Supporting Information

Synthesis and Reactivity of Zr MOFs Assembled from P^NN^NP -Ru Pincer Complexes Abebu A. Kassie[†], Pu Duan[‡], Matthew B. Gray[†], Klaus Schmidt-Rohr[‡], Patrick M. Woodward[†], Casey R. Wade*[†]

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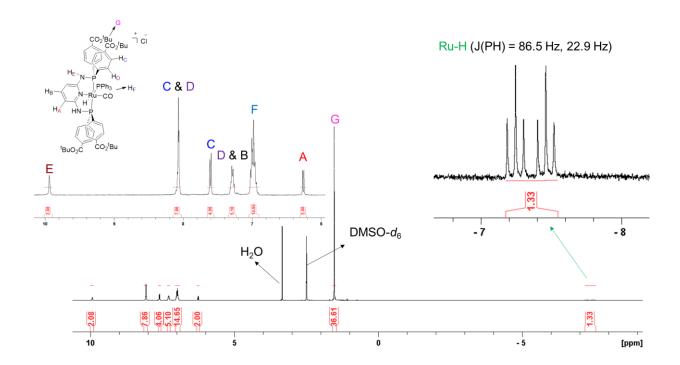
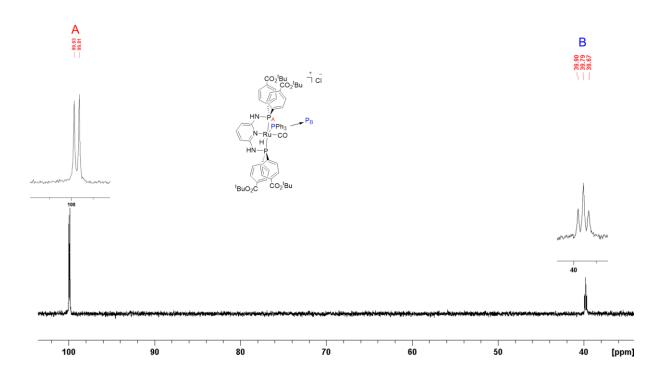


Figure S1. ¹H NMR spectrum of [^tBu₄L-RuH(CO)(PPh₃)]Cl in DMSO-d₆.



 $\textbf{Figure S2.} \ ^{31}P\{^{1}H\} \ NMR \ spectrum \ of \ [^{t}Bu_{4}L-RuH(CO)(PPh_{3})]Cl \ in \ DMSO-d_{6}.$

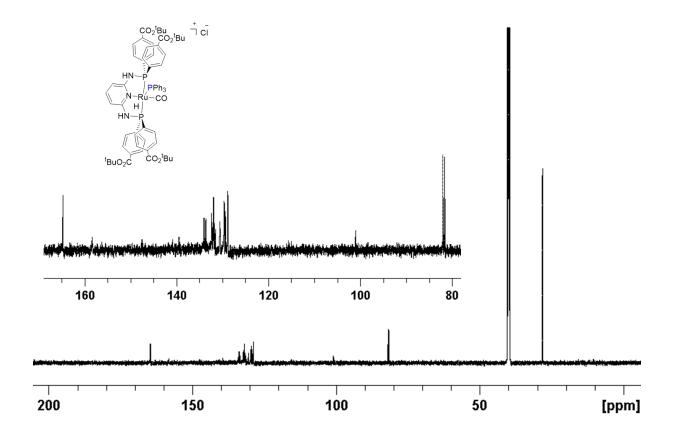


Figure S3. ¹³C{¹H} NMR spectrum of [^tBu₄L-RuH(CO)(PPh₃)]Cl in DMSO-d₆.

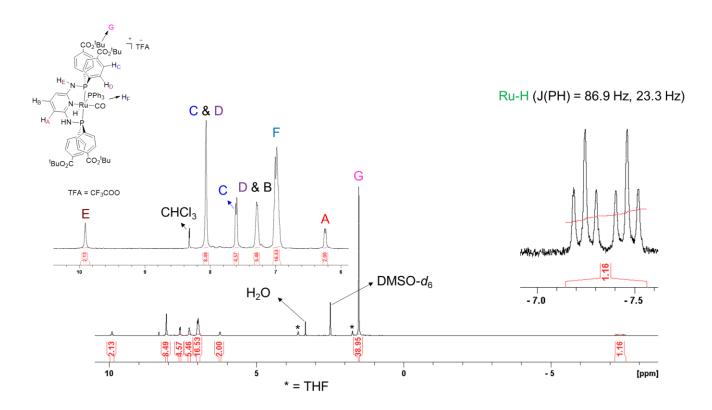
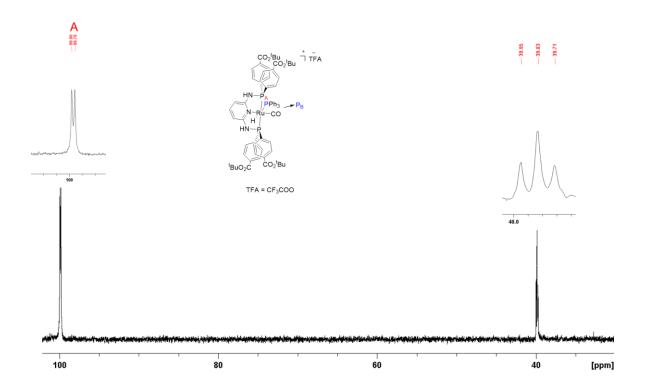


Figure S4. ¹H NMR spectrum of [^tBu₄L-RuH(CO)(PPh₃)]TFA in DMSO-d₆.



 $\textbf{Figure S5.} \ ^{31}P\{^{1}H\} \ NMR \ spectrum \ of \ [^{t}Bu_{4}L-RuH(CO)(PPh_{3})]TFA \ in \ DMSO-d_{6}.$

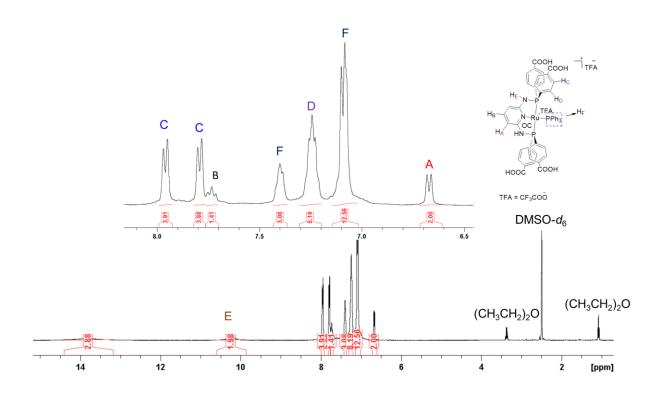


Figure S6. ¹H NMR spectrum of [H₄L-Ru(TFA)(CO)(PPh₃)]TFA in DMSO-d₆.

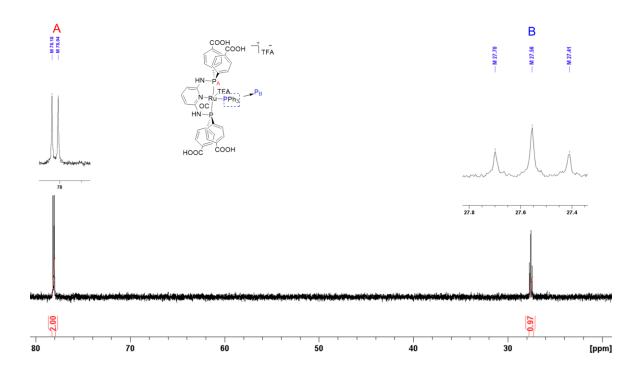


Figure S7. ³¹P {¹H} NMR spectrum of [H₄L-Ru(TFA)(CO)(PPh₃)]TFA in DMSO-d₆.

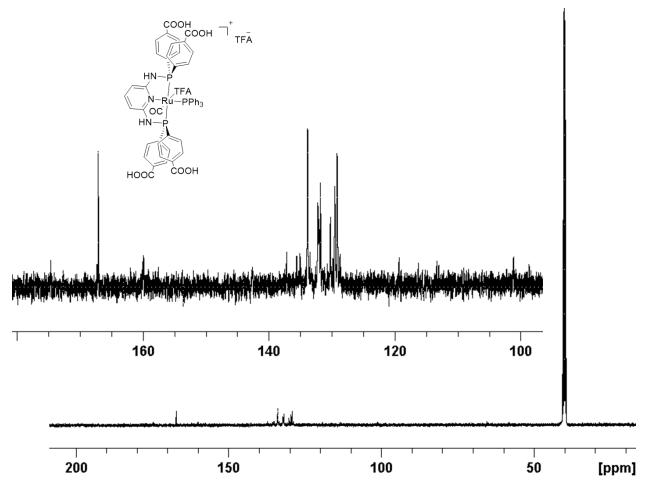


Figure S8. ¹³C { ¹H } NMR spectrum of [H₄L-Ru(TFA)(CO)(PPh₃)]TFA in DMSO-d₆.

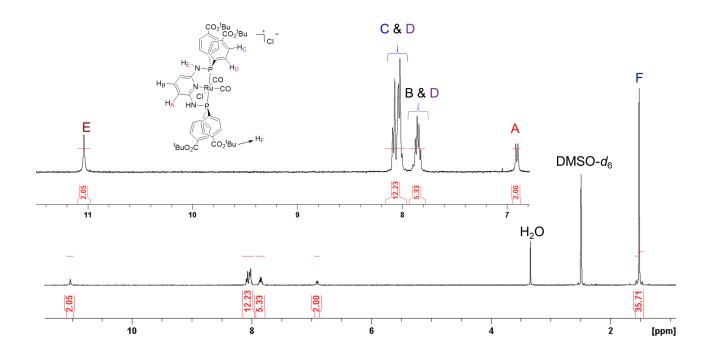


Figure S9. ¹H NMR spectrum of [^tBu₄L-RuCl(CO)₂]Cl in DMSO-d₆.

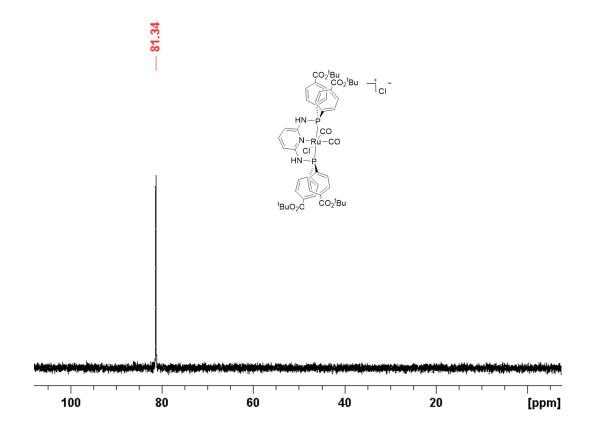


Figure S10. ³¹P { ¹H } NMR spectrum of [^tBu₄L-RuCl(CO)₂]Cl in DMSO-d₆

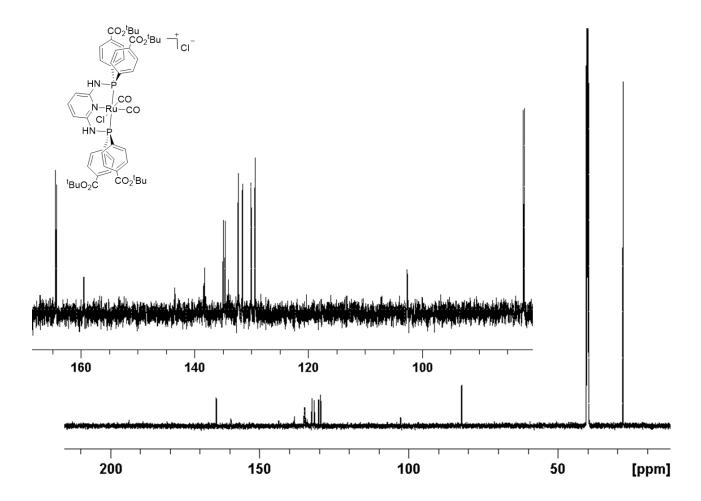


Figure S11. ¹³C { ¹H } NMR spectrum of [^tBu₄L-RuCl(CO)₂]Cl in DMSO-d₆

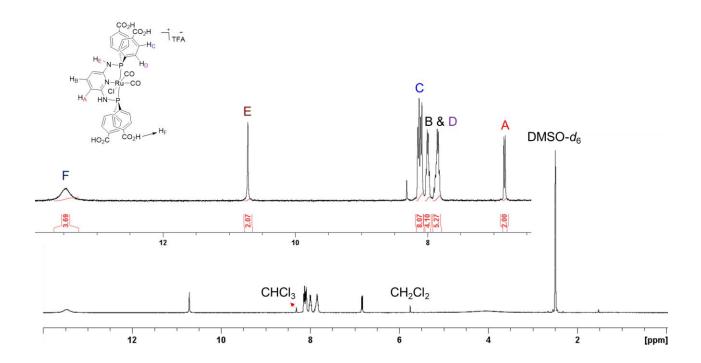


Figure S12. ¹H NMR spectrum of [H₄L-RuCl(CO)₂]TFA in DMSO-d₆.

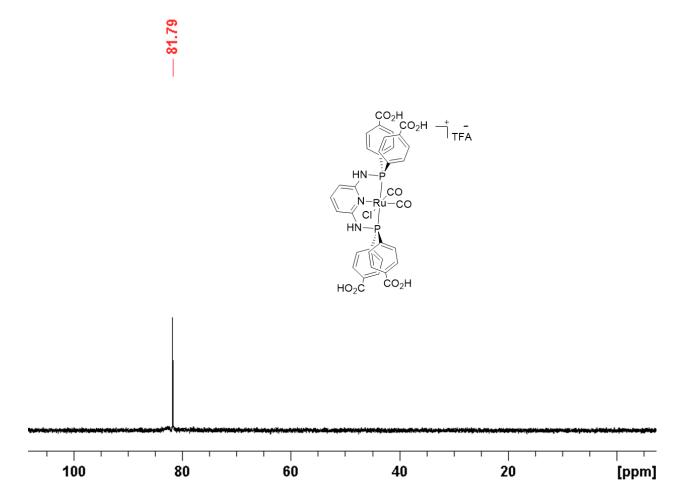


Figure S13. ^{31}P { ^{1}H } NMR spectrum of [H₄L-RuCl(CO)₂]TFA in DMSO-d₆.

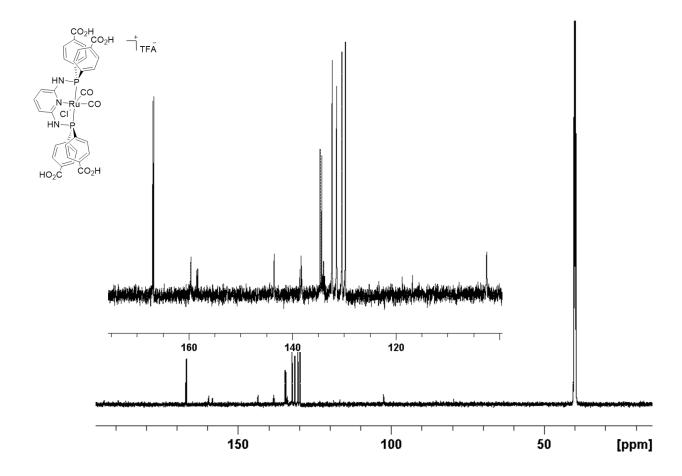


Figure S14. ¹³C {¹H} NMR spectrum of [H₄L-RuCl(CO)₂]TFA in DMSO-d₆.

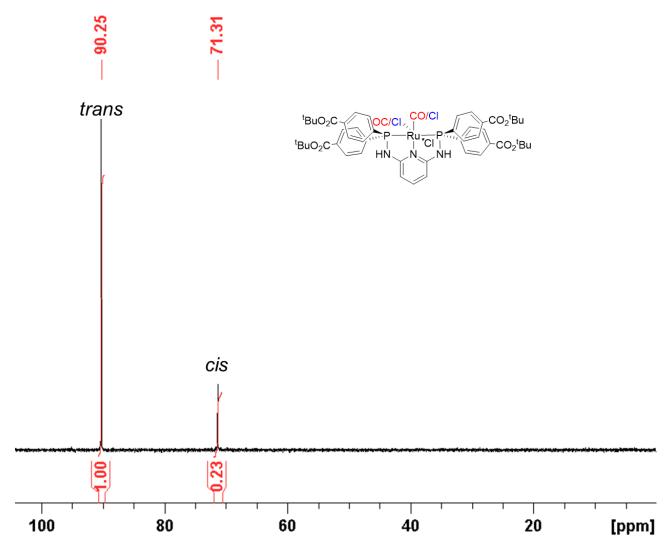


Figure S15. ³¹P { ¹H} NMR spectrum of *cis/trans*-^tBu₄L-RuCl₂(CO) in DMSO-d6.

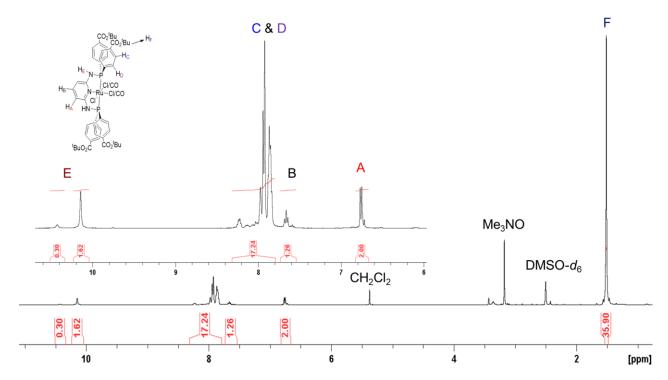


Figure S16. ¹H NMR spectrum of *cis/trans*-^tBu₄L-RuCl₂(CO) in DMSO-d₆.

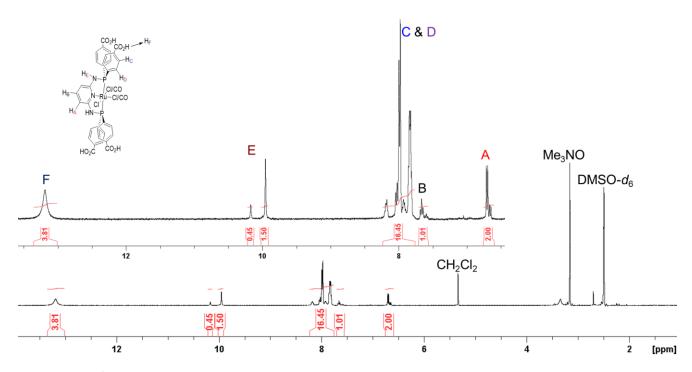


Figure S17. ¹H NMR spectrum of cis/trans-H₄L-RuCl₂(CO) in DMSO-d₆

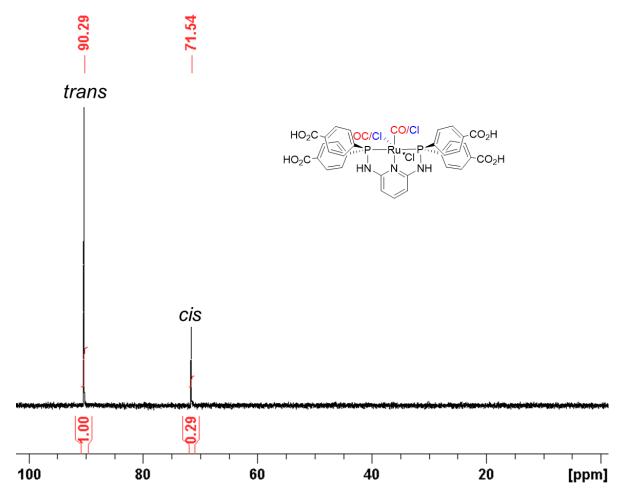


Figure S18. ³¹P { ¹H} NMR spectrum of *cis/trans*- H₄L-RuCl₂(CO) in DMSO-d₆

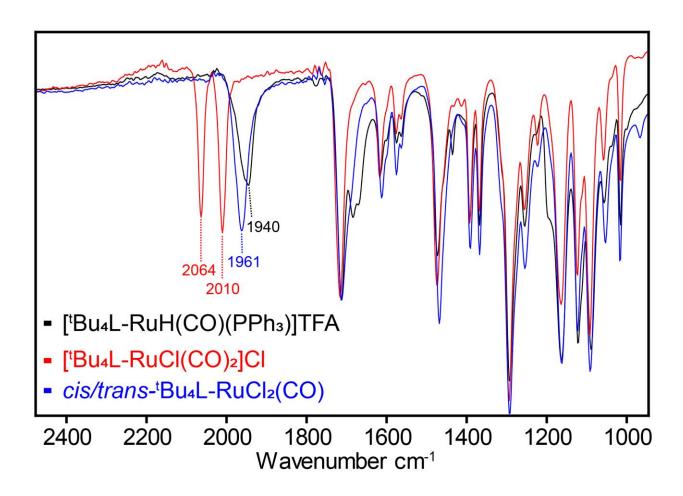


Figure S19. ATR-IR spectra of ^tBu₄L-Ru-P^NN^NP pincer complexes

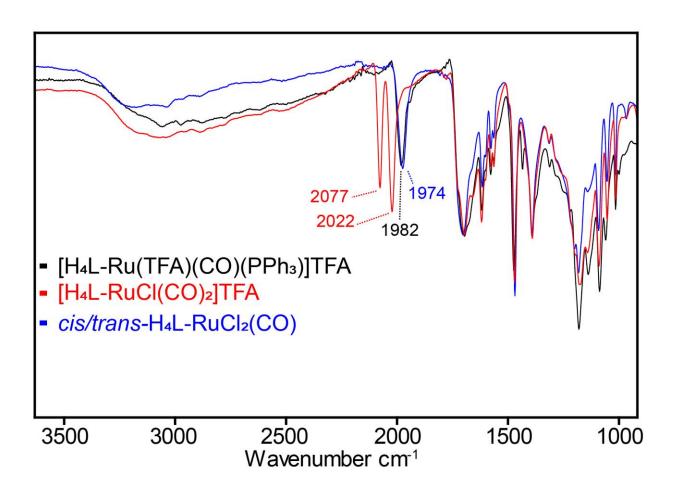


Figure S20. ATR-IR spectra of H₄L-Ru-P^NN^NP pincer complexes

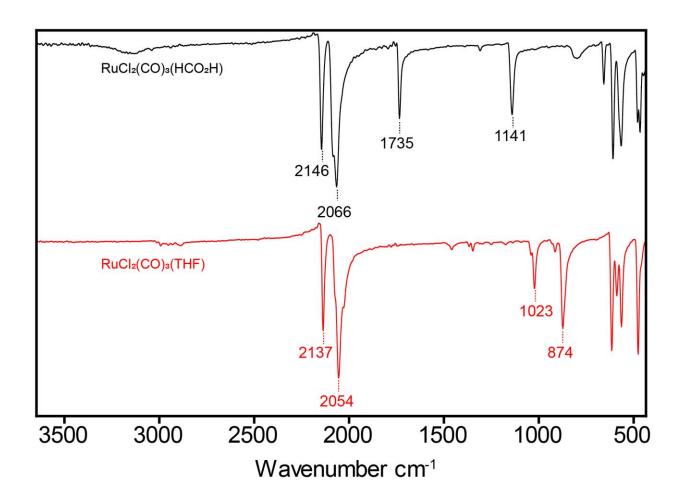


Figure S21. ATR-IR spectra of RuCl₂(CO)₃(HCO₂H) and RuCl₂(CO)₃(THF)

Synchrotron X-ray Powder Diffraction, Structure Solution, and Rietveld Refinement of 1

Synchrotron X-ray Powder diffraction (SXPD) data for **1** was collected on the 11-BM beamline at the Advanced Photon Source (APS, Argonne National Laboratory). Measurements were taken on a powder sample sealed in a 0.8 mm ID Kapton capillary at 298 K using a photon wavelength of $\lambda = 0.414536$ Å. Subsequent Pawley fits and Rietveld refinement were performed using TOPAS-Academic (v6) over the data range $2\theta = 0.5 - 10.0^{\circ}$ and $0.5 - 20.0^{\circ}$, respectively. Indexing the SXPD data gave a hexagonal unit cell (a = 31.937(7) Å, c = 15.798(4) Å) with *P6/mmm* as a possible space group. An initial structure model was constructed with *P6/mmm* space group symmetry and Rietveld refinement was carried out using simulated annealing with two rigid bodies, a D_{4h} $Zr_6O_4(OH)_4(OAc)_4$ cluster and idealized [L-RuCl₃]⁴⁻ linker. The position and orientation of each rigid body is constrained by symmetry; the torsion angles of the benzoate group were allowed to freely refine, as described previously. Constraints were placed on the Zr-acetate and Zr-benzoate bond distances, to guarantee chemically reasonable Zr-O bond lengths. The best fit to the data provided $R_{wp} = 14.03$ with final lattice parameters of a = 31.9437(6) Å, c = 15.8051(3) Å.

Table S1. Fractional coordinates of the asymmetric unit for framework structure 1.

Label	Element	Xfrac	Yfrac	Zfrac
Ru	Ru	0.186100	0.372200	0.000000
Cla	Cl	0.229870	0.459741	0.000000
Clb	Cl	0.110287	0.372200	0.000000
P1	P	0.181952	0.363905	-0.148726
N1	N	0.152066	0.304132	-0.147269
C1	С	0.137403	0.274806	-0.074540
C2	С	0.111950	0.223900	-0.076341
C3	С	0.099062	0.198124	0.000274
N2	N	0.149818	0.299637	0.000101
C11	С	0.151269	0.390328	0.205106
C12	С	0.161653	0.437831	0.190923
C13	С	0.136862	0.456403	0.236143
C14	С	0.101685	0.427469	0.295546
C15	С	0.091301	0.379966	0.309729
C16	С	0.116093	0.361394	0.264509
C17	С	0.075075	0.447403	0.344083
O11	O	0.054313	0.430335	0.409705
O12	0	0.076722	0.485714	0.307436
Zr1a	Zr	0.422372	0.422372	0.500000
Zr2a	Zr	0.468309	0.531691	0.610953
O1a	О	0.463860	0.463860	0.603326
O2a	О	0.506627	0.565653	0.500000
O3a	О	0.429834	0.570166	0.567662
C3a	С	0.418676	0.581324	0.500000

C3b	С	0.391499	0.608501	0.500000
O4a	О	0.519326	0.480674	0.745654
C4a	С	0.500000	0.500000	0.784719
C4b	С	0.500000	0.500000	0.879866

Pawley refinement of 1

The Pawley refinement was performed using synchrotron X-ray powder diffraction data of **1**. The Pawley fits were carried out in P6, P6/m, and P6/mmm space groups using a data range of $0.5 - 10^{\circ} 2\theta$, a 7 term Chebyshev polynomial, a 1/x term (low angle scattering), a PVII peak profile, a simple axial model term, a zero-point correction, and cell parameter refinement. An R_{wp} of ~12.6 was found for the Pawley fit, which is not significantly different than the Rietveld refined R_{wp} of 14.03 in P6/mmm, indicating the reasonableness of the Rietveld refined structure.

Table S2. Pawley refinement parameters for 1 in *P6/mmm* space group.

Parameters	Value
2θ _{min} (°)	0.5
2θ _{max} (°)	10.0
λ(°)	0.414536
a (Å)	31.937(7)
c (Å)	15.798(4)
R_{wp}	12.598
Goodness of Fit	1.972

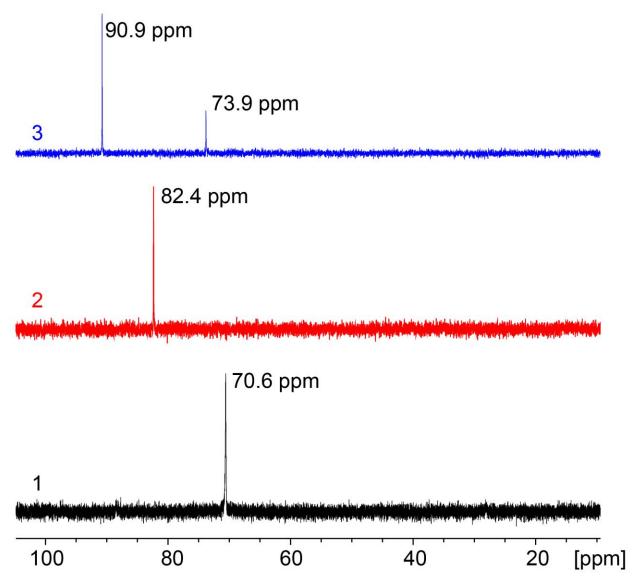


Figure S22. CsF- and acid-digested ³¹P { ¹H } NMR spectra of **1**, **2** and **3**. 1 was digested with CsF/DMSO-d₆/D₂O while 2 and 3 were digested with CF₃CO₂H/DMSO-d₆.

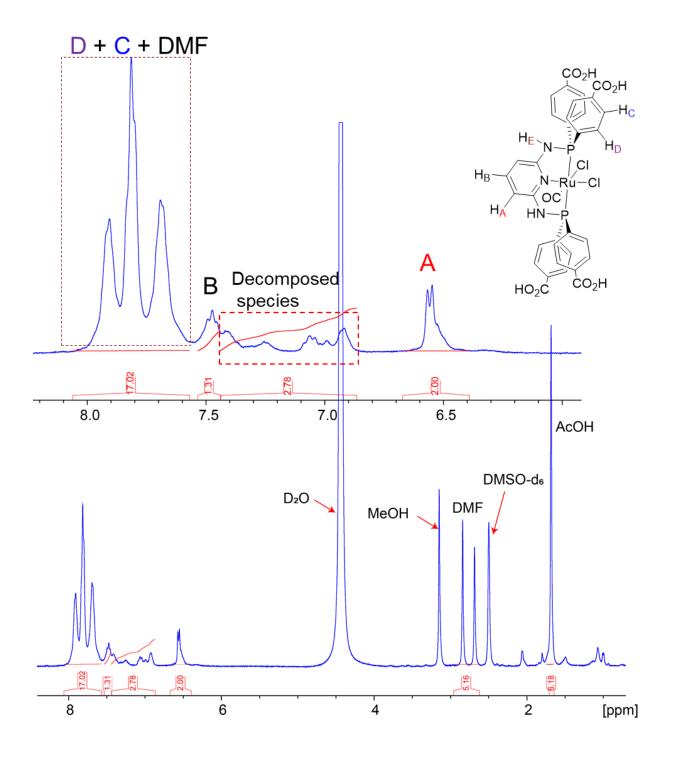


Figure S23. CsF-digested ¹H NMR spectrum (DMSO-d₆/D₂O) of **1** after MeOH solvent exchange.

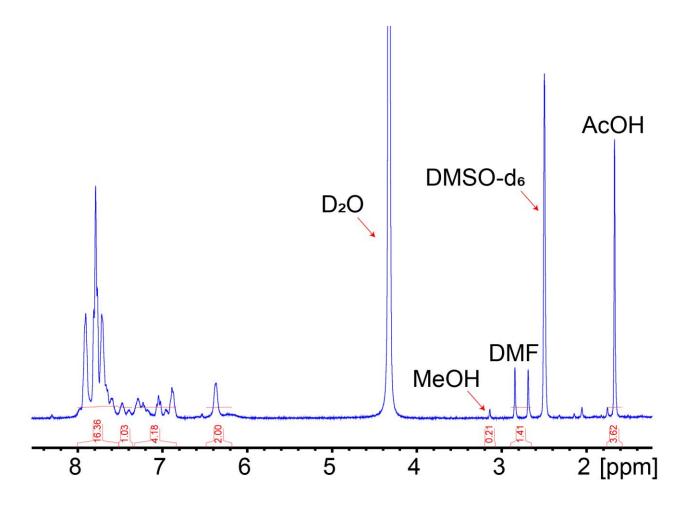


Figure S24. CsF-digested ¹H NMR spectrum (DMSO-d₆/D₂O) of 1 after activation.

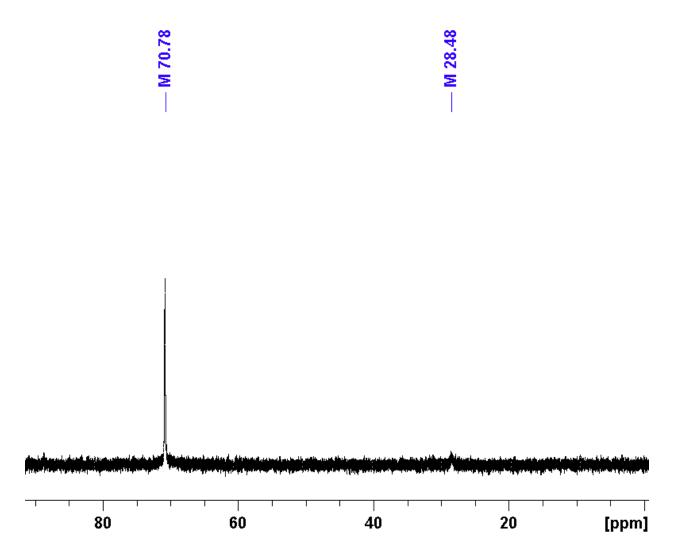


Figure S25. CsF-digested $^{31}P\{^{1}H\}$ NMR spectrum (DMSO-d₆/D₂O) of 1 after activation.

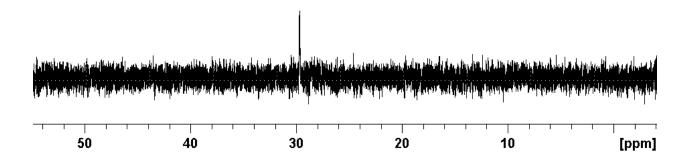


Figure S26. $^{31}P\{^{1}H\}$ NMR spectrum for MOF reaction supernatant of 1.

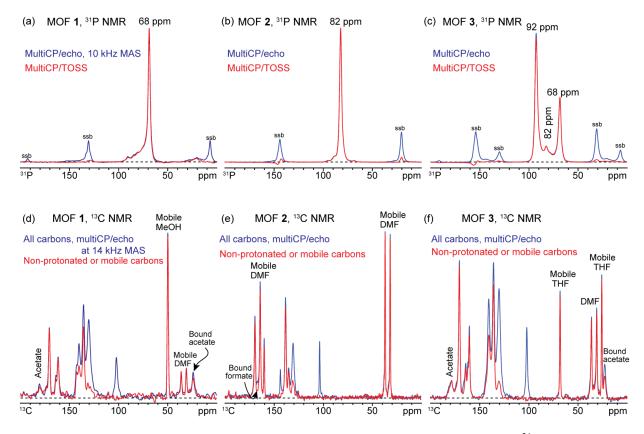


Figure S27. Solid-state NMR spectra of (a, d) 1, (b, e) 2 and (c, f) 3. (a-c): ³¹P NMR spectra recorded at 10 kHz MAS without (top blue line) and with (bottom red line) total suppression of spinning sidebands. "ssb": spinning sideband. (d-f) Quantitative multiCP ¹³C NMR spectra without (top blue line) and with (bottom red line) recoupled ¹H dipolar dephasing, recorded at 14 kHz MAS. The spectrum in red shows nonprotonated carbons and highly mobile segments. Bound acetate and formate are identified by the signal reduction of their CH_n groups after dipolar dephasing, and by inhomogeneous line broadening. For rotating CH₃ groups in immobilized molecules, dephasing to 57% of the full signal is expected.

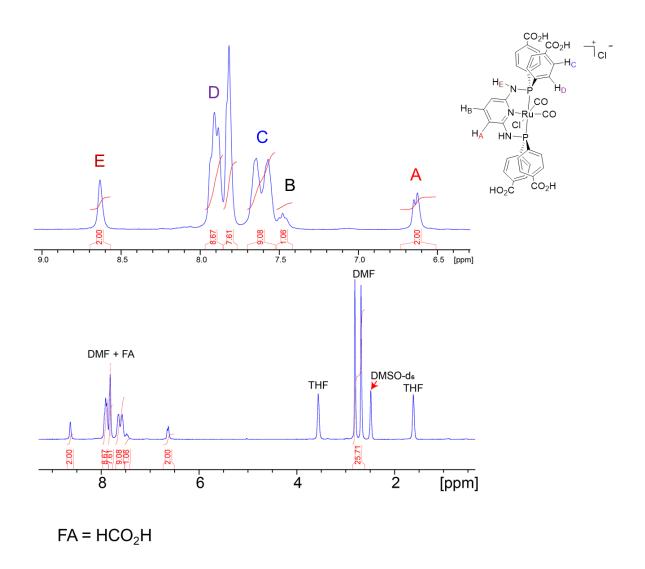


Figure S28. Acid-digested ¹H NMR spectrum (CF₃CO₂H/DMSO-d₆) of 2 after THF washing.

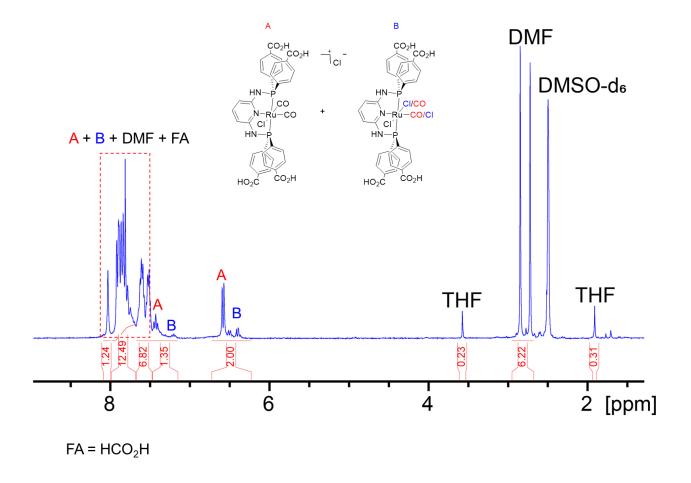


Figure S29. Acid-digested ¹H NMR spectrum (CF₃CO₂H/DMSO-d₆) of **2** after activation.

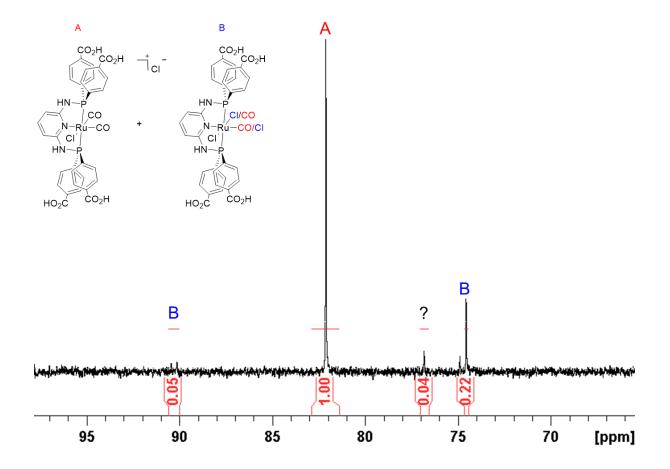


Figure S30. Acid-digested ³¹P{¹H} NMR spectrum (CF₃CO₂H/DMSO-d₆) of **2** after activation.

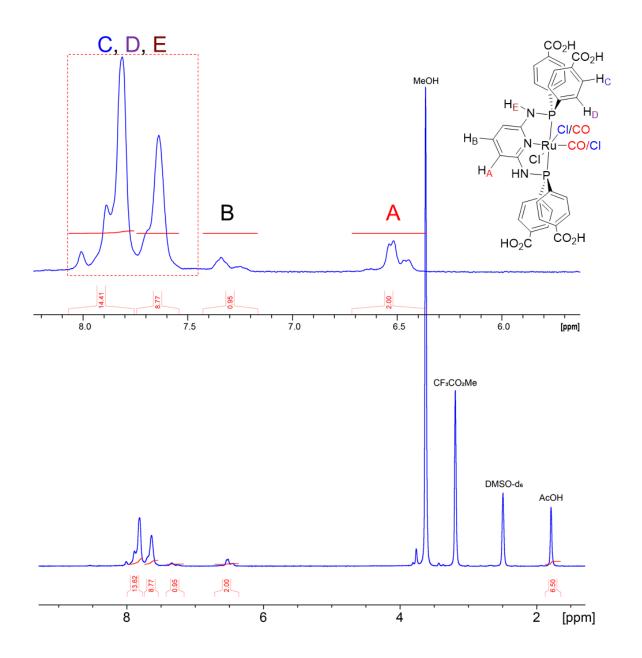
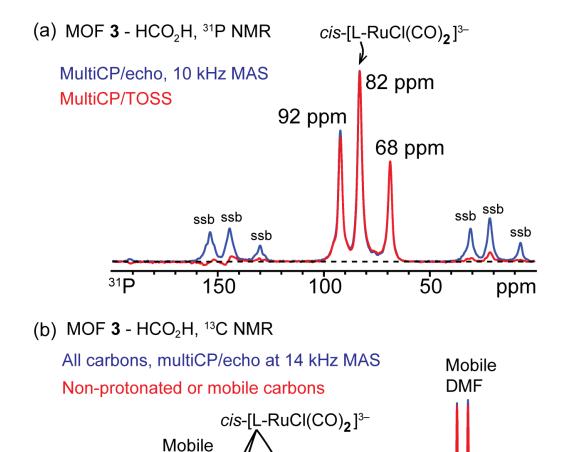


Figure S31. Acid-digested ¹H NMR spectrum (CF₃CO₂H/DMSO-d₆) of **3** after MeOH solvent exchange.



DMF

150

Bound formate

Figure S32. Solid-state ³¹P and ¹³C NMR spectra of MOF **3** synthesized with HCO₂H as the modulator. (a): ³¹P NMR spectra recorded at 10 kHz MAS without (top blue line) and with (bottom red line) total suppression of spinning sidebands. "ssb": spinning sideband. (b) Quantitative multiCP ¹³C NMR spectra without (top blue line) and with (bottom red line) recoupled ¹H dipolar dephasing, recorded at 14 kHz MAS. Bound formate is identified by the signal reduction after dipolar dephasing.

100

50

ppm

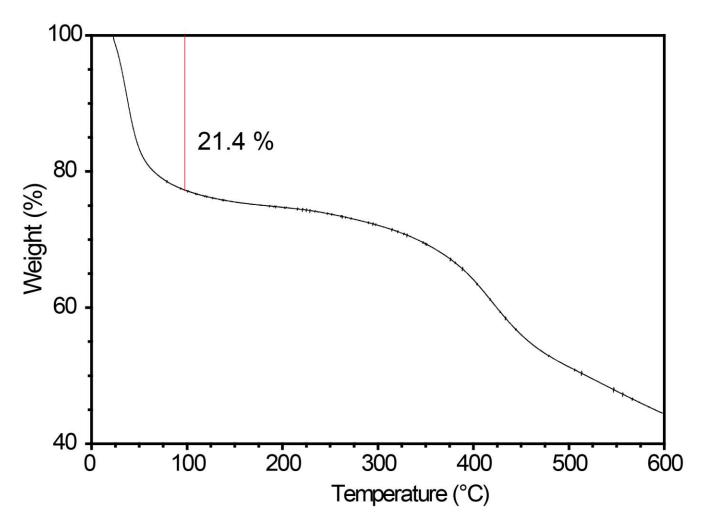


Figure S33. TGA for MeOH soaked sample of **1** measured at a ramp rate of 5 $^{\circ}$ C/min under flowing N₂ (50 mL/min).

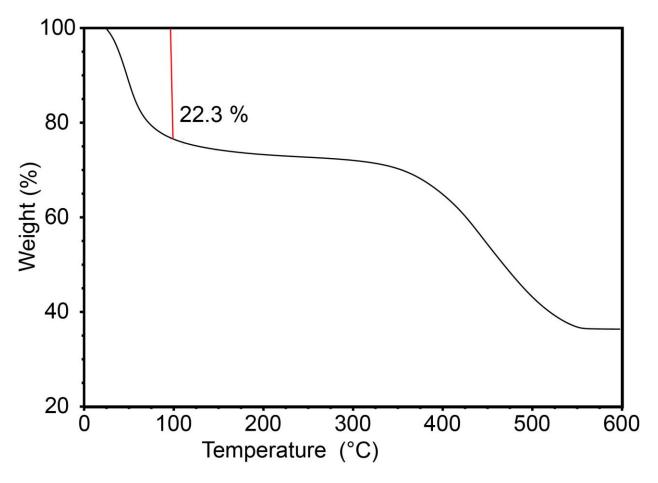


Figure S34. TGA for MeOH soaked sample of **3** measured at a ramp rate of 5 $^{\circ}$ C/min under flowing N₂ (50 mL/min).

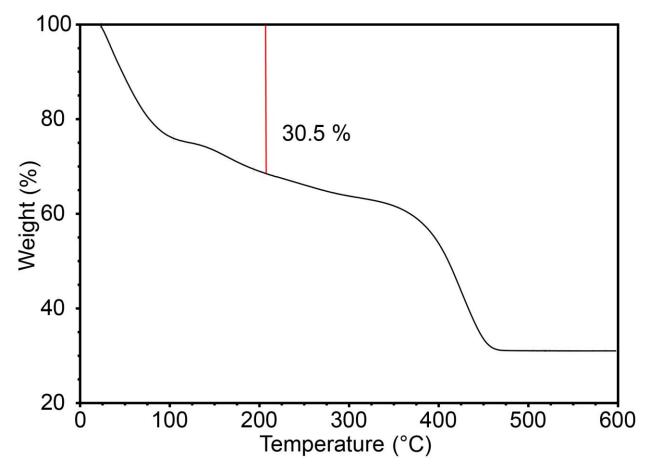


Figure S35. TGA for THF-exchanged sample of **2** measured at ramp rate of 5 °C/min under flowing N_2 (50 mL/min). ¹H NMR analysis of THF-exchanged MOF prior to TGA showed the presence of both THF and DMF solvents. As a result, 30.5 % mass loss up to 200 °C is attributed to volatilization of these solvents.

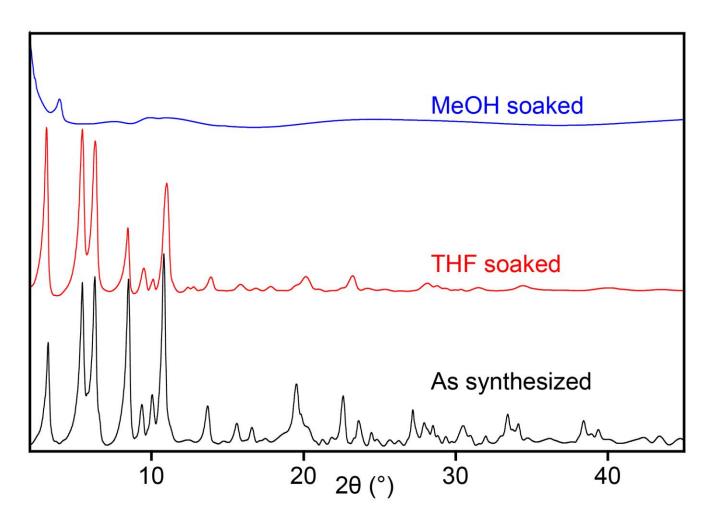


Figure S36. XRPD patterns (Cu-K α radiation, $\lambda = 1.5418$ Å) for as synthesized, THF and MeOH solvent exchanged samples of **2**.

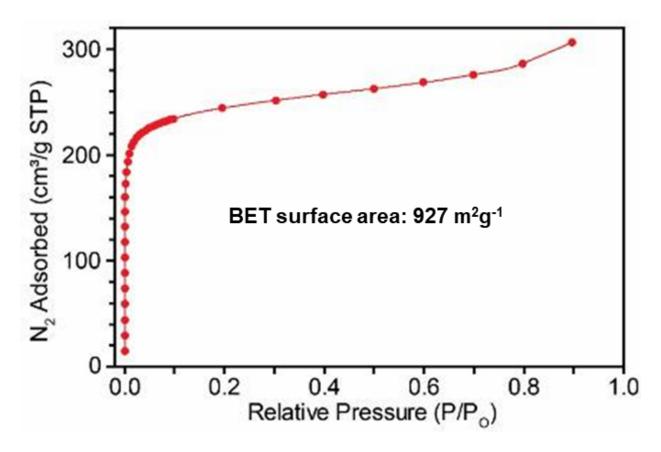


Figure S37. N_2 adsorption isotherm (77 K) for MeOH soaked sample of **1** after desolvation at 100 $^{\circ}$ C and 10 $^{-4}$ torr for 16 h.

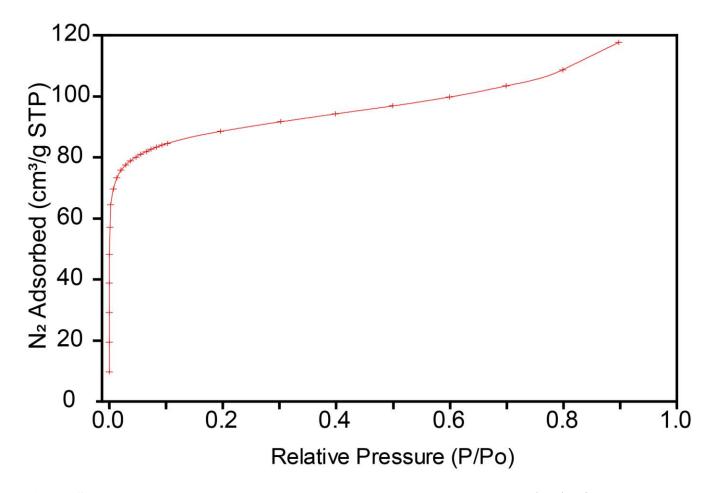


Figure S38. N_2 adsorption isotherm (77 K) for THF soaked sample of **2** after desolvation at 100 °C and 10^{-4} torr for 16 h.

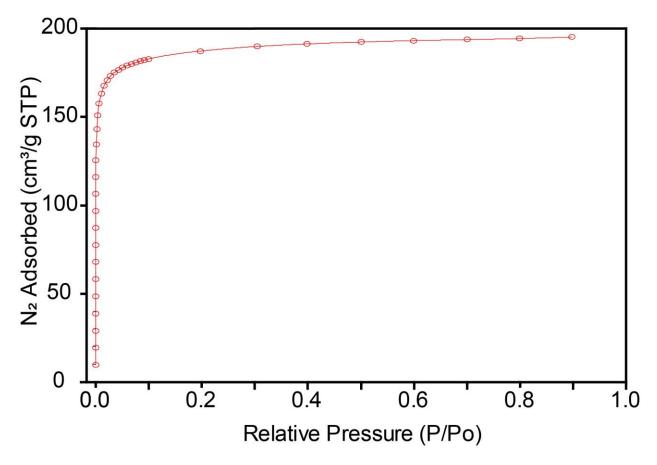


Figure S39. N_2 adsorption isotherm (77 K) for MeOH soaked sample of **3** after desolvation at 100 °C and 10^{-4} torr for 16 h.

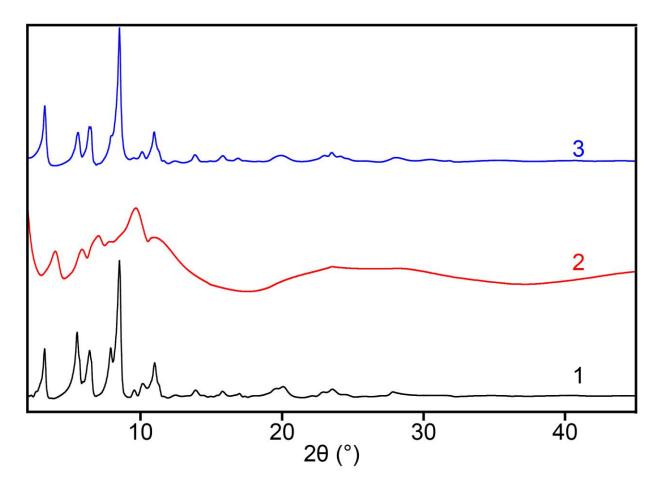


Figure S40. XRPD patterns (Cu-K α radiation, $\lambda = 1.5418$ Å) for activated samples of **1**, **2** and **3**.

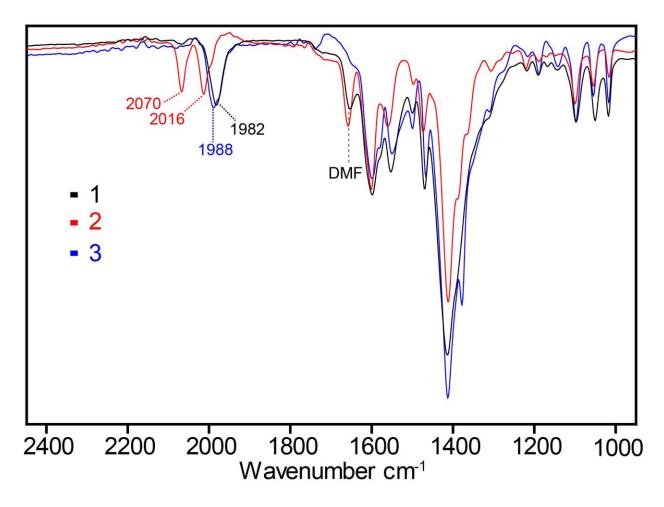


Figure S41. ATR-IR spectra for samples of 1, 3 (MeOH soaked), and 2 (THF soaked).

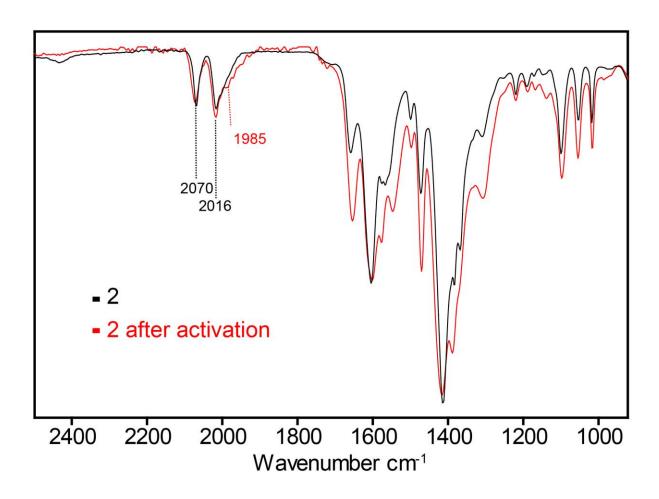


Figure S42. ATR-IR spectra for 2 before and after activation.

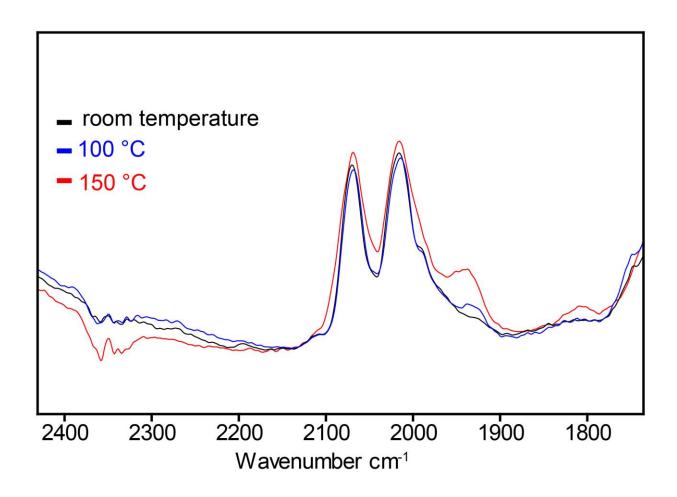


Figure S43. Diffuse reflectance IR spectra of **2** at room temperature and have heating to 100 and 150 $^{\circ}$ C under an N₂ atmosphere.

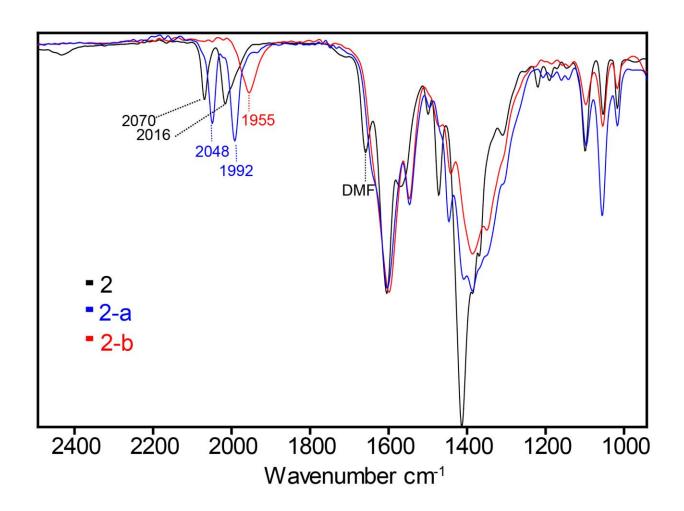


Figure S44. ATR-IR spectra of 2, 2-a, and 2-b.

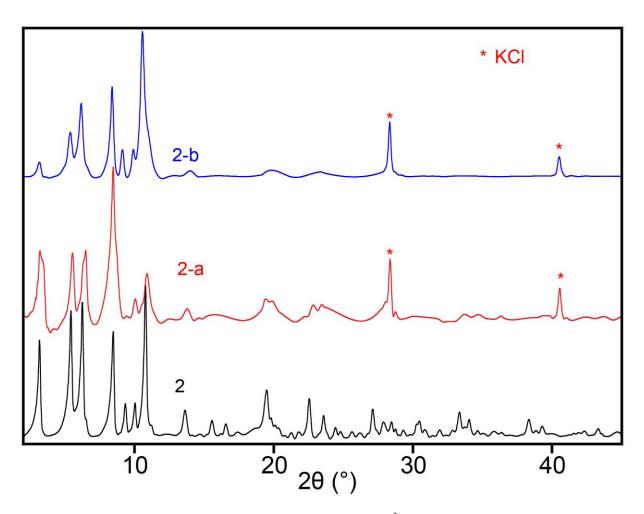


Figure S45. XRPD patterns (Cu-K α radiation, $\lambda = 1.5418$ Å) of **2**, **2-a** and **2-b**.

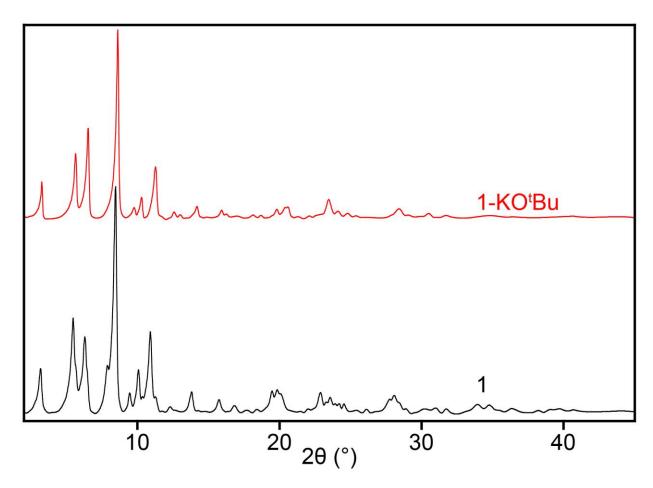


Figure S46. XRPD patterns (Cu-K α radiation, λ = 1.5418 Å) of 1 and 1-KO t Bu.

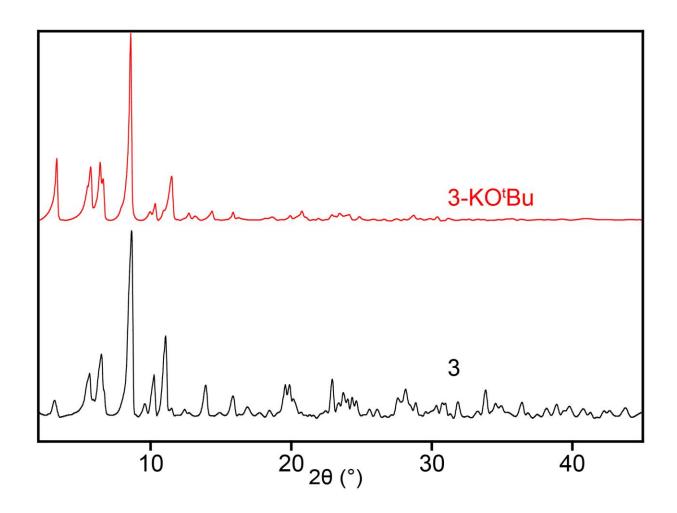


Figure S47. XRPD patterns (Cu-K α radiation, $\lambda = 1.5418$ Å) of **3** and **3-KO^tBu**.

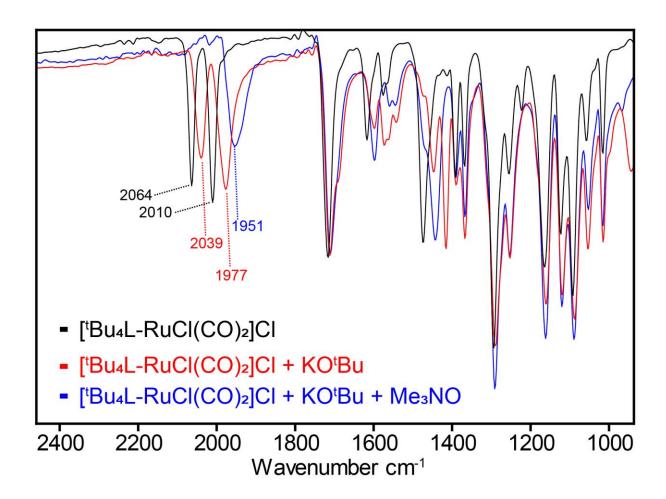


Figure S48. ATR-IR spectra for [^tBu₄L-RuCl(CO)₂]Cl reaction with KO^tBu and Me₃NO.

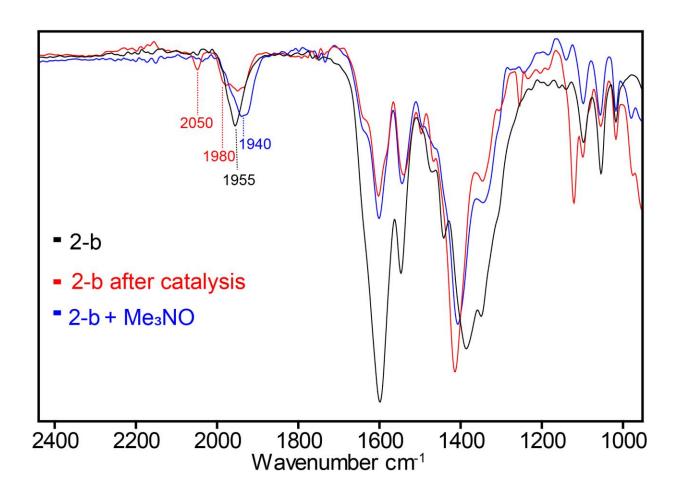
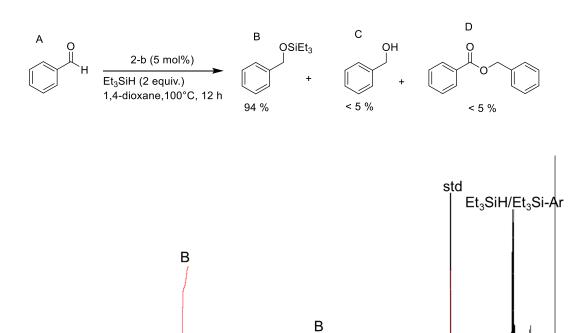


Figure S49. ATR-IR spectra for **2-b** before and after catalysis, and regeneration of **2-b** with Me_3NO .

Table S3. Hydrosilylation of aryl aldehydes catalyzed by 2-b^a

Entry	Substrate	Product	% Yield ^b
1	OMe	OSIEt ₃	91
2	~°	OSiEt ₃	86
3	F ₃ C-\(\bigc\)\(\overline{O}\)	F_3C OSiEt $_3$	92
4	MeO-	MeO-OSiEt ₃	69
5	Ph_O O Ph	Ph_OOSiEt ₃	9
6°		OSiPh ₃	< 5

"Reaction conditions: substrate (0.2 mmol), catalyst (0.01 mmol), Et₃SiH (0.4 mmol),1,4-dioxane (1 mL), 12 h, 100 °C. ^bYields were determined by ¹H NMR with respect to an internal standard (hexamethylbenzene). ^cPh₃SiH (0.4 mmol) was used in place of Et₃SiH.



D

6

A + D

Α

10

DMSO-d₆

2

[ppm]

Figure S50. 1 H NMR spectrum for hydrosilylation of benzaldehyde with **2-b**. (Substrate: hexamethylbenzene = 3.8:1) . Asterisk (*) is used to denote suppressed 1,4-dioxane.

4

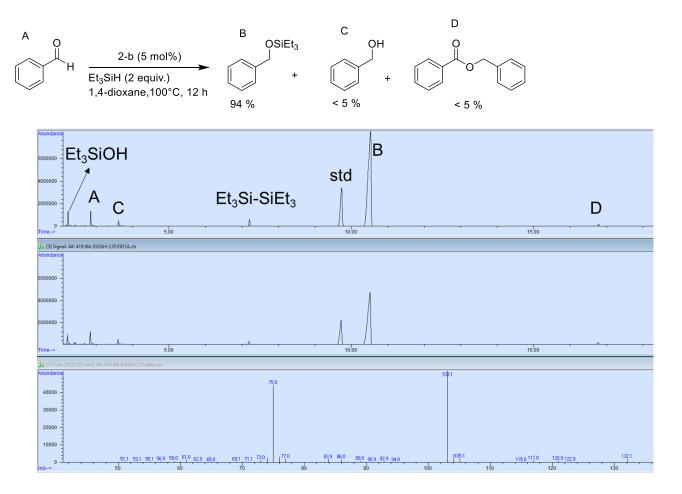


Figure S51. GC/MS chromatogram for the hydrosilylation of benzaldehyde with 2-b.

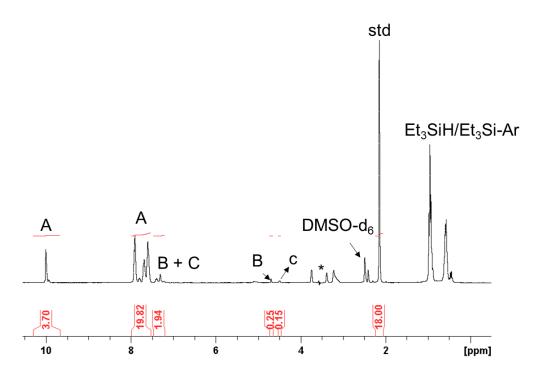


Figure S52. ¹H NMR spectrum for hydrosilylation of benzaldehyde with **2**. (Substrate: hexamethylbenzene = 3.8:1). Asterisk (*) is used to denote suppressed 1,4-dioxane.

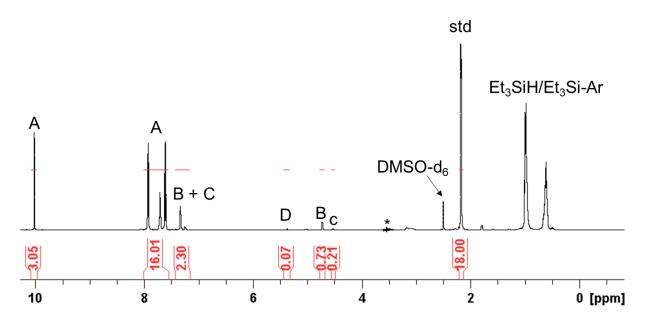


Figure S53. 1 H NMR spectrum for hydrosilylation of benzaldehyde with **2-a**. (Substrate: hexamethylbenzene = 3.8:1). Asterisk (*) is used to denote suppressed 1,4-dioxane.

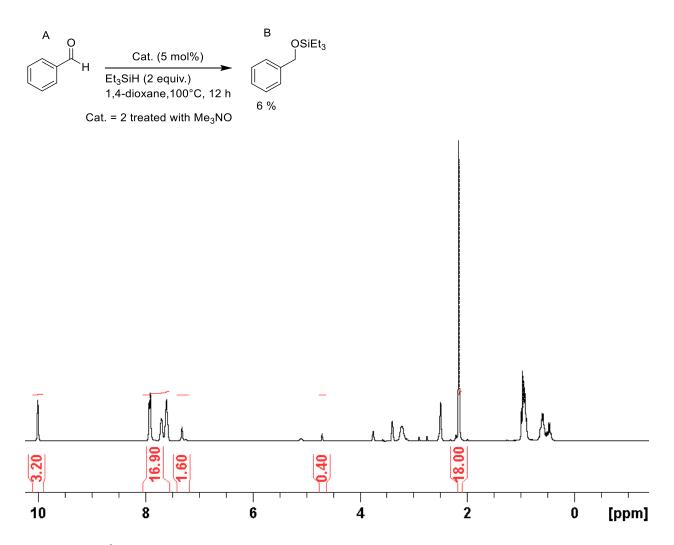


Figure S54. ¹H NMR spectrum for hydrosilylation of benzaldehyde with **2** treated with Me₃NO. (Substrate: hexamethylbenzene = 3.3:1).

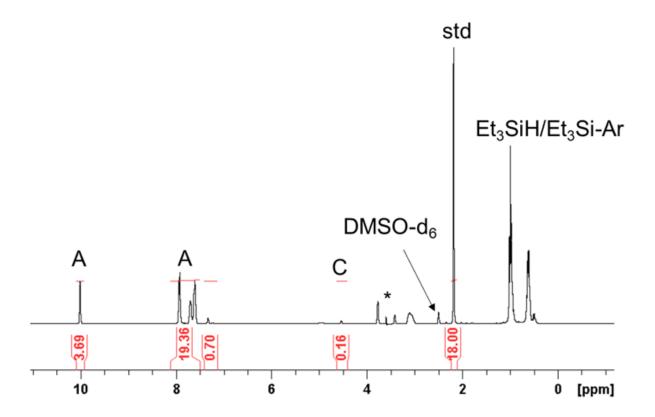


Figure S55. 1 H NMR spectrum for hydrosilylation of benzaldehyde with **1**.(Substrate: hexamethylbenzene = 3.98:1). Asterisk (*) is used to denote suppressed 1,4-dioxane.

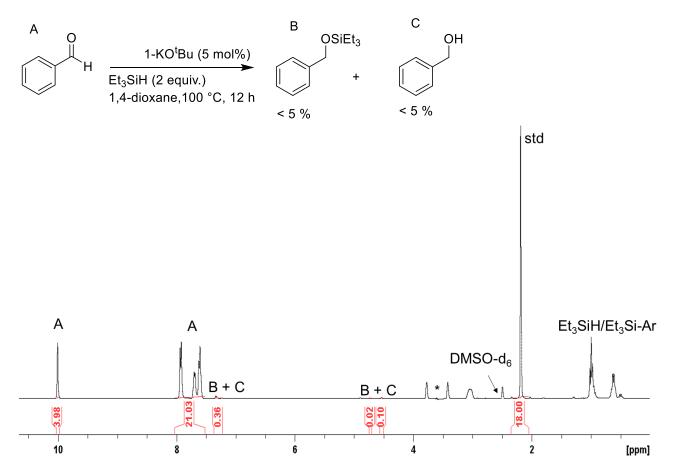


Figure S56. ¹H NMR spectrum for hydrosilylation of benzaldehyde with **1-KO**^t**Bu**. (Substrate: hexamethylbenzene = 4:1). Asterisk (*) is used to denote suppressed 1,4-dioxane.

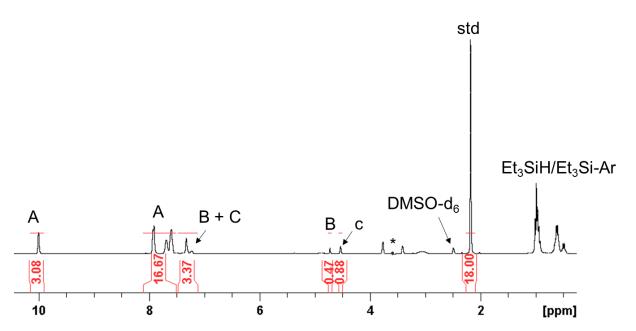


Figure S57. ¹H NMR spectrum for hydrosilylation of benzaldehyde with **3**. (Substrate: hexamethylbenzene = 3.8:1). Asterisk is used to denote suppressed 1,4-dioxane.

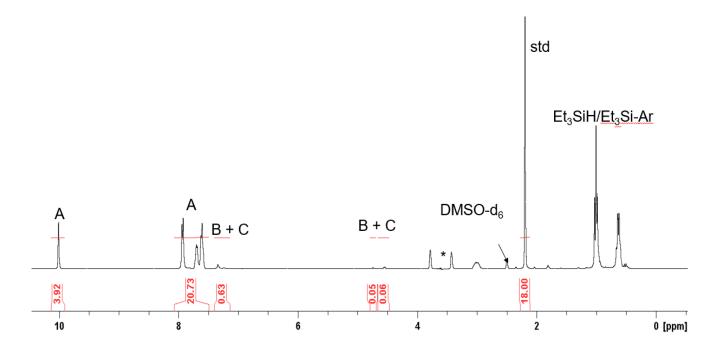


Figure S58. ¹H NMR spectrum for hydrosilylation of benzaldehyde with **3-KO**^t**Bu**. (Substrate: hexamethylbenzene = 4:1). Asterisk is used to denote suppressed 1,4-dioxane.

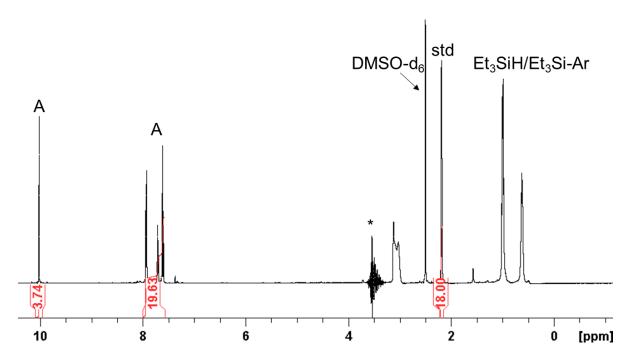


Figure S59. ¹H NMR spectrum for hydrosilylation of benzaldehyde with [^tBu₄L-RuCl(CO)₂]Cl. (Substrate: hexamethylbenzene = 3.8:1). Asterisk (*) is used to denote suppressed 1,4-dioxane.

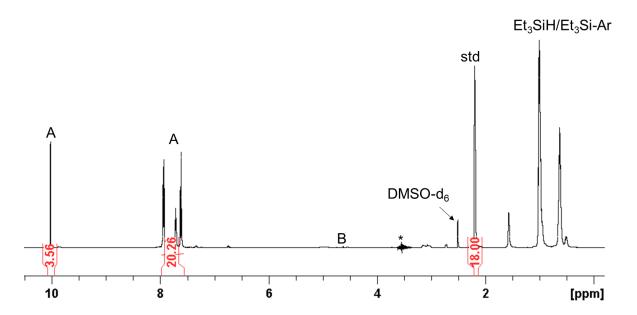


Figure S60. ¹H NMR spectrum for hydrosilylation of benzaldehyde with cis/trans-^tBu₄L-RuCl₂(CO). (Substrate: hexamethylbenzene = 3.8:1). Asterisk (*) is used to denote suppressed 1,4-dioxane.

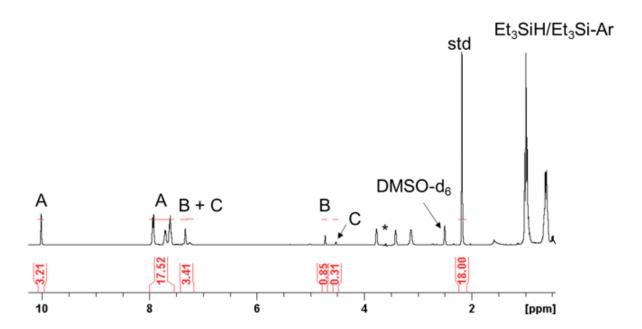
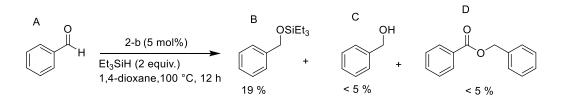


Figure S61. ¹H NMR spectrum for hydrosilylation of benzaldehyde with [^tBu₄L-RuCl(CO)₂]Cl pretreated with KO^tBu and Me₃NO. (Substrate: hexamethylbenzene = 3.8:1). Asterisk (*) is used to denote suppressed 1,4-dioxane.



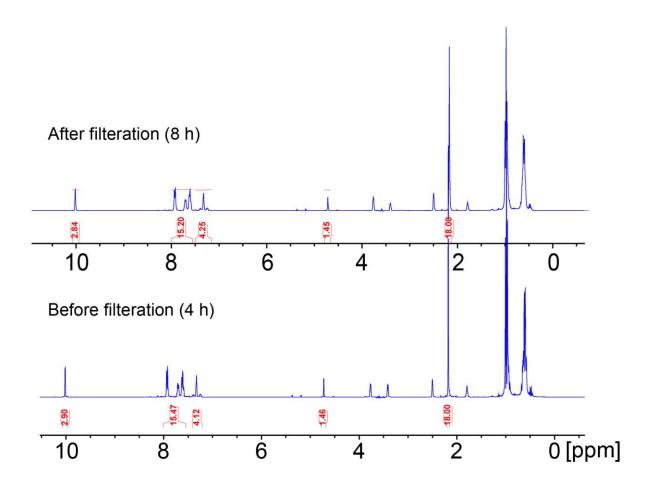


Figure S62. ¹H NMR spectra before (bottom) and after (top) hot filtration for hydrosilylation of benzaldehyde with **2-b**. (Substrate: hexamethylbenzene = 3.8:1). Asterisk (*) is used to denote suppressed 1,4-dioxane.

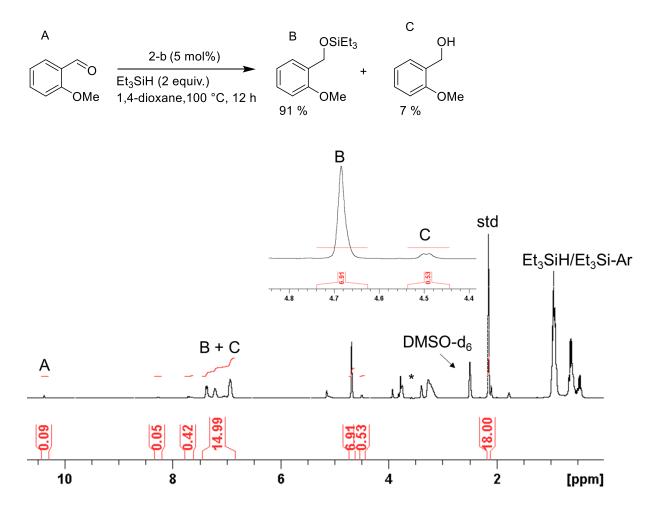


Figure S63. ¹H NMR spectrum for hydrosilylation of o-anisaldehyde with **2-b**. (Substrate: hexamethylbenzene = 3.8:1). Asterisk (*) is used to denote suppressed 1,4-dioxane.

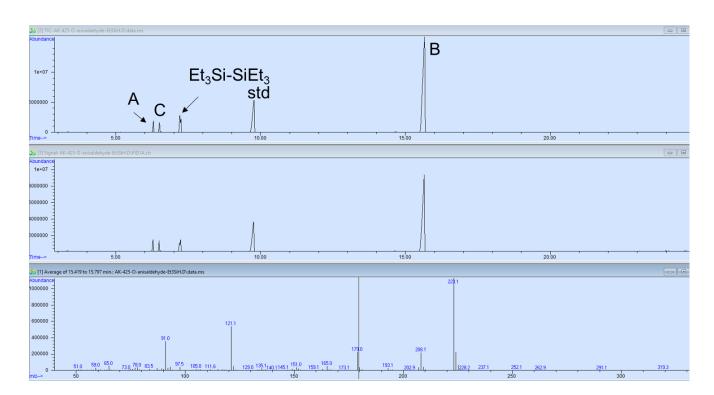


Figure S64. GC/MS chromatogram for the hydrosilylation of O-anisaldehyde with **2-b**.

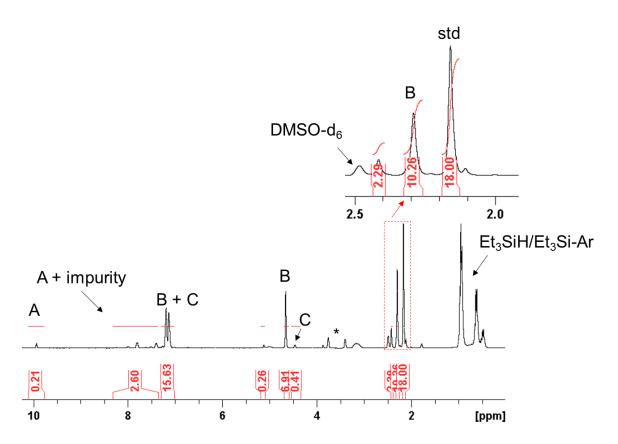


Figure S65. ¹H NMR spectrum for hydrosilylation of 4-methylbenzaldehyde with **2-b**. (Substrate: hexamethylbenzene = 4:1). The substrate had some impurity that was not removed after distillation. GC/MS analysis of the substrate predicts the impurity as methyl benzoate. Asterisk (*) is used to denote suppressed 1,4-dioxane.

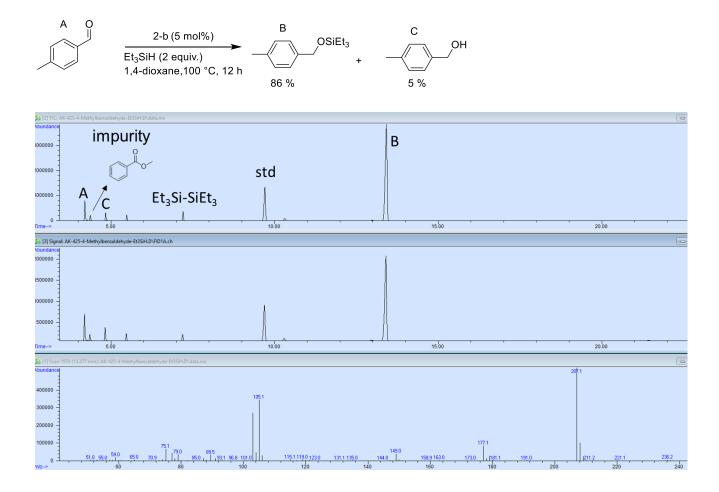


Figure S66. GC/MS chromatogram for the hydrosilylation of 4-methylbenzaldehyde with **2-b**.

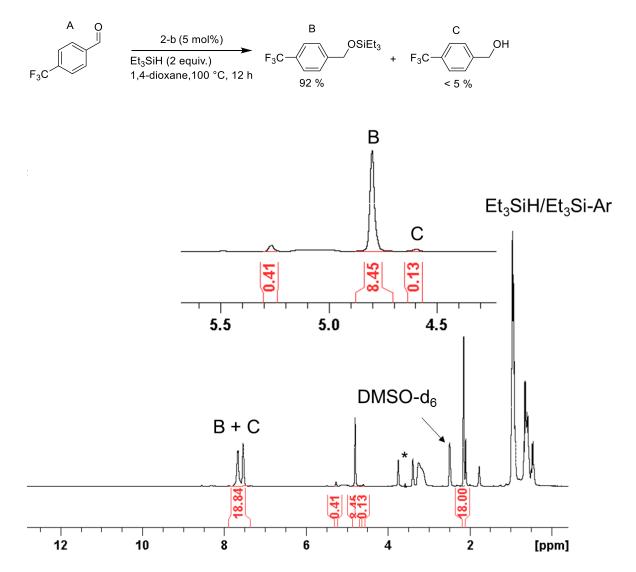


Figure S67. ¹H NMR spectrum for hydrosilylation of 4-(Trifluoromethyl)benzaldehyde with **2-b**. (Substrate: hexamethylbenzene = 4.6:1). Asterisk (*) is used to denote suppressed 1,4-dioxane.

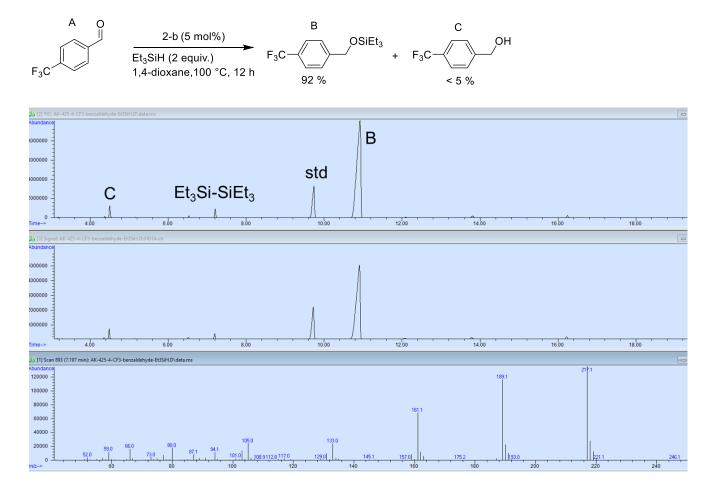


Figure S68. GC/MS chromatogram for the hydrosilylation of 4-(Trifluoromethyl)benzaldehyde with **2-b**.

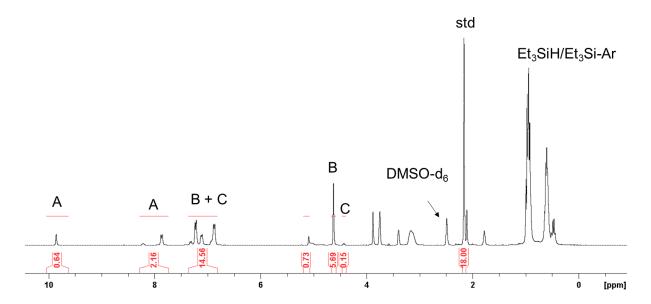


Figure S69. ¹H NMR spectrum for for the hydrosilylation of 4-methoxybenzaldehyde with **2-b**. (Substrate: hexamethylbenzene = 4.1:1). Asterisk (*) is used to denote suppressed 1,4-dioxane.

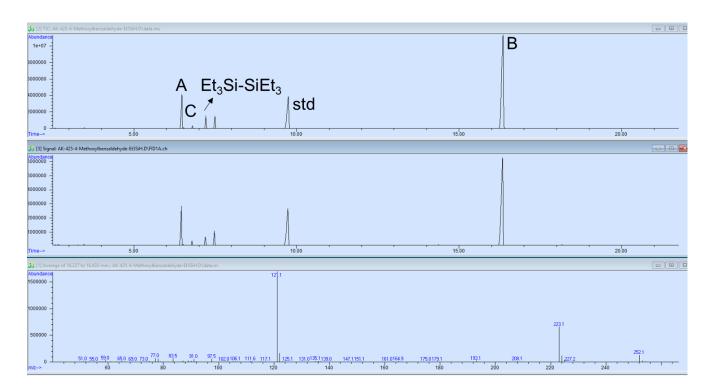


Figure S70. GC/MS chromatogram for the hydrosilylation of 4-methoxybenzaldehyde with **2-b**.

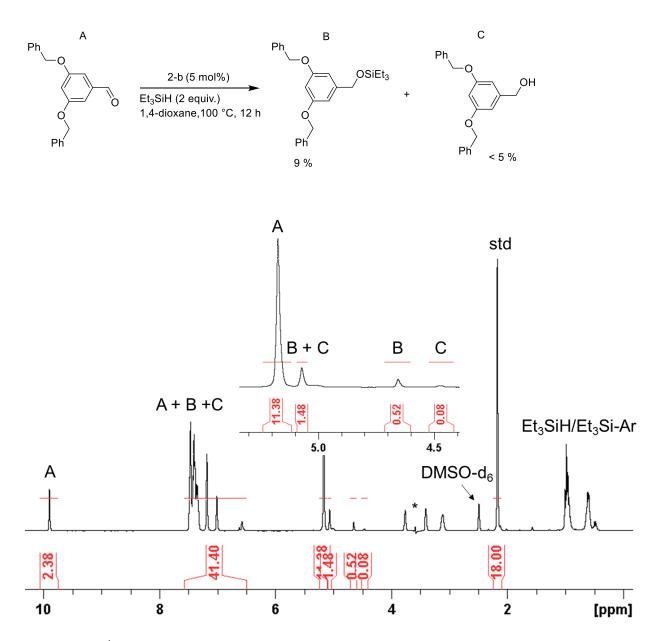
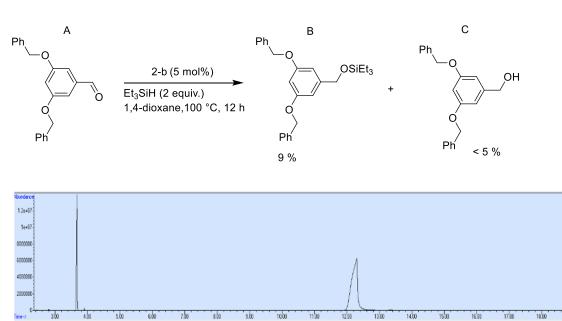


Figure S71. 1 H NMR spectrum for the hydrosilylation of 3,5-dibenzyloxybenzaldehyde with **2-b**. (Substrate: hexamethylbenzene = 2.9:1)



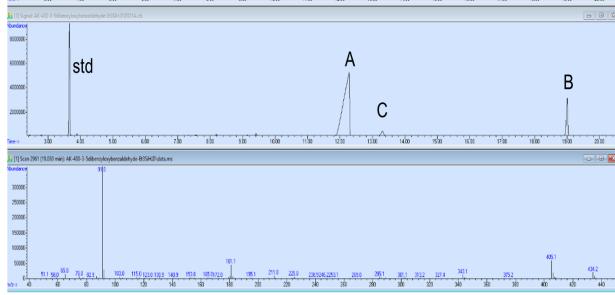
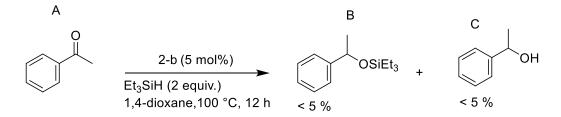


Figure S72. GC/MS chromatogram for the hydrosilylation of 3,5-dibenzyloxybenzaldehyde with **2-b**.



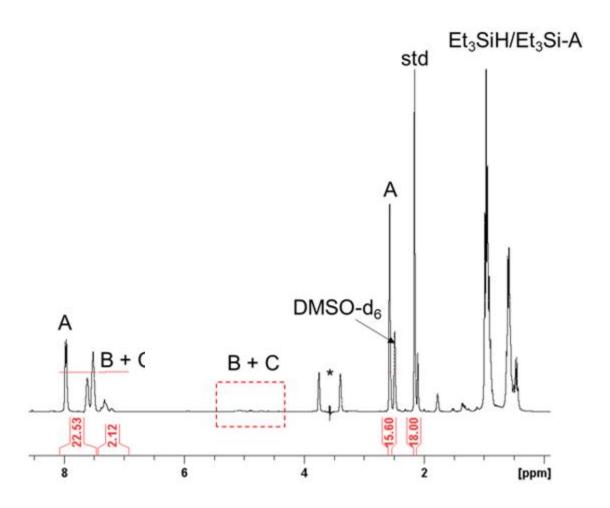


Figure S73. ¹H NMR spectrum for the hydrosilylation of acetophenone with **2-b**. (Substrate: hexamethylbenzene = 4.6:1)

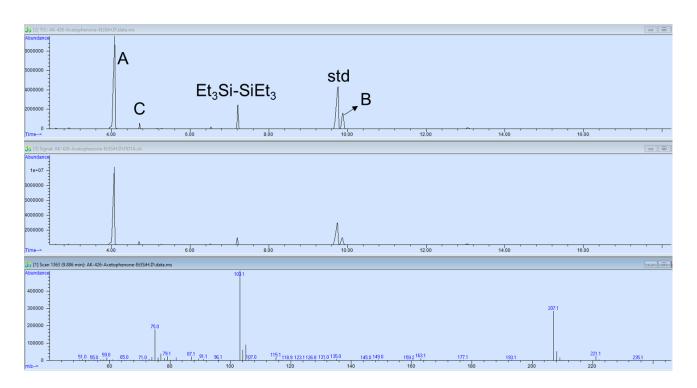


Figure S74. GC/MS chromatogram for the hydrosilylation of acetophenone with **2-b**.

REFERENCES

(1) Kassie, A. A.; Duan, P.; McClure, E. T.; Schmidt-Rohr, K.; Woodward, P. M.; Wade, C. R. Postsynthetic Metal Exchange in a Metal–Organic Framework Assembled from Co(III) Diphosphine Pincer Complexes. *Inorg. Chem.* **2019**, *58*, 3227–3236.