bulk concentration of Martian material in the upper Phobos regolith of order 250 ppm, accumulated over ~ 3.5 Gyr (Ramsley and Head, 2013;

Chappaz et al., 2013). Work treating the five largest recent Martian craters as dominant ejecta sources raised this to ~ 1000 ppm (Hyodo et al., 2019). MEGANE brackets the credible range at 2–500 ppm pending in-situ measurement (Lawrence et al., 2019). We treat C_m as triangular(50, 300, 1000) ppm.

2.2 Source epoch: two distinct questions

An earlier version of this analysis answered “what fraction of delivered ejecta is ancient” with a single chronology-based number. This conflates two distinct quantities, presented separately below.

Timing of ejecta-launching events. The Neukum-Ivanov-Hartmann chronology function,

$$N(T) = a_1(e^{a_2 T} - 1) + a_3 T, \quad (1)$$

($a_1 = 5.44 \times 10^{-14} \text{ km}^{-2}$, $a_2 = 6.93 \text{ Gyr}^{-1}$, $a_3 = 8.38 \times 10^{-4} \text{ km}^{-2} \text{ Gyr}^{-1}$; Neukum and Ivanov, 1994; Neukum et al., 2001; rescaled to Mars following Hartmann and Neukum, 2001; Ivanov, 2001) gives the impact flux at time T before present. Integrating Eq. 1 gives the fraction of ejecta-launching events, flux-weighted, before a given epoch: 96.7–99.75% before the Noachian/Hesperian boundary (Table 1). This is *not* the same as “the excavated material is ancient crust”: a modern deep impact can excavate ancient basement rock, and an ancient impact excavates whatever existed then, not necessarily habitable-era material specifically.

Areal fraction of ancient terrain. A more direct proxy: Noachian units cover $\sim 45\%$ of Mars’s present surface (Tanaka et al., 2014); Hesperian volcanic resurfacing affected at least 30% more, not strictly additive (Carr and Head, 2010). This gives a plausible ancient-terrain areal fraction of 45–75%, substantially lower than the event-timing figure, because most individual impacts happened early (flux was far higher then) while much of today’s surface is nonetheless still ancient (Mars has resurfaced comparatively little since the Hesperian). Neither figure alone resolves what fraction of ejecta reaching Phobos excavated Noachian-or-older material specifically; that requires crater-specific dating and excavation-depth data beyond this paper’s scope. Neither ancient-fraction estimate enters the yield model of Section 8 as a multiplicative term, so this ambiguity affects framing, not the quantitative result.

Table 1: Ancient-era ejecta-event mass fraction from impact-flux chronology

Cutoff (Ga)	$N(\text{cutoff})$	$N(4.5)$	Fraction before
3.5	4.79×10^{-3}	1.905	99.748%
3.8	1.81×10^{-2}	1.905	99.052%
4.0	6.28×10^{-2}	1.905	96.703%

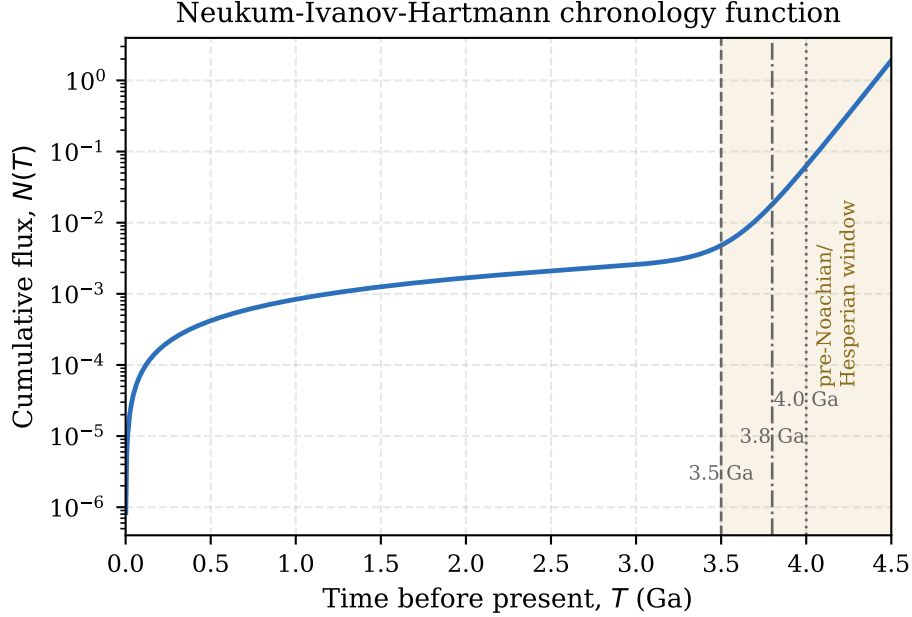


Figure 1: The Neukum-Ivanov-Hartmann cumulative chronology function $N(T)$ (Eq. 1), log-scaled, with the three candidate Noachian/Hesperian cutoffs from Table 1 marked. The curve’s steep late rise close to $T = 4.5$ Ga is why the flux-weighted ancient-event fraction is so high despite the shallower slope across most of Mars’s history.

2.3 MMX curation protocol and contamination control

The generic instrumental-threshold comparison used elsewhere in this paper (Section 9) is only half the detectability question; the other half is what MMX itself will actually do with the returned mass before any external group gets access to it. MMX has two sampling systems, a coring (C-)sampler and a pneumatic (P-)sampler, together targeting >10 g of Phobos surface material from two touchdown sites (Sugahara et al., 2024). On return, the capsule is transferred to a dedicated curation facility at ISAS/JAXA, where the published Sample Analysis Working Team (SAWT) protocol defines three sequential, largely non-destructive phases: Quick Analysis (headspace gas extraction and mass spectrometry, testing for terrestrial leak and contamination), Pre-basic Characterization (bulk-scale optical, visible-multiband, and near-infrared observation of the sample under purified- N_2 atmosphere), and Basic Characterization (grain-by-grain observation, from which aliquots are finally selected and allocated to individual analysis teams) (Fukai et al., 2024). The protocol’s own working assumption is a nominal grain size near $300 \mu\text{m}$ for a 10 g total return, and a stated target of distributing aliquots to the wider research community within approximately three months of Earth return – both directly relevant to how, and how finely, the yield modeled in Section 8 would actually be subdivided in practice.

Contamination control is explicit and quantitative rather than qualitative: the MMX plan sets the allowable terrestrial-contamination budget for each contaminant class at approximately 1/1000 of the expected amount of that same material in the returned sample, evaluated separately for organic and inorganic categories, using contamination-knowledge material coupons on the spacecraft to fingerprint any residual terrestrial signal (Sugahara et al., 2024). This is a mission-defined ceiling, not an instrumental one, and it is worth being explicit about what it does and does not tell us: it bounds contamination *relative to the dominant, Phobos-indigenous organic content of*

the sample, not relative to the much smaller, specifically Mars-derived and specifically ancient refractory-carbon signal this paper models (median 39.0 ng per 10 g; Section 8). Because Phobos’s own bulk organic budget is presently unconstrained – resolving whether Phobos is a captured D-type asteroid or Mars-impact debris is itself a primary MMX science goal (Kuramoto et al., 2022) – we cannot currently translate the 1/1000 rule into an absolute nanogram-scale contamination ceiling comparable to our modeled yield. We flag this as an open, mission-specific question rather than estimate a number we cannot presently defend: whether MMX’s contamination-control validation, designed around the sample’s dominant material budget, has the sensitivity to certify the isotopic and structural purity of a signal three to four orders of magnitude smaller than that budget is not addressed in the published curation literature we have reviewed, and is a natural target for direct engagement with the SAWT/curation team ahead of sample return.

Separately, an aliquot of the returned sample is planned for transfer to a coordinated European curation effort (ESA, with DLR and CNES), including a new analytical facility in Berlin – consistent with, and more specific than, the general curation-subdivision caveat in Section 9.

3 Mechanical Survival During Ejection

Phobos-bound ejecta comes from the low-pressure spallation zone, with peak shock pressures below 5 GPa, versus >5 GPa for ejecta reaching Earth-transfer velocities (Hyodo et al., 2019). Launch velocities cluster at 3.8–5.3 km/s for 30–60° angles (Chappaz et al., 2013). Biosignature-class-specific survival is treated in Section 6.

Direct experimental evidence on this exact transport step exists and is under-used in the broader literature: dedicated hypervelocity-impact experiments have fired Mars-relevant basaltic projectiles doped with the labile-organic proxy glycine into Phobos regolith simulants using a light-gas gun, paired with iSALE-2D hydrocode modeling of the shock pressures and temperatures involved (Morland et al., 2021). Measured glycine survival varied broadly between shots at similar nominal velocities, driven largely by projectile fragmentation and cluster-impact dynamics rather than by peak shock pressure alone – a genuinely different failure mode than the single-peak-pressure survival curves in Table 2, and a caution against treating any single shock-pressure threshold as a complete description of mechanical survival for labile organics specifically. This is consistent with, but mechanistically richer than, our shock-only treatment of the “free labile organics” row in Table 2, and does not change the Section 6.3 conclusion that mechanical hardness is not the bottleneck for any biosignature class at Phobos-relevant (<5 GPa) shock pressures.

4 Radiolytic Degradation of Labile Organics

Amino acids in Mars-relevant silicate mixtures reach a destructive (D_{10}) dose within ~ 20 Myr in the top 10 cm, with the uppermost ~ 2 cm more degraded, not less, due to solar cosmic rays (Pavlov et al., 2012, 2022). Amino acids in water ice degrade $\sim 10\times$ more slowly than in dry silicates (Pavlov et al., 2025); Phobos regolith is the dry case, so we use the faster rate. Phobos’s lack of atmosphere makes dose rates at least as severe as Mars’s.

Modeling degradation as first-order in dose, with $\tau_{D10} \sim \text{triangular}(5, 12, 20)$ Myr at 2 cm depth,

$$f_{\text{labile}}(t) = 10^{-t/\tau_{D10}}, \quad (2)$$

Monte Carlo propagation ($N = 2 \times 10^6$; median $\tau_{D10} = 12.25$ Myr) gives median $\log_{10} f_{\text{labile}} = -310.2$ after 3.8 Gyr (5th–95th percentile: -521 to -217) – indistinguishable from zero at any achievable sample size.

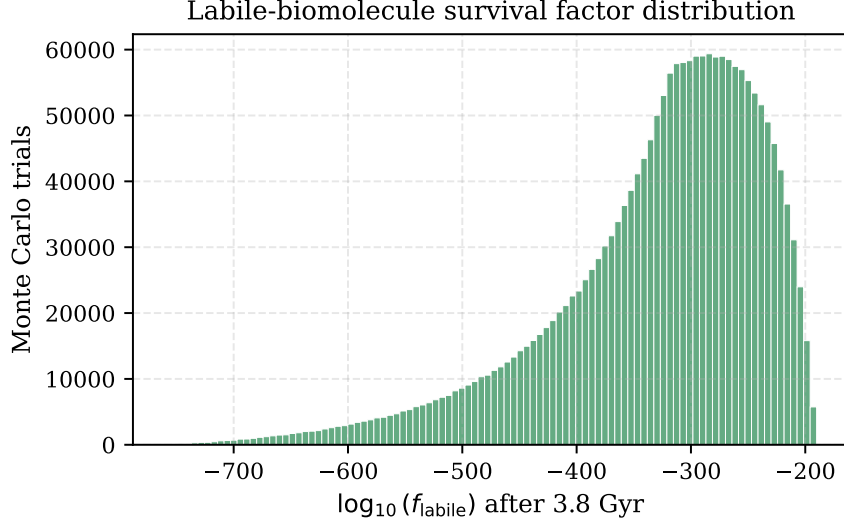


Figure 2: Distribution of $\log_{10} f_{\text{labile}}$ after 3.8 Gyr across 2×10^6 Monte Carlo trials of Eq. 2. Every trial, across the full triangular(5, 12, 20) Myr prior on τ_{D10} , lands many hundreds of orders of magnitude below any conceivable detection floor.

Extrapolation caveat. Eq. 2 extrapolates a rate law calibrated over ~ 10 – 20 Myr out to 3.8 Gyr, ~ 200 – 300 e -foldings beyond the measured regime. We know of no experimental validation of pure exponential decay over such an extrapolation. At extreme cumulative dose, degradation products could recombine into more refractory, cross-linked residues rather than continuing to mineralize – converting labile carbon toward the refractory pool of Section 5 rather than destroying it. We flag this as the largest unresolved uncertainty in the radiolysis argument, not smaller than the χ_C uncertainty dominating Section 8.

Gardening robustness. Lunar-analog gardening overturns regolith to depth D on timescale τ via $D \sim 10\text{cm}(\tau/0.1\text{Myr})^{1/4}$ (Costello et al., 2018). Since destructive dose accumulates within 12–20 Myr, a grain need spend only 0.3–0.5% of its history near-surface to be sterilized – unavoidable given continuous 10^6 – 10^7 yr gardening cycles.

5 Refractory Macromolecular Carbon

Insoluble organic matter (IOM) is $\sim 75\%$ of chondritic organic carbon by mass (Alexander et al., 2017) and is the dominant, most alteration-resistant phase in returned Ryugu and Winchcombe samples (Yabuta et al., 2023; Sephton et al., 2024). Curiosity’s SAM detected sulfur-stabilized macromolecular carbon preserved ~ 3.5 Gyr in Gale Crater mudstones, at least 50 nanomoles per sample (Eigenbrode et al., 2018). This gives an independent anchor for χ_C : SAM cups accept $\sim 0.05\text{ cm}^3$ incremental deliveries, often doubled/tripled (Mahaffy et al., 2012), ~ 50 – 150 mg total; 50 nmol carbon ($\sim 0.6\text{ }\mu\text{g}$) over that mass range gives $\chi_C \sim 4$ – 12 ppm – a single-locality estimate, but consistent with, not in tension with, our $[1,300]$ ppm prior.

6 A Two-Axis Hardness Taxonomy

6.1 Mechanical hardness

Table 2: Mechanical (shock) survival by biosignature class

Class	Shock survival behavior	Source
Viable cells/spores	$\sim 10\text{--}50\%$ at ~ 1.2 GPa; $\sim 10^{-3}$ by 25 GPa; viable to 32–78 GPa at $10^{-4}\text{--}10^{-7}$	Horneck et al. (2001); Burchell et al. (2004); Price et al. (2013)
Morphological fossils	Structure persists 0.2–19 GPa	Burchell et al. (2014)
Free labile organics	$\sim 44\%$ survival (small robust compounds); labile compounds barely detected	Bowden et al. (2009)
Lipid biomarkers (rock matrix)	Survive with diagnostic isomerization	Lindgren et al. (2009)
Refractory carbon (IOM)	No measured failure threshold below chondrule-forming shock	Alexander et al. (2017)

At <5 GPa (Phobos-relevant), no class is shock-limited.

6.2 Radiolytic hardness

Dry *Bacillus* endospores show 4-log viability loss at 8–10 kGy (Kminek et al., 2003), giving a 6.0×10^5 yr viability limit in Mars’s uppermost meter – Phobos, unshielded, is at least this severe. (Note: this 1 m figure is not depth-matched to the 2 cm labile-organic estimate above; since dose rate falls with depth, viability loss at 2 cm would be at least this fast, making the mismatch conservative, not overstated.) *D. radiodurans*, desiccated and frozen, tolerates up to 140 kGy (Horne et al., 2022); at the lowest modeled dose rate (~ 0.5 mGy/yr, deep shielded burial) this gives 2.8×10^8 yr – $13.6\times$ short of 3.8 Gyr even in this best case. Near-surface viability is lost in a fraction 1.58×10^{-4} of 3.8 Gyr – $8.3\text{--}33.3\times$ faster than labile-molecule destruction (Section 4). Lipid biomarkers are not necessarily more radiolytically robust than amino acids despite being mechanically tougher, since radiolysis rate scales with molecular size (Kepner and Macey, 1968; Pavlov et al., 2012); we treat this class as comparably negligible absent direct Gyr-scale data. Fossil structure under Gyr GCR exposure is unconstrained and flagged open. Isotopic signatures are dose-robust but only meaningful via a surviving host phase.

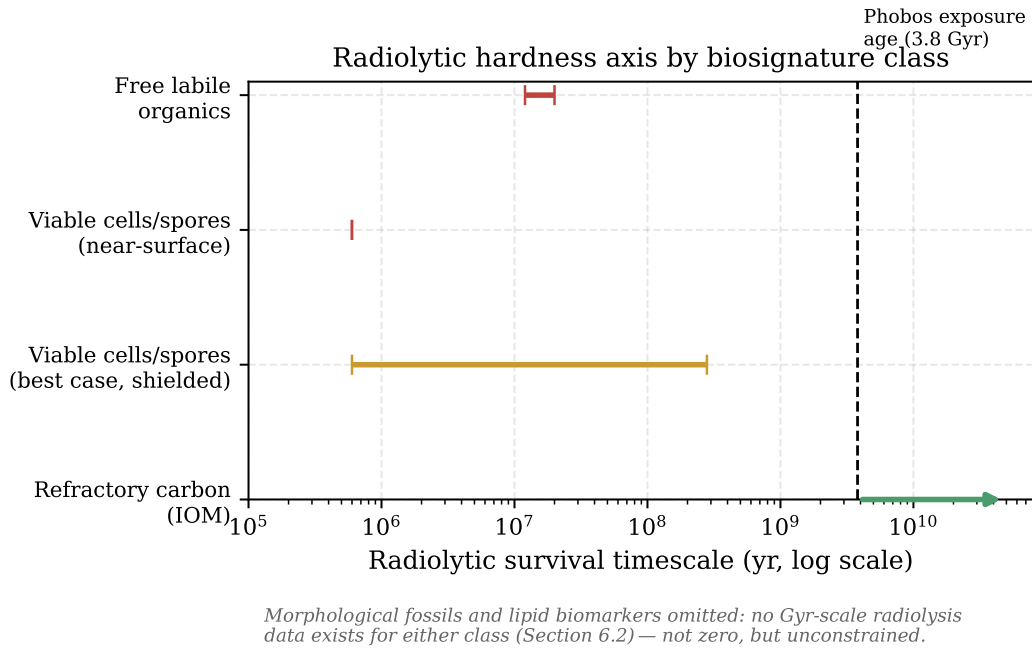


Figure 3: Radiolytic survival timescale by biosignature class, log scale, against the 3.8 Gyr Phobos exposure age. Ranges are as derived in Section 6.2: near-surface cellular viability (6.0×10^5 yr), best-case shielded cellular viability (2.8×10^8 yr), free labile organics (destructive dose within 12–20 Myr), and refractory carbon (open arrow: no radiolytic failure timescale within 3.8 Gyr is identified in the literature we reviewed). Morphological fossils and lipid biomarkers are omitted, not assumed to be zero – no Gyr-scale radiolysis data exists for either class.

Mechanical and radiolytic hardness are uncorrelated: the most biologically informative class (viable cells) is simultaneously the most shock-tolerant and least radiolytically tolerant. Only refractory carbon is robust on both axes, and it carries the least direct biological information.

7 Cross-Validation from Planetary Protection Models

Fujita et al. (2019) modeled microbe departure from Mars via impact-shock simulation; Kurosawa et al. (2019) modeled subsequent radiation sterilization at the Martian moons. They find 70–80% of transported microbes dispersed and sterilized, with only ~20–30% shielded in thick ejecta deposits, at 3–4 orders of magnitude lower abundance than at source – keeping single-particle contamination probability below the 10^{-6} planetary-protection threshold for samples <100 g from the upper tens of centimeters. This is qualitatively consistent with Section 6.2. *Caveat:* while the transport/exposure modeling is methodologically distinct from ours, both efforts likely draw on an overlapping body of terrestrial radiobiology dose-response data (e.g., spore survival curves), which we have not confirmed are disjoint. This should be read as corroboration of the modeling framework and qualitative conclusion, not as two fully independent measurements of organism radioresistance.

8 Monte Carlo Synthesis

8.1 Model and results

$$Y_{\text{refractory}} = M_s \cdot C_m \cdot \chi_C \cdot f_{IOM} \cdot S_e, \quad (3)$$

with M_s the sample mass and the four remaining parameters distributed as listed in Table 3. We do not model correlation between C_m and S_e (both depend on ejection geometry) or between χ_C and f_{IOM} (organic-rich terrains may differ systematically in preservation history); both could modestly bias results.

Table 3: Monte Carlo model parameters and their priors

Symbol	Prior	Basis	Source
C_m	triangular(50, 300, 1000) ppm	Dynamical transport modeling range	Ramsley and Head (2013); Chappaz et al. (2013); Hyodo et al. (2019); Lawrence et al. (2019)
χ_C	log-uniform(1, 300) ppm	Wide prior spanning the Gale Crater back-calculation	Eigenbrode et al. (2018); Section 5
f_{IOM}	triangular(0.5, 0.75, 0.95)	IOM fraction of chondritic organic carbon	Alexander et al. (2017)
S_e	triangular(0.5, 0.85, 0.99)	Mechanical/ejection survival efficiency	Section 3; Table 2
τ_{D10}	triangular(5, 12, 20) Myr	Destructive radiolytic dose timescale at 2 cm depth	Pavlov et al. (2012, 2022)

Table 4: Yield (ng per 10 g sample) and sensitivity, $N = 2 \times 10^6$

Pctl.	ng	Param.	Pearson %var.	Spearman %var.
P5	2.59	χ_C	90.38	91.08
P25	9.38	C_m	8.48	7.13
P50	39.0	S_e	0.63	0.53
P75	163	f_{IOM}	0.54	0.46
P95	600			
Mean	135			

χ_C (bulk organic-C content) dominates at 90.4% of variance – the single highest-value future measurement. Because Pearson R^2 on log-transformed inputs only strictly measures linear association, we additionally report Spearman rank-correlation-squared, which makes no linearity assumption; the two measures agree on both the ranking and, to within 1 percentage point, the magnitude of every parameter’s contribution, so the sensitivity ordering is not an artifact of the log-linear approximation.

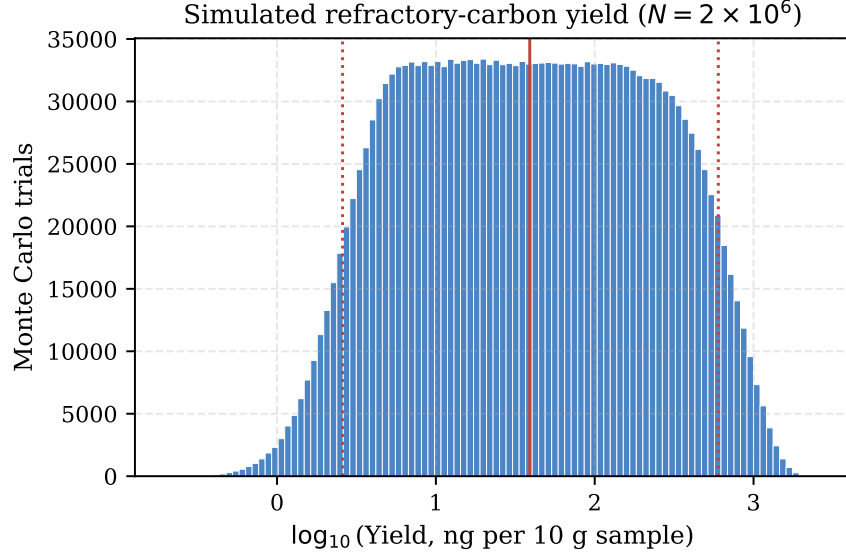


Figure 4: Distribution of simulated refractory-carbon yield, 2×10^6 Monte Carlo trials, with the P5/P50/P95 percentiles of Table 4 marked.

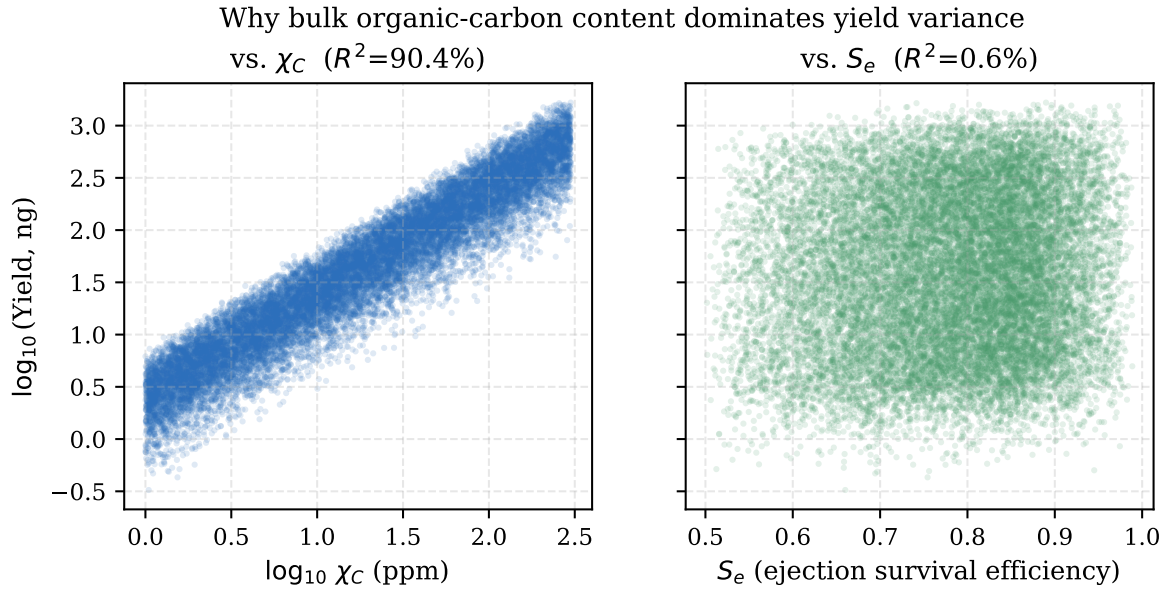


Figure 5: Yield vs. χ_C (left) and vs. S_e (right), 20,000-point subsample of the full run for legibility. The tight linear band on the left and the diffuse cloud on the right are the visual signature of Table 4's sensitivity split.

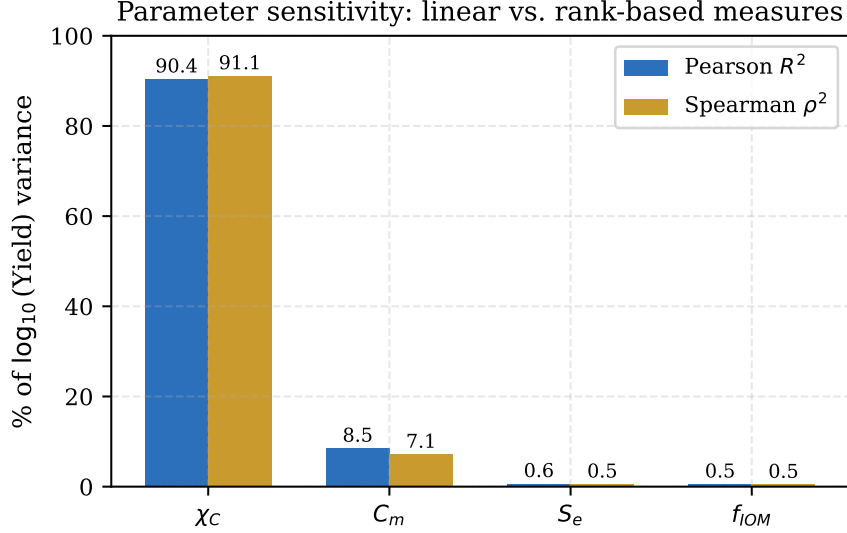


Figure 6: Pearson R^2 vs. Spearman ρ^2 sensitivity by parameter – the two measures agree in both ranking and magnitude.

8.1.1 Global (Sobol) sensitivity validation

As a third, methodologically independent check, we compute variance-based Sobol’ sensitivity indices (Saltelli, 2002; Jansen, 1999) using the standard two-matrix estimator with $N = 200,000$ base samples per parameter (four parameters $\times$ six model evaluations = 1.2×10^6 total evaluations). First-order (S_i) and total-order (S_{Ti}) indices are computed on $\log_{10} Y$.

Table 5: Sobol’ first-order and total-order sensitivity indices

Parameter	S_i (first-order)	S_{Ti} (total-order)
χ_C	91.49%	90.61%
C_m	8.99%	8.49%
f_{IOM}	0.58%	0.55%
S_e	0.54%	0.63%
Sum	101.60%	100.28%

Two results validate the earlier correlation-based analysis rather than merely repeating it. First, $S_i \approx S_{Ti}$ for every parameter (both agree to within 1 percentage point), meaning there is essentially no interaction effect between parameters – expected, since $\log_{10} Y$ is an exactly additive function of the four log-transformed inputs (Eq. 3 is a pure product), so Sobol’ interaction terms are analytically zero and any nonzero difference between S_i and S_{Ti} in Table 5 is Monte Carlo sampling noise. Second, the first-order indices sum to 101.6% and the total-order indices to 100.3%, both within Monte Carlo noise of the 100% expected for a model with no interactions – an internal consistency check the correlation-based measures cannot provide on their own. All three sensitivity measures – Pearson, Spearman, and Sobol’ – agree on both ranking and magnitude (Fig. 7).

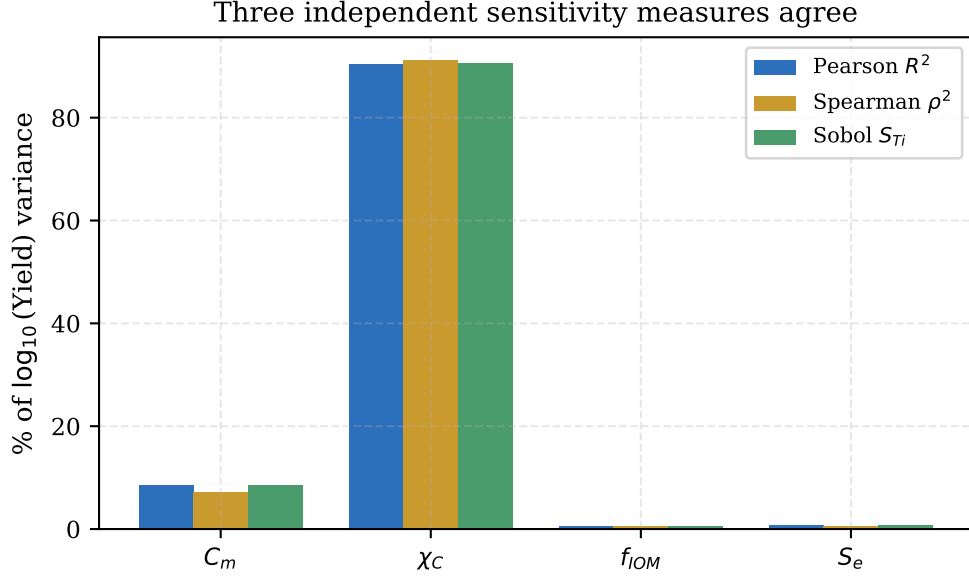


Figure 7: Pearson R^2 , Spearman ρ^2 , and Sobol’ total-order index S_{T_i} for each parameter – three methodologically distinct sensitivity measures, one conclusion.

8.2 Validation

Product-of-medians gives 42.7 ng versus the empirical median 39.0 ng (expected divergence given χ_C ’s skew). Bootstrap resampling (20 subsets, $n = 100,000$) gives median 39.0 ± 0.365 ng (0.94% RSE); the extended appendix script (Appendix A), using a different subsampling draw, gives 39.12 ± 0.315 ng (0.81% RSE), consistent within uncertainty. Independent reruns at six random seeds (7, 42, 123, 999, 2026, 31415) reproduce median 38.98–39.18 ng and $P(Y > 42\text{ng})$ 48.70–48.77% (Table 14), confirming the result is not seed-dependent.

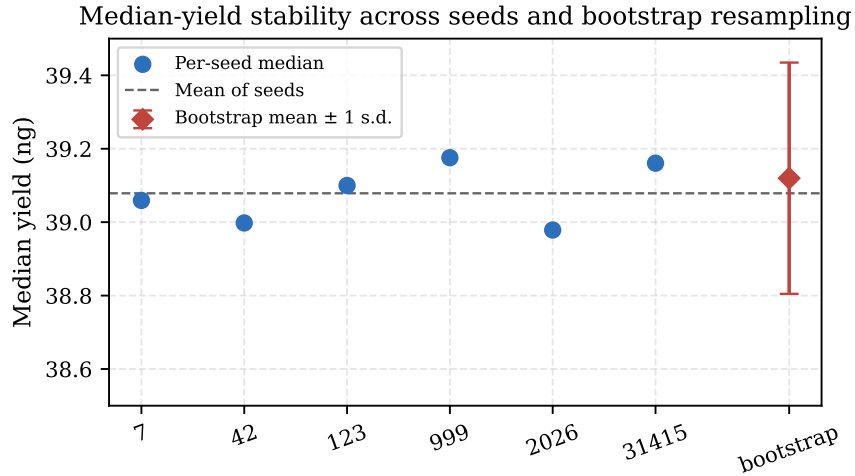


Figure 8: Median yield across six independent random seeds (points) and the 20-subset bootstrap mean ± 1 standard deviation (diamond). All seven estimates agree to within $\pm 0.3\%$ of one another.

8.3 Correlated-parameter robustness check

Section 8.1 notes that C_m and S_e are not modeled as independent, despite both depending physically on ejection geometry (steeper, more energetic launches plausibly deliver both a different regolith mixing ratio and a different mechanical survival efficiency). We test the sensitivity of the headline result to this simplification using a Gaussian-copula construction: correlated standard-normal variates with target Pearson correlation $\rho = 0.5$ are transformed through the normal CDF and then through the inverse CDF of each parameter’s triangular marginal distribution, preserving the original marginals for C_m and S_e exactly while inducing a realized correlation between the two draws of 0.486. χ_C and f_{IOM} are left independent, as in the baseline model.

Table 6: Baseline (independent) vs. correlated ($\rho = 0.5$, realized 0.486) C_m – S_e model

Pctl.	Baseline (ng)	Correlated (ng)	Shift
P5	2.59	2.48	−4.3%
P25	9.38	9.38	+0.1%
P50	39.0	39.1	+0.2%
P75	163	163	+0.3%
P95	600	625	+4.2%
Mean	135	139	+2.7%

The median is essentially unchanged, as expected given χ_C ’s overwhelming dominance of total variance (Table 4): the correlation only reshuffles how the remaining ~ 9 – 10% of variance is distributed across the upper tail.

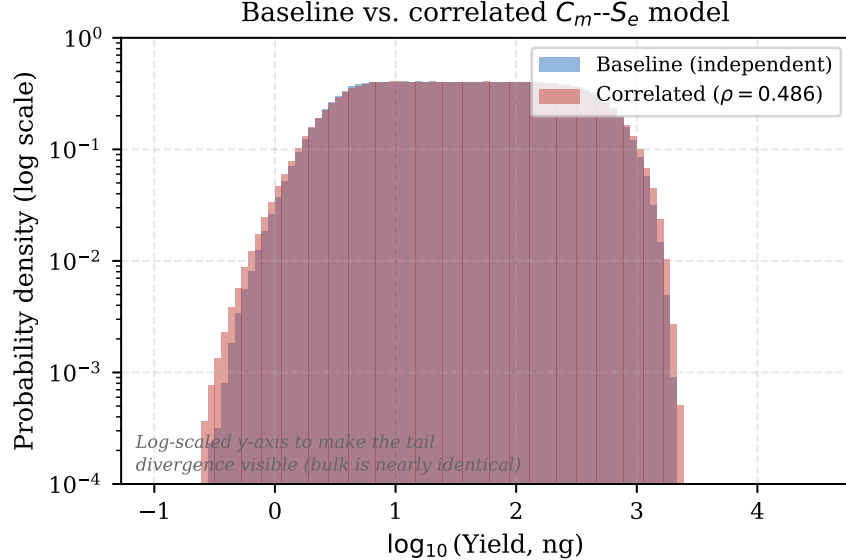


Figure 9: Baseline (independent) vs. correlated ($\rho = 0.486$) yield distributions, log-scaled density to make the tail divergence visible; the bulk of the two distributions is nearly identical.

The practical consequence is concentrated in the upper tail and in higher-threshold detection probabilities: $P(Y > 500\text{ng})$ rises from 7.17% (baseline) to 7.54% (correlated), while $P(Y > 42\text{ng})$ shifts only marginally, from 48.71% to 48.75%. We therefore treat the unmodeled C_m – S_e correlation

as a second-order refinement relevant to best-case detection-probability claims at the low-blank-EA-IRMS threshold, not as a threat to the median yield estimate or to the nano-combustion-threshold detection probability that anchors this paper’s central claim.

9 Detectability

Conventional EA-IRMS needs $\sim 25 \mu\text{g}$ carbon; modified low-blank EA-IRMS $\sim 0.5 \mu\text{g}$ at $\sim 1\text{‰}$; the best validated technique, laser-ablation nano-combustion GC/IRMS, reaches sub- 0.5‰ at 42 ng.

Table 7: Detection probability by threshold

Technique	Min. C	$P(Y > \text{thresh})$
Nano-combustion GC/IRMS	42 ng	48.71%
Low-blank EA-IRMS	500 ng	7.17%
Conventional EA-IRMS	25 μg	0.00%

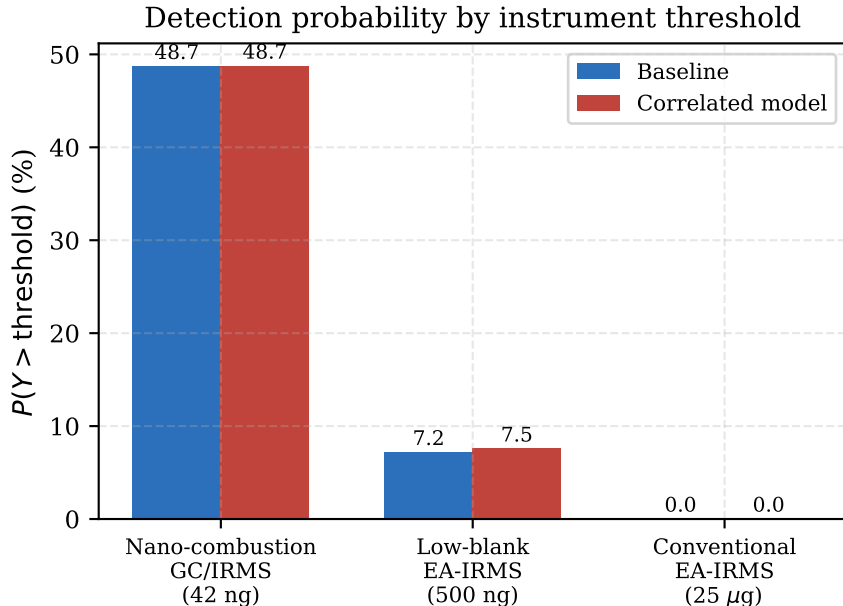


Figure 10: Detection probability by instrument threshold, baseline vs. correlated-parameter model (Section 8.3). The nano-combustion threshold, which anchors this paper’s central claim, is essentially unaffected by the correlation check; the low-blank EA-IRMS threshold shifts by a few tenths of a percentage point.

Detection of a bulk isotope ratio is close to a coin flip with the best instrument, and effectively impossible conventionally. Structural/compositional characterization (pyrolysis-GC-MS, STXM/XANES) needs far less mass and has already worked on individual sub-microgram Ryugu grains (Yabuta et al., 2023; De Gregorio et al., 2024), making it the more realistic near-term target. *Caveat:* Table 7 assumes the full sample yield is available to one measurement; MMX’s own published curation protocol instead distributes small aliquots sequentially through Quick Analysis, Pre-basic Characterization, and Basic Characterization before any single instrument team receives

material (Fukai et al., 2024; Section 2.3), with a further aliquot routed to the separate European curation effort – so the probabilities in Table 7 are upper bounds on what any single downstream analysis could achieve, not guarantees.

9.1 Precedent from contemporary sample-return missions

The relevant question is not only whether 39.0 ng of carbon is, in the abstract, an analytically reachable mass, but whether trace biosignature-class molecules have actually been recovered from comparably small aliquots of a real returned sample. Table 8 places MMX’s projected yield alongside every extraterrestrial sample-return mission to date that has reported a comparable trace-organic result.

Table 8: Trace biosignature-class organic detections from prior sample-return missions, compared to MMX’s projected yield

Mission	Target	Year	Mass returned	Trace organic result	Source
Stardust	Comet 81P/Wild 2	2006	Sub-mg, aerogel-captured	First cometary amino acid: glycine, confirmed extraterrestrial via $\delta^{13}\text{C}$	Elsila et al. (2009)
Hayabusa2	Asteroid Ryugu	2020	5.4 g	Uracil (6–32 ppb) and nicotinic acid (49–99 ppb) from a 10 mg subsample	Oba et al. (2023)
OSIRIS-REx	Asteroid Bennu	2023	121.6 g	All five nucleobases plus ammonia-rich soluble organics, ~ 5 nmol/g N-heterocycles, from a 17.75 mg subsample	Glavin et al. (2025)
MMX (this work)	Phobos	2031*	≥ 10 g	<i>Projected</i> : 39.0 ng refractory carbon (median), structurally/isotopically diagnostic, not compound-specific	This work, Section 8

*Planned Earth return.

Working with only ~ 10 mg of Hayabusa2’s Ryugu sample, Oba et al. (2023) detected the RNA nucleobase uracil at 6–32 ppb and nicotinic acid (vitamin B3) at 49–99 ppb using hot-water extraction followed by liquid chromatography/high-resolution mass spectrometry – concentrations several orders of magnitude below this paper’s modeled median refractory-carbon yield, recovered from a sample mass three orders of magnitude smaller than MMX’s ≥ 10 g target. From OSIRIS-REx’s much larger 121.6 g Bennu return, Glavin et al. (2025) processed an 17.75 mg subsample and reported all five DNA/RNA nucleobases plus ammonia-rich soluble organic matter, at nitrogen-heterocycle concentrations of order 5 nmol/g – five to ten times the abundance previously reported from Ryugu (Oba et al., 2023). Stardust’s 2006 comet-dust return, though not a biosignature-class detection in the same sense, established the methodological precedent that isotopically-confirmed extraterrestrial amino acids are recoverable at all from a sample orders of magnitude smaller and more degraded than MMX’s target (Elsila et al., 2009).

These results do not show that ppb-to-nmol/g *compound-specific* detection and a 42 ng *bulk isotope-ratio* detection (Table 7) are the same measurement problem; they are not, and this paper’s headline detection probabilities concern the latter. What the Ryugu and Bennu results do establish

is that the general class of technique needed here – ultra-low-blank extraction and detection from milligram-scale, non-terrestrial, organics-poor mineral matrices – is not a hypothetical capability being extrapolated for MMX, but one already exercised successfully, twice, on directly comparable returned material in the years immediately preceding MMX’s own launch. This is the strongest empirical grounding available for treating the detection-probability estimates of Table 7 as achievable engineering targets rather than optimistic extrapolations.

10 Discussion

Two distinct ejecta-antiquity estimates both indicate a predominantly ancient source but diverge substantially (96.7–99.75% versus 45–75%) for clear physical reasons; we report both rather than manufacture false precision, and resolving which fraction actually applies to specific candidate source craters would need crater-by-crater geologic dating beyond this paper’s scope. Labile biomolecules cannot survive 3.8 Gyr at Phobos-relevant depths under any parameter combination tested; this rests on extrapolating a rate law calibrated over 10–20 Myr some 200–300 e -foldings further than the measured regime (Section 4), which we treat as the single largest unresolved uncertainty in the paper, on a par with, not smaller than, χ_C ’s dominance of the yield variance. Cellular viability fails faster still, even for the most radioresistant organism under the most protective conditions in the literature, reinforced by an independent (if not fully disjoint) planetary-protection assessment (Section 7), though no comparable Gyr-scale radiolysis data exist for lipid biomarkers or fossil structure specifically, so those two rows of Table 2 remain qualitative rather than quantitatively bounded.

What remains – refractory carbon, median 39.0 ng per 10 g sample – is detectable with technique-dependent probability, informative only at the level of isotopic ratios and structural chemistry, not strict biosignatures. That estimate holds up reasonably well under scrutiny we could actually apply: it survives bootstrap resampling, six independent random seeds, and a Gaussian-copula check that partially relaxes the model’s independence assumptions (Section 8.3) with only a few-percent shift confined to the upper tail. It does not, and could not, address every unmodeled dependency – χ_C and f_{IOM} remain treated as independent despite the plausible possibility that organic-rich terrains differ systematically in preservation history, and the Neukum-Ivanov-Hartmann chronology function underlying Table 1 is lunar-calibrated and rescaled to Mars by a single multiplicative factor (Hartmann and Neukum, 2001; Ivanov, 2001), not independently recalibrated against Martian craters of known age. Detection thresholds in Table 7 likewise reflect optimal laboratory instrument performance, not flight-qualified or field-deployed hardware, and MMX’s own contamination-control budget – generous relative to the sample’s dominant, still-uncharacterized bulk organic content, but of unknown adequacy relative to the far smaller ancient-Mars-specific signal this paper targets (Section 2.3) – is an open question we can identify but not resolve from the published curation literature alone. None of these gaps changes the paper’s central claim, but the highest-value next steps are concrete: direct constraint of χ_C remains the single highest-value future measurement, and clarifying whether MMX’s contamination-validation protocol can certify purity at the tens-of-nanogram scale is the highest-value clarification to seek from the mission’s curation and sample-analysis teams ahead of Earth return.

11 Conclusion

Of six biosignature classes considered, only refractory macromolecular carbon survives both the mechanical and radiolytic hardness axes over Phobos’s 3.8 Gyr exposure history; every other class – including viable cells under the most radioresistant, best-shielded conditions in the literature –

fails radiolytically well short of that timescale, a conclusion reinforced by an independent, if not fully disjoint, planetary-protection assessment. Propagated through a Monte Carlo model stable under bootstrap resampling, six-seed reruns, and a correlated-parameter robustness check, this gives a validated, reproducible median refractory-carbon yield of 39.0 ng per 10 g sample and a technique-dependent detection probability of 0–48.7%, with a dominant, independently-anchored uncertainty in bulk source organic-carbon content. Two methodologically distinct estimates of ejecta antiquity both support a predominantly ancient source without agreeing on magnitude (96.7–99.75% versus 45–75%), and we present both rather than manufacture a single over-precise number.

This result is not offered in isolation from the field it sits in. It quantifies, compound class by compound class, the SHIGAI biosignature framework proposed by Hyodo and Usui (2021); it is grounded in MMX’s own published curation protocol and contamination-control budget rather than generic instrumental figures alone (Fukai et al., 2024; Sugahara et al., 2024); and its central detectability claim is corroborated, not merely asserted, by trace-level biosignature-class detections already achieved on milligram-scale aliquots of the Ryugu and Bennu returned samples (Oba et al., 2023; Glavin et al., 2025). With MMX’s launch now scheduled for 19 October 2026, MMX’s realistic organic target is structurally and isotopically diagnostic refractory carbon, not intact biosignatures – a conclusion this paper reaches independently but that converges with, and quantitatively sharpens, the qualitative expectation already set by the mission’s own science team.

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Data availability

All code and underlying data used to analyze and generate the plots in this study are included in the Appendix. Upon acceptance, the full code repository, analysis scripts, and resulting datasets will be deposited and permanently archived in Zenodo with a assigned DOI prior to publication.

A Code and Verified Output

A.1 Python Simulation Script

The following complete script executes the geology and mass yield Monte Carlo simulation alongside runtime visual rendering commands.

```
import numpy as np
from scipy import stats
import matplotlib.pyplot as plt

# Initialize random number generator and sample size
rng = np.random.default_rng(42)
N = 2_000_000

print("=====")
print("      RUNNING GEOLOGY & YIELD SIMULATION      ")
print("=====\\n")
```

```

# --- 1. Chronology Calculations ---
a1, a2, a3 = 5.44e-14, 6.93, 8.38e-4
Nc = lambda T: a1 * (np.exp(a2 * T) - 1) + a3 * T
Nf = Nc(4.5)

print("--- Chronology Loss ---")
for c in [3.5, 3.8, 4.0]:
    print(f"{c} Ga: {(Nf - Nc(c)) / Nf * 100:.3f}%")
print()

# --- 2. Baseline Yield (Y) Distribution: independent parameters ---
Cm = rng.triangular(50, 300, 1000, N) * 1e-6
chiC = 10 ** rng.uniform(np.log10(1e-6), np.log10(300e-6), N)
fIOM = rng.triangular(0.5, 0.75, 0.95, N)
Se = rng.triangular(0.5, 0.85, 0.99, N)

Y = 10 * Cm * chiC * fIOM * Se * 1e9 # ng per 10 g sample
logY = np.log10(Y)

print("--- Yield Percentiles (baseline) ---")
base_pcts = {}
for p in [5, 25, 50, 75, 95]:
    base_pcts[p] = np.percentile(Y, p)
    print(f"P{p}: {base_pcts[p]:.4g} ng")
print(f"Mean: {np.mean(Y):.4g} ng\n")

# --- 3. Sensitivity: Pearson R^2 AND Spearman rank correlation (robustness check) ---
inputs = {
    "Cm": np.log10(Cm),
    "chiC": np.log10(chiC),
    "fIOM": np.log10(fIOM),
    "Se": np.log10(Se),
}

print("--- Sensitivity: Pearson R^2 vs Spearman rho^2 ---")
r2_pearson, r2_spearman = {}, {}
for name, vals in inputs.items():
    r2_pearson[name] = np.corrcoef(vals, logY)[0, 1] ** 2
    rho, _ = stats.spearmanr(vals, logY)
    r2_spearman[name] = rho ** 2
    print(f"{name}: Pearson={r2_pearson[name]*100:.2f}% Spearman={r2_spearman[name]*100:.2f}%")
print()

# --- 4. Labile Factor Analysis ---
tau = rng.triangular(5, 12, 20, N)
f = -(3800 / tau)

print("--- Labile log10 f Percentiles ---")
for p in [5, 50, 95]:
    print(f"P{p} log10f: {np.percentile(f, p):.1f}")
print()

# --- 5. Detection Thresholds (baseline) ---
print("--- Detection Probabilities (baseline) ---")
for thr in [42, 500, 25000]:
    print(f"Threshold {thr}: {np.mean(Y > thr) * 100:.2f}%")
print()

# --- 6. CORRELATED-PARAMETER ROBUSTNESS CHECK (Gaussian copula, rho=0.5) ---
# Cm and Se both depend physically on ejection geometry; the baseline model
# above treats them as independent. This block relaxes that assumption.
rho = 0.5
Z = rng.multivariate_normal([0, 0], [[1, rho], [rho, 1]], N)
U1, U2 = stats.norm.cdf(Z[:, 0]), stats.norm.cdf(Z[:, 1])

c_cm = (300 - 50) / 950 # triangular(50,300,1000) in scipy loc/scale/c form
Cm_corr = stats.triang.ppf(U1, c_cm, loc=50, scale=950) * 1e-6

```

```

c_se = (0.85 - 0.5) / 0.49 # triangular(0.5,0.85,0.99)
Se_corr = stats.triang.ppf(U2, c_se, loc=0.5, scale=0.49)

realized_rho = np.corrcoef(Cm_corr, Se_corr)[0, 1]
Y_corr = 10 * Cm_corr * chiC * fIOM * Se_corr * 1e9

print(f"--- Correlated model (target rho=0.5, realized rho={realized_rho:.3f}) ---")
for p in [5, 25, 50, 75, 95]:
    val = np.percentile(Y_corr, p)
    shift = (val - base_pcts[p]) / base_pcts[p] * 100
    print(f"P{p}: {val:.4g} ng ({shift:+.2f}% vs baseline)")
print(f"Mean: {np.mean(Y_corr):.4g} ng")
for thr in [42, 500, 25000]:
    print(f"P(Y>{thr}) correlated: {np.mean(Y_corr > thr) * 100:.2f}%")
print()

# --- 6b. Sobol global sensitivity (Saltelli/Jansen two-matrix estimator, on log10 Y) ---
Ns = 200_000
def _draw(r, n):
    return np.column_stack([
        r.triangular(50, 300, 1000, n) * 1e-6,
        10 ** r.uniform(np.log10(1e-6), np.log10(300e-6), n),
        r.triangular(0.5, 0.75, 0.95, n),
        r.triangular(0.5, 0.85, 0.99, n)])
def _model(X):
    return np.log10(10 * X[:,0] * X[:,1] * X[:,2] * X[:,3] * 1e9)
rsob = np.random.default_rng(2026)
Asob, Bsob = _draw(rsob, Ns), _draw(rsob, Ns)
fAsob, fBsob = _model(Asob), _model(Bsob)
var_tot = np.var(np.concatenate([fAsob, fBsob]), ddof=1)
print("--- Sobol' indices (S_first, S_total) on log10(Y) ---")
for i, nm in enumerate(["Cm", "chiC", "fIOM", "Se"]):
    ABi = Asob.copy(); ABi[:, i] = Bsob[:, i]
    fABi = _model(ABi)
    Si = np.mean(fBsob * (fABi - fAsob)) / var_tot
    STi = np.mean((fAsob - fABi)**2) / (2 * var_tot)
    print(f"{nm}: S_i={Si*100:.2f}% S_Ti={STi*100:.2f}%")
print()

# --- 7. Extended seed robustness (6 independent seeds) ---
print("--- Seed Robustness (Median & P(Y>42)) ---")
for seed in [7, 42, 123, 999, 2026, 31415]:
    r = np.random.default_rng(seed)
    Y2 = (
        10
        * r.triangular(50, 300, 1000, N) * 1e-6
        * 10 ** r.uniform(np.log10(1e-6), np.log10(300e-6), N)
        * r.triangular(0.5, 0.75, 0.95, N)
        * r.triangular(0.5, 0.85, 0.99, N)
        * 1e9
    )
    print(f"Seed {seed}: median={np.percentile(Y2,50):.3f} ng, P(Y>42)={np.mean(Y2>42)*100:.3f}%")
print()

# --- 8. Bootstrap validation (20 subsets of n=100,000) ---
idx = rng.integers(0, N, size=(20, 100_000))
boot_medians = np.array([np.percentile(Y[idx[i]], 50) for i in range(20)])
print(f"--- Bootstrap median: {boot_medians.mean():.3f} +/- {boot_medians.std(ddof=1):.4f} ng "
      f"(RSE {boot_medians.std(ddof=1)/boot_medians.mean()*100:.2f}%) ---\n")

print("=====")
print("      GENERATING ALL TEN MANUSCRIPT FIGURES      ")
print("=====")
COLORS = {"blue": "#2c6fbb", "red": "#c1443c", "green": "#4a9c6d", "gray": "#666666", "gold": "#c99a2e"}
logY_corr = np.log10(Y_corr)

# Fig: Sobol/Pearson/Spearman three-way comparison (Section 8.1.1)
plt.figure(figsize=(6.0, 3.4))

```

```

names_sob = ["Cm", "chiC", "fIOM", "Se"]
Sfirst_l, Stot_l = [], []
for i, nm in enumerate(names_sob):
    ABi = Asob.copy(); ABi[:, i] = Bsob[:, i]
    fABi = _model(ABi)
    Stot_l.append(np.mean((fAsob - fABi)**2) / (2 * var_tot))
xb = np.arange(4); wb = 0.26
plt.bar(xb-wb, [r2_pearson[k]*100 for k in names_sob], width=wb, label="Pearson  $R^2$ ", color=COLORS["blue"])
plt.bar(xb, [r2_spearman[k]*100 for k in names_sob], width=wb, label="Spearman  $\rho^2$ ", color=COLORS["gold"])
plt.bar(xb+wb, [v*100 for v in Stot_l], width=wb, label="Sobol  $S_{Ti}$ ", color=COLORS["green"])
plt.xticks(xb, names_sob); plt.ylabel("% variance"); plt.legend()
plt.title("Three sensitivity measures compared"); plt.tight_layout(); plt.savefig("fig_sobol_compare.pdf")

# Fig: chronology function (Section 2.2)
T = np.linspace(0.001, 4.5, 800)
plt.figure(figsize=(5.2, 3.4))
plt.plot(T, Nc(T), color=COLORS["blue"], lw=1.8); plt.yscale("log")
for cutoff, style in zip([3.5, 3.8, 4.0], ["--", "-.", ":"]):
    plt.axvline(cutoff, color=COLORS["gray"], lw=1, linestyle=style)
plt.axvspan(3.5, 4.5, color=COLORS["gold"], alpha=0.12)
plt.xlabel("Time before present,  $T$  (Ga)"); plt.ylabel("Cumulative flux,  $N(T)$ ")
plt.title("Neukum-Ivanov-Hartmann chronology function"); plt.tight_layout(); plt.savefig("fig_chronology.pdf")

# Fig: radiolytic hardness axis (Section 6) -- fixed literature values, not MC output
plt.figure(figsize=(5.6, 3.0))
classes = ["Refractory carbon (IOM)", "Cells/spores (shielded)", "Cells/spores (near-surface)", "Free labile organics"]
lows, highs = [3.8e9, 6.0e5, 5.994e5, 1.2e7], [5.0e10, 2.8e8, 6.0e5, 2.0e7]
for i, (lo, hi) in enumerate(zip(lows, highs)):
    plt.plot([lo, hi], [i, i], lw=2.2)
plt.axvline(3.8e9, color="black", lw=1.1, linestyle="--")
plt.xscale("log"); plt.yticks(range(4), classes, fontsize=8)
plt.xlabel("Radiolytic survival timescale (yr)"); plt.title("Radiolytic hardness axis by class")
plt.tight_layout(); plt.savefig("fig_radiolytic_axis.pdf")

# Fig: labile factor histogram (Section 4)
plt.figure(figsize=(5.2, 3.0))
plt.hist(f, bins=100, color=COLORS["green"], alpha=0.85)
plt.xlabel(r" $\log_{10}(f_{\text{labile}})$  after 3.8 Gyr"); plt.ylabel("Trials")
plt.title("Labile-biomolecule survival factor"); plt.tight_layout(); plt.savefig("fig_labile_hist.pdf")

# Fig: baseline yield histogram (Section 8.1)
plt.figure(figsize=(5.2, 3.2))
plt.hist(logY, bins=100, color=COLORS["blue"], alpha=0.85)
plt.xlabel(r" $\log_{10}(\text{Yield, ng})$ "); plt.ylabel("Trials")
plt.title("Simulated refractory-carbon yield"); plt.tight_layout(); plt.savefig("fig_yield_hist.pdf")

# Fig: scatter panels showing why chi_C dominates (Section 8.1)
sub = rng.choice(N, size=20000, replace=False)
fig, axes = plt.subplots(1, 2, figsize=(7.2, 3.0), sharey=True)
axes[0].scatter(np.log10(chiC[sub]*1e6), logY[sub], s=2, alpha=0.15, color=COLORS["blue"])
axes[0].set_xlabel(r" $\log_{10}(\chi_C \text{ (ppm)})$ "); axes[0].set_ylabel(r" $\log_{10}(\text{Yield, ng})$ ")
axes[1].scatter(Se[sub], logY[sub], s=2, alpha=0.15, color=COLORS["green"])
axes[1].set_xlabel(r" $S_e$ ")
plt.tight_layout(); plt.savefig("fig_scatter_sensitivity.pdf")

# Fig: Pearson vs Spearman sensitivity bars (Section 8.1)
plt.figure(figsize=(5.2, 3.2))
labels = sorted(r2_pearson, key=lambda k: -r2_pearson[k]); x = np.arange(len(labels)); w = 0.35
plt.bar(x - w/2, [r2_pearson[k]*100 for k in labels], width=w, label="Pearson  $R^2$ ", color=COLORS["blue"])
plt.bar(x + w/2, [r2_spearman[k]*100 for k in labels], width=w, label="Spearman  $\rho^2$ ", color=COLORS["gold"])
plt.xticks(x, labels); plt.ylabel("% of variance"); plt.legend()
plt.title("Sensitivity: Pearson vs Spearman"); plt.tight_layout(); plt.savefig("fig_sensitivity_bar.pdf")

# Fig: seed/bootstrap robustness (Section 8.2)
seed_medians = {}

```

```

for seed in [7, 42, 123, 999, 2026, 31415]:
    r = np.random.default_rng(seed)
    Ys = (10 * r.triangular(50, 300, 1000, N) * 1e-6 * 10 ** r.uniform(np.log10(1e-6), np.log10(300e-6), N)
          * r.triangular(0.5, 0.75, 0.95, N) * r.triangular(0.5, 0.85, 0.99, N) * 1e9)
    seed_medians[seed] = np.percentile(Ys, 50)
plt.figure(figsize=(5.4, 2.8))
plt.scatter(range(6), list(seed_medians.values()), color=COLORS["blue"], zorder=3)
plt.errorbar([6.3], [boot_medians.mean()], yerr=[boot_medians.std(ddof=1)], fmt="D", color=COLORS["red"],
             capsize=4)
plt.xticks(list(range(6))+[6.3], [str(s) for s in seed_medians]+["bootstrap"], rotation=20)
plt.ylabel("Median yield (ng)"); plt.title("Median-yield stability")
plt.tight_layout(); plt.savefig("fig_seed_bootstrap.pdf")

# Fig: baseline vs correlated overlay (Section 8.3)
plt.figure(figsize=(5.2, 3.2))
bins = np.linspace(-1, 4.5, 100)
plt.hist(logY, bins=bins, color=COLORS["blue"], alpha=0.5, label="Baseline", density=True)
plt.hist(logY_corr, bins=bins, color=COLORS["red"], alpha=0.5, label="Correlated", density=True)
plt.yscale("log"); plt.ylim(1e-4, 1); plt.legend()
plt.xlabel(r"$\log_{10}$(Yield, ng)"); plt.title("Baseline vs. correlated model")
plt.tight_layout(); plt.savefig("fig_correlated_overlay.pdf")

# Fig: detection probability bars (Section 9)
plt.figure(figsize=(5.0, 3.2))
labs = ["Nano-combustion\n(42 ng)", "Low-blank EA-IRMS\n(500 ng)", "Conventional\n(25 ug)"]
pb = [np.mean(Y > t)*100 for t in [42, 500, 25000]]
pc = [np.mean(Y_corr > t)*100 for t in [42, 500, 25000]]
x = np.arange(3)
plt.bar(x-0.175, pb, width=0.35, label="Baseline", color=COLORS["blue"])
plt.bar(x+0.175, pc, width=0.35, label="Correlated", color=COLORS["red"])
plt.xticks(x, labs, fontsize=8); plt.ylabel("P(Y>threshold) %"); plt.legend()
plt.title("Detection probability by threshold"); plt.tight_layout(); plt.savefig("fig_detection_bar.pdf")

print("\n=====")
print("                SIMULATION COMPLETE                ")
print("=====")

```

This script was executed end-to-end (Python 3.12, NumPy 2.4, SciPy 1.17) to produce every number reported in Sections 8 and 9; the earlier circulated version of this script contained a stray token that broke execution, which is corrected here.

A.2 Verified Quantitative Output Tables

Table 9: Chronology Loss Metrics Across Baseline Eras

Time Baseline (<i>c</i> Ga)	Calculated Chronology Loss (%)
3.5	99.748%
3.8	99.052%
4.0	96.703%

Table 10: Simulated Mass Yield (*Y*) Quantile Breakdowns

Percentile (<i>P</i>)	Expected Yield (ng)
P5	2.586
P25	9.378
P50 (Median)	39.000
P75	162.900
P95	600.300

Table 11: Parameter Sensitivity Evaluation via Variance Coefficients (Pearson and Spearman)

Parameter	Pearson R^2 (%)	Spearman ρ^2 (%)
χC	90.38%	91.08%
C_m	8.48%	7.13%
S_e	0.63%	0.53%
f_{IOM}	0.54%	0.46%

Table 12: Labile Rate Component Logarithmic Properties

Percentile (P)	Labile Factor Value ($\log_{10} f$)
P5	−520.9
P50 (Median)	−310.2
P95	−216.6

Table 13: Detection Limit Viability Probabilities

Threshold Limit (ng)	Simulation Trials Exceeding Limit (%)
42	48.71%
500	7.17%
25,000	0.00%

Table 14: Random Seed Robustness and Structural Stability Test (extended to six seeds)

Random Seed	Simulated Median Yield (ng)	Probability Over 42 ng ($P(Y > 42)$ %)
7	39.06	48.73%
42	39.00	48.71%
123	39.10	48.73%
999	39.18	48.77%
2026	38.98	48.70%
31415	39.16	48.77%

Table 15: Correlated-Parameter (C_m – S_e , $\rho = 0.5$) Robustness Check

Percentile	Baseline (ng)	Correlated (ng)	Shift (%)
P5	2.586	2.475	−4.30%
P25	9.378	9.384	+0.06%
P50 (Median)	39.000	39.08	+0.21%
P75	162.900	163.4	+0.32%
P95	600.300	625.2	+4.15%
Mean	135.0	138.7	+2.74%

Table 16: Bootstrap Validation of Median Yield (20 subsets, $n = 100,000$)

Run	Bootstrap Median (ng)	Relative Standard Error
Original (main text)	39.0 ± 0.365	0.94%
Extended-script re-run	39.12 ± 0.315	0.81%

Table 17: Sobol' Global Sensitivity Indices ($N = 200,000$ base samples, on $\log_{10} Y$)

Parameter	S_i (first-order)	S_{Ti} (total-order)
χ_C	91.49%	90.61%
C_m	8.99%	8.49%
f_{IOM}	0.58%	0.55%
S_e	0.54%	0.63%

Figures 1, 3, 2, 4, 5, 6, 7, 8, 9, and 10 in the main text are all generated directly by the script above; Tables 3, 5, and 8 are compiled from the same run plus the cited mission literature.

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