

Supporting Information

From High Loading to High Activity: Unraveling the Correlation in High Performance Single-Atom Catalysts Design

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In the Electronic Supplementary Material section, the following parts are included:

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1. Calculation Details

The binding energy of a single TM atom ($E_{b,mono}$), binding energy of a TM dimer ($E_{b,di}$), adsorption energy (ΔE), and clustering energy ($E_{cluster}$) were computed using the following equations.

$$E_{b,mono} = (E_{TM-GY} - E_{GY} - nE_{TM}) / n \quad (n = 1, 2) \quad (1)$$

$$E_{b,di} = (E_{2TM-GY} - E_{GY} - 2E_{TM}) / 2 \quad (2)$$

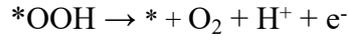
$$\Delta E = E_{X@TM-GY} - E_{TM-GY} - E_X \quad (X = O, OH, OOH) \quad (3)$$

$$E_{cluster} = E_{b,mono} - E_{b,di} \quad (4)$$

Where E_{GY} , E_{TM} , and E_{TM-GY} are the energies of the pristine GY, isolated TM atoms, and GY adsorbing TM atoms, respectively, while n denotes the number of adsorbed TM atoms. E_{2TM-GY} corresponds to the energy of GY with an adsorbed TM dimer. $E_{X@TM-GY}$ and E_X denote the energy of the catalyst adsorbing X species and the energy of isolated X in the gas phase, respectively. $E_{cluster}$ quantifies the binding energy

difference between single TM atoms and dimers on the surface. When E_{cluster} is negative – indicating higher stability for single-atom adsorption than dimer adsorption – aggregation of single atoms is thermodynamically suppressed [1, 2].

Using Nørskov's electrocatalytic framework [3], we simulate acidic (pH = 0) water splitting at active sites via four elementary steps, as follows:



Where * is the active site of the catalyst, and *OH, *O, and *OOH corresponding three reaction intermediates.

The Gibbs free energy change (ΔG) was calculated at each reaction step as follows [4]:

$$\Delta G = \Delta E + \Delta \text{ZPE} - T\Delta S + \Delta G_U - \Delta G_{\text{pH}} \quad (5)$$

Where ΔE represents the total energy change derived from DFT simulations. The ΔZPE and ΔS values obtained from frequency calculations represent the zero-point energy correction and entropy correction at 298.15 K and 1 bar, respectively. Note that water's reference state at this temperature is 0.035 bar, corresponding to the liquid-vapor equilibrium condition. The electrode potential contribution to Gibbs free energy follows $\Delta G_U = -eU$, with U defined vs RHE. $\Delta G_{\text{pH}} = 0.059 \times \text{pH}$. Given the condition pH = 0 in this study, this term evaluates to zero.

To quantify catalytic activity, the OER overpotential of catalysts can be calculated using [5]:

$$\eta = \max [\Delta G_1, \Delta G_2, \Delta G_3, \Delta G_4] / e - 1.23 \text{ V} \quad (6)$$

where 1.23 V is the potential for an ideal OER catalyst at pH = 0.

2. Figures

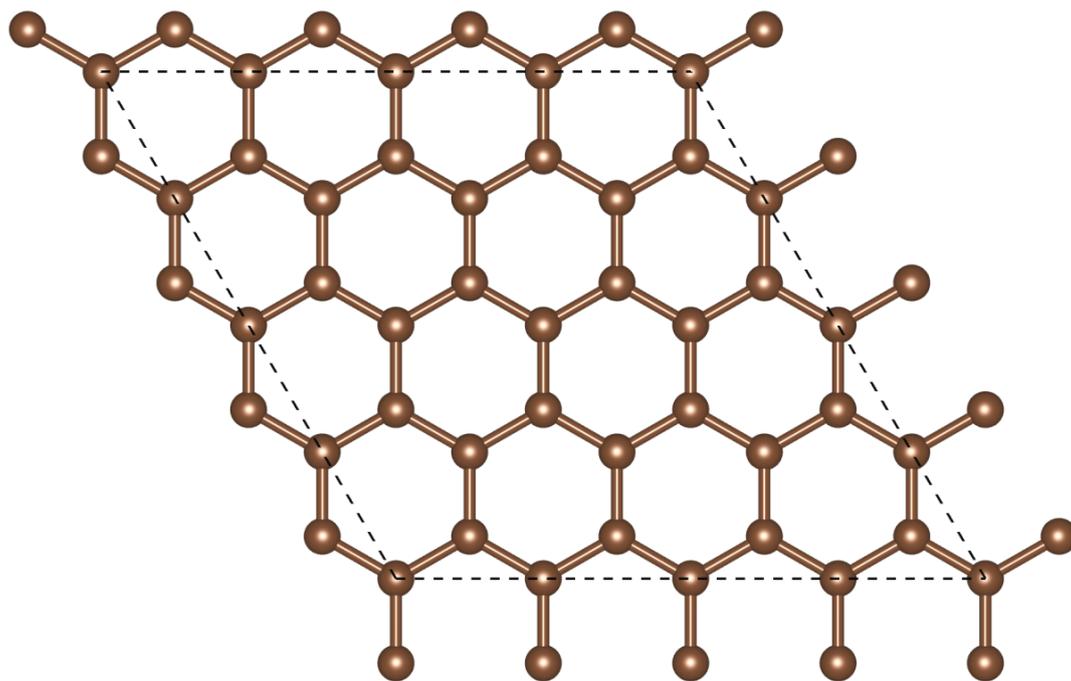


Figure S1. Atomic structure of the 4×4 graphene supercell.

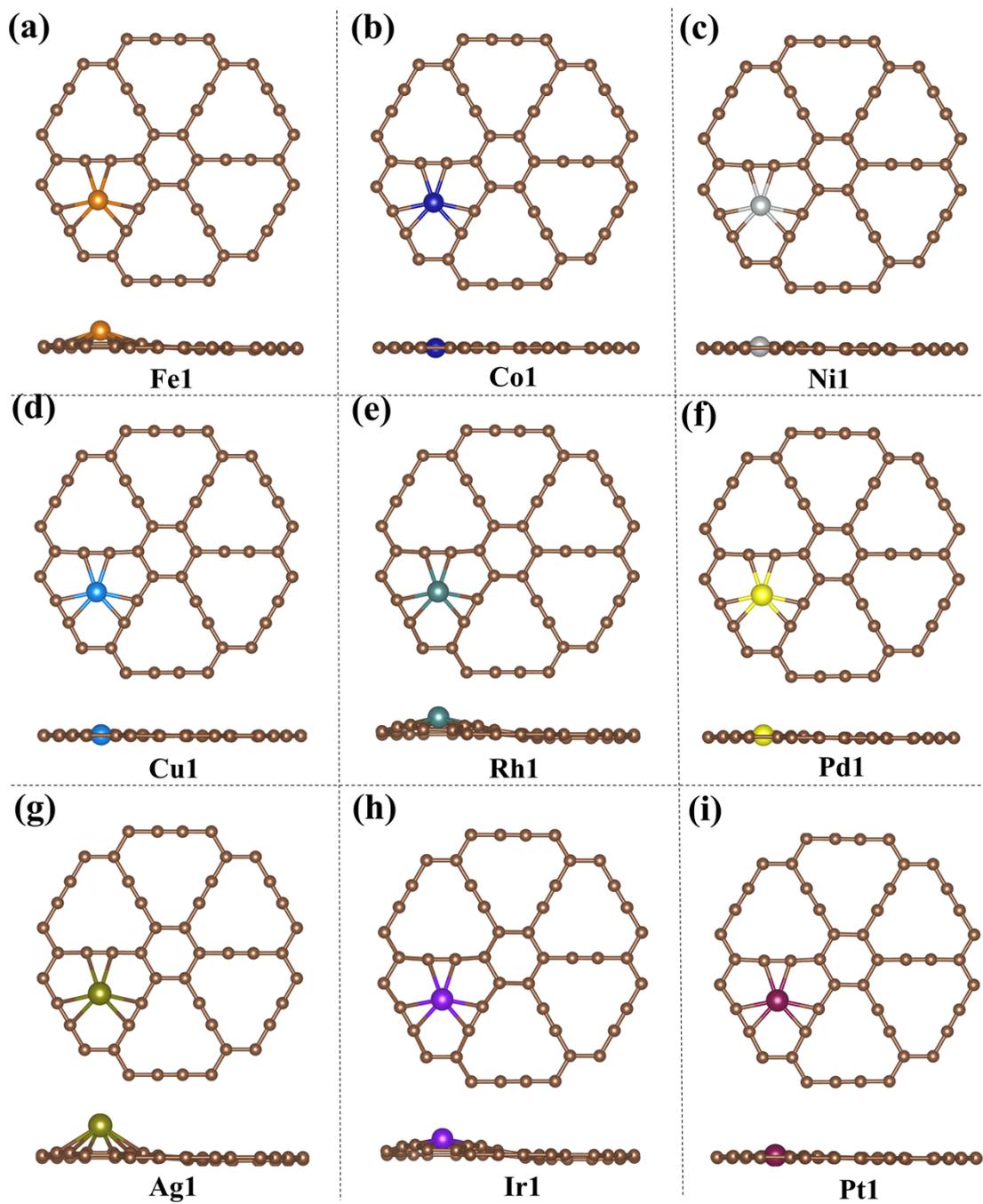


Figure S2. (a-i) Top and side views of the optimized atomic structures of low-loading TM-GY (TM = Fe, Co, Ni, Cu, Rh, Pd, Ag, Ir, and Pt).

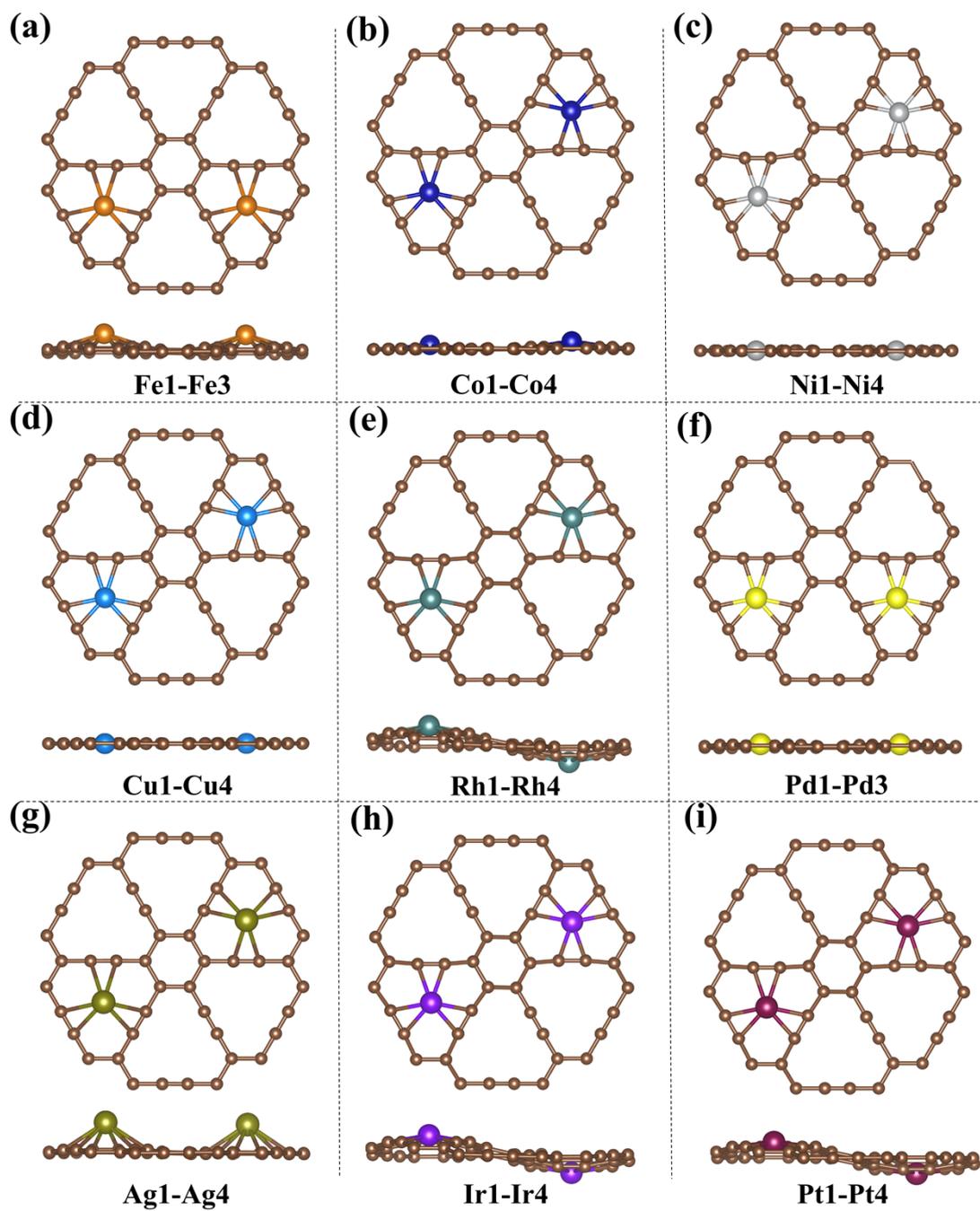


Figure S3. (a-i) Top and side views of the optimized atomic structures of high-loading TM-GY (TM = Fe, Co, Ni, Cu, Rh, Pd, Ag, Ir, and Pt).

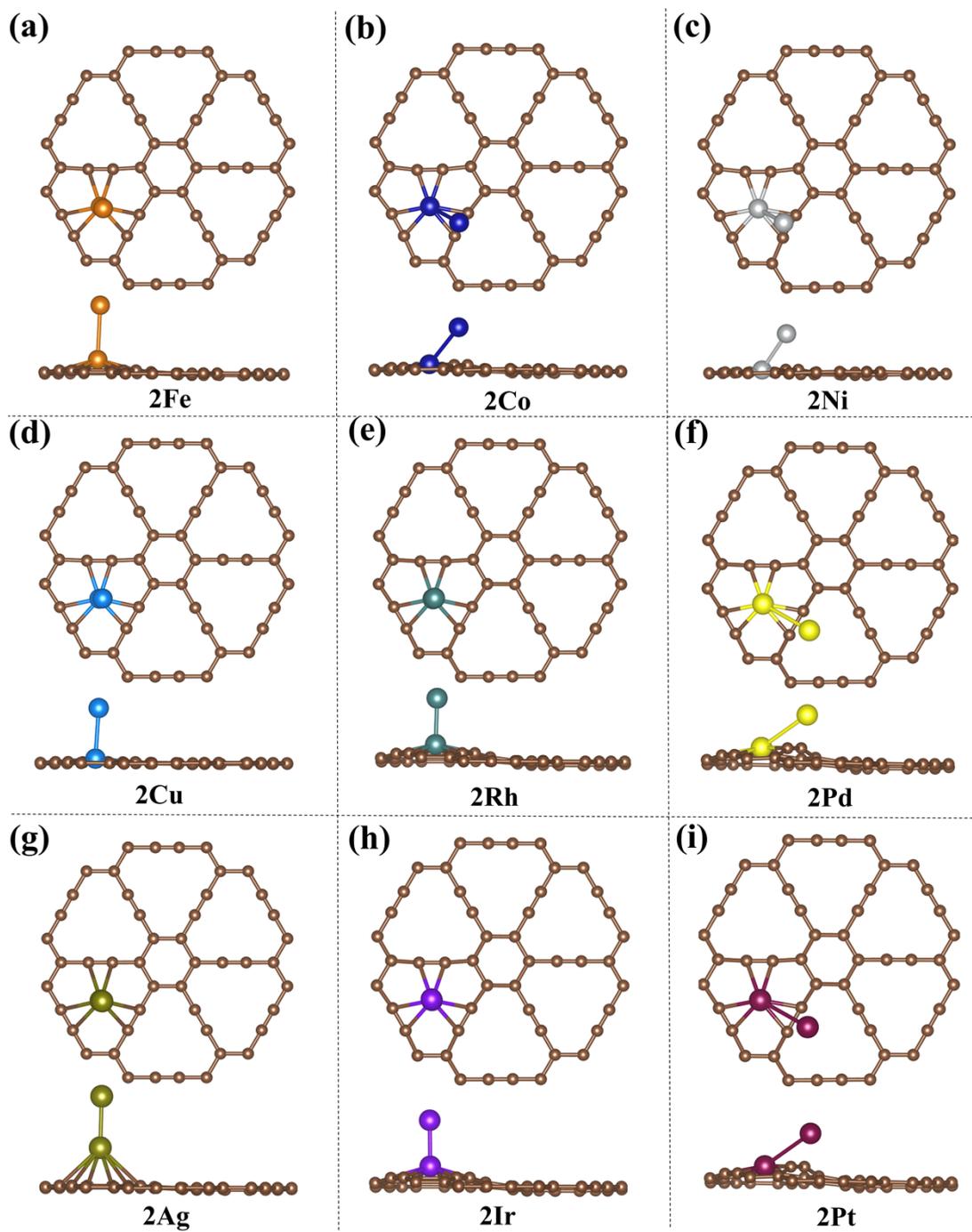


Figure S4. (a-i) Top and side views of optimized atomic structures for TM dimers (TM = Fe, Co, Ni, Cu, Rh, Pd, Ag, Ir, and Pt) adsorbed on GY surfaces.

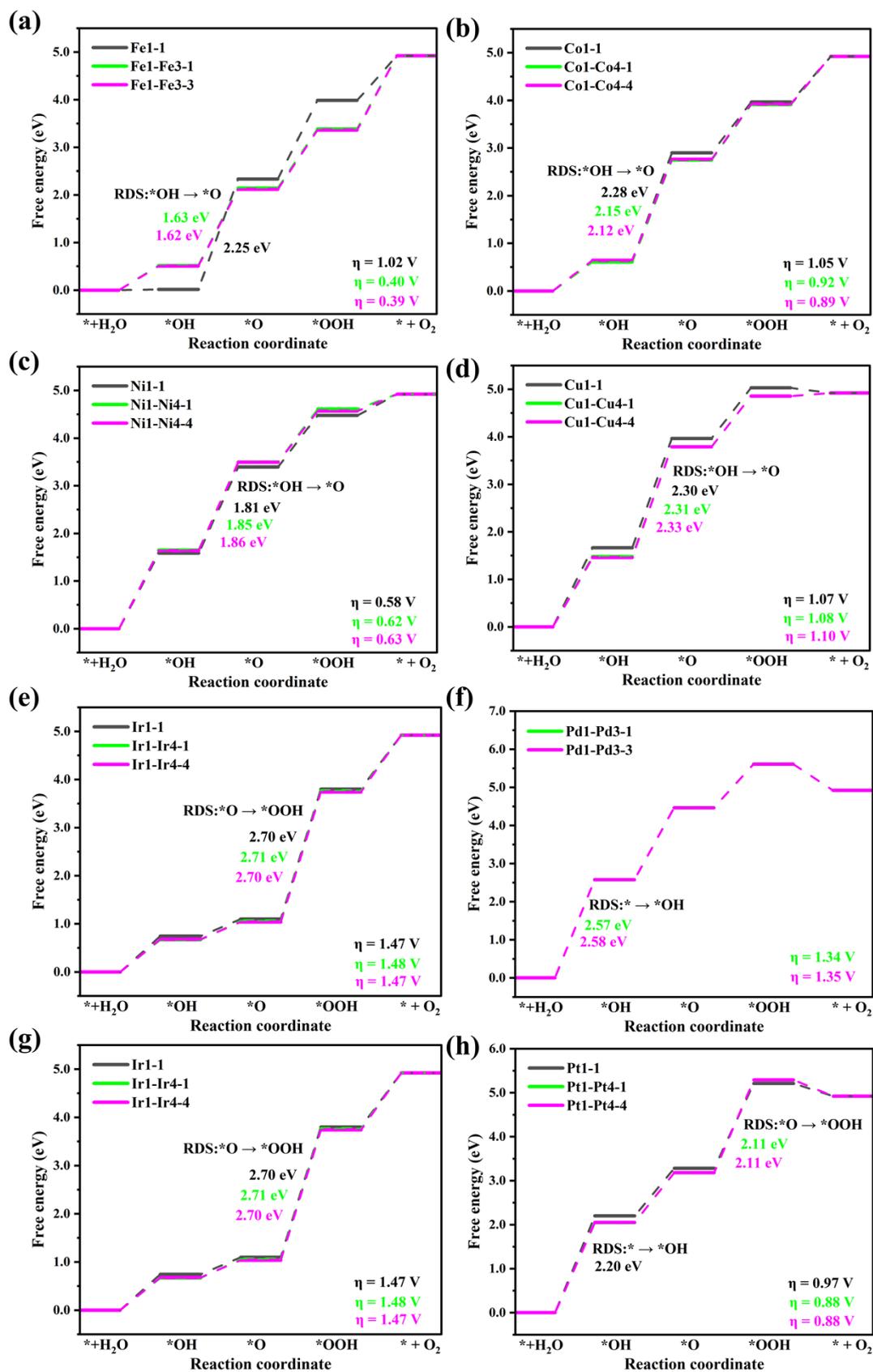


Figure S5. (a-h) OER Gibbs free energy diagrams and overpotentials of low- and high-loading TM-GY (TM = Fe, Co, Ni, Cu, Rh, Pd, Ir, and Pt). The numerals 1, 3 and 4 denote the TM site labeling.

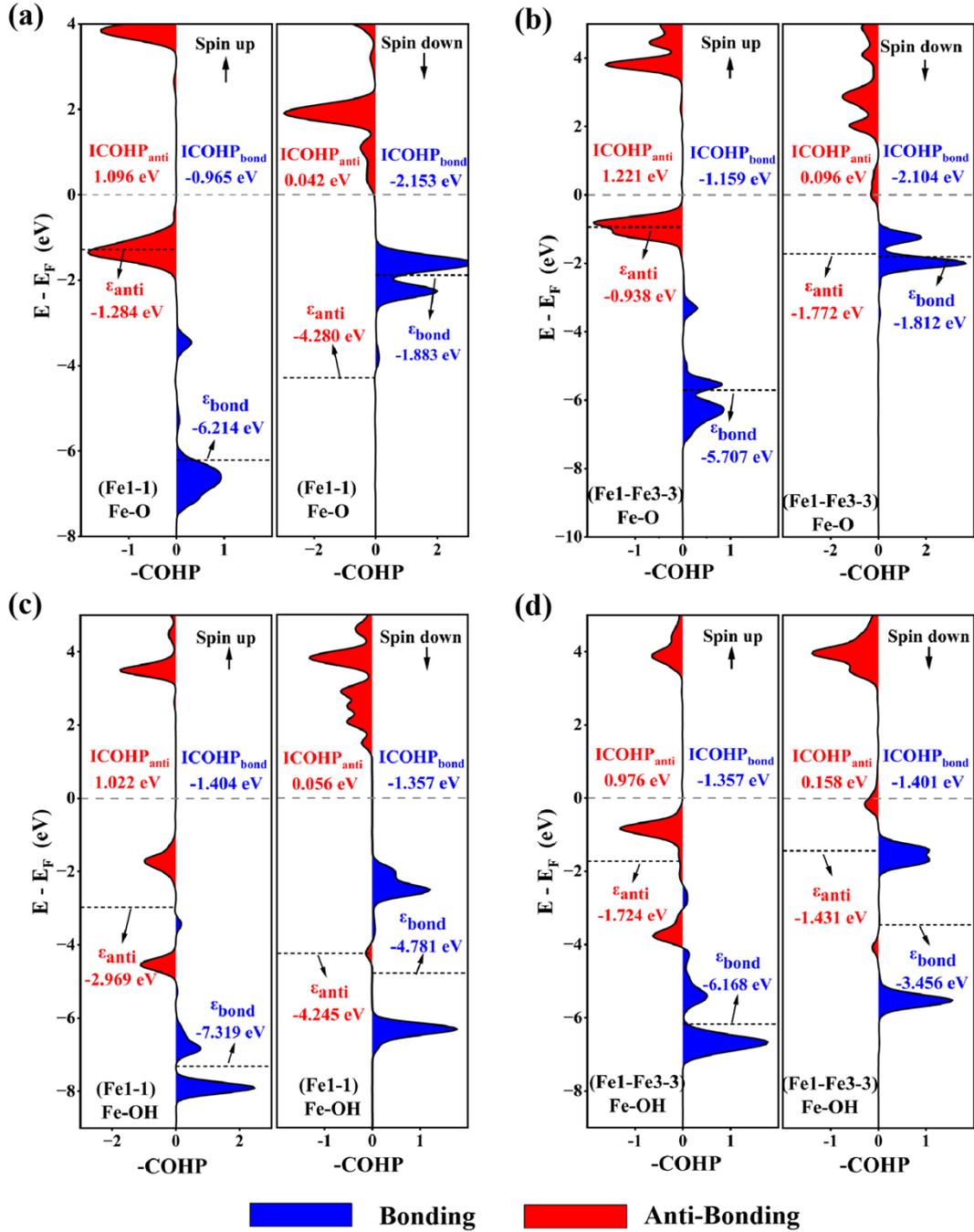


Figure S6. Spin-polarized COHP analysis for Fe-O bond : (a) *O at Fe1-1 site, (b) *O at Fe1-Fe3-3 site, (c) *OH at Fe1-1 site, and (d) *OH at Fe1-Fe3-3 site. The numerals 1, and 3 denote the TM site labeling.

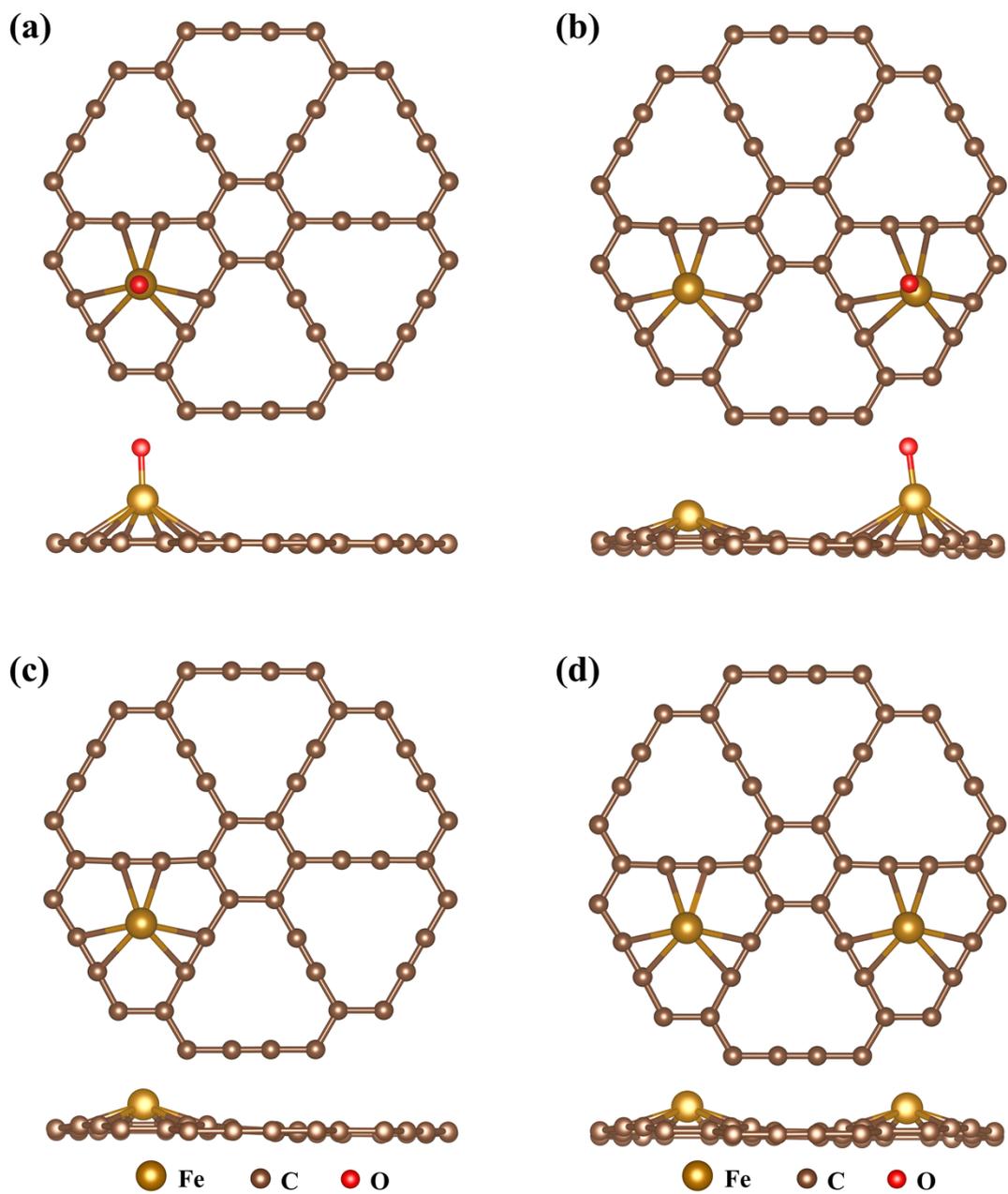


Figure S7. Side and top views of the optimized structures: (a) *O on Fe1-1 (b) *O on Fe1-Fe3-3 (c) Fe1 (d) Fe1-Fe3.

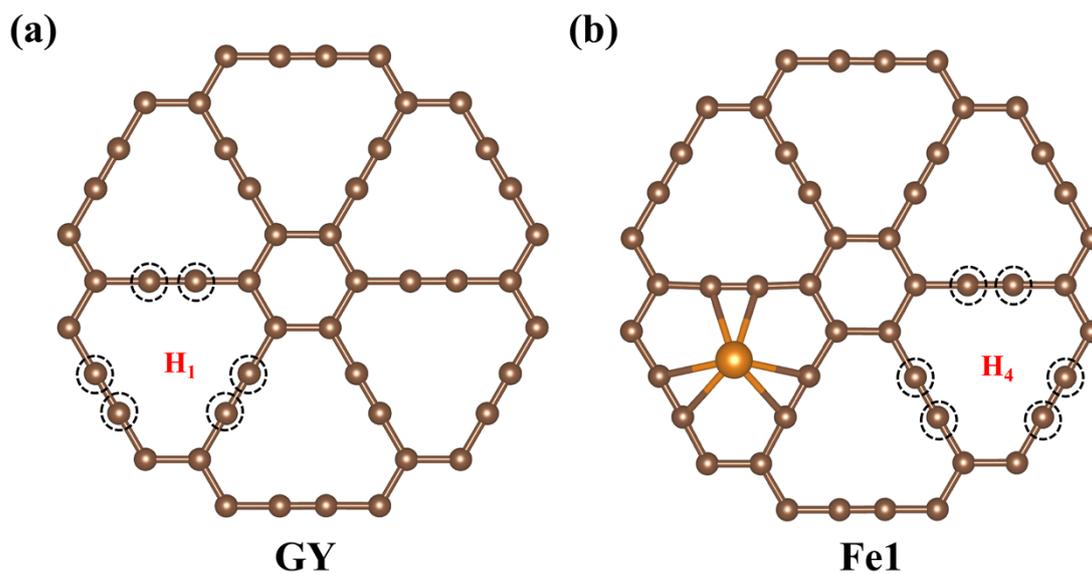


Figure S8. The carbon atoms represented by (a) GY-H1 and (b) Fe1-H3 in Figure S9.

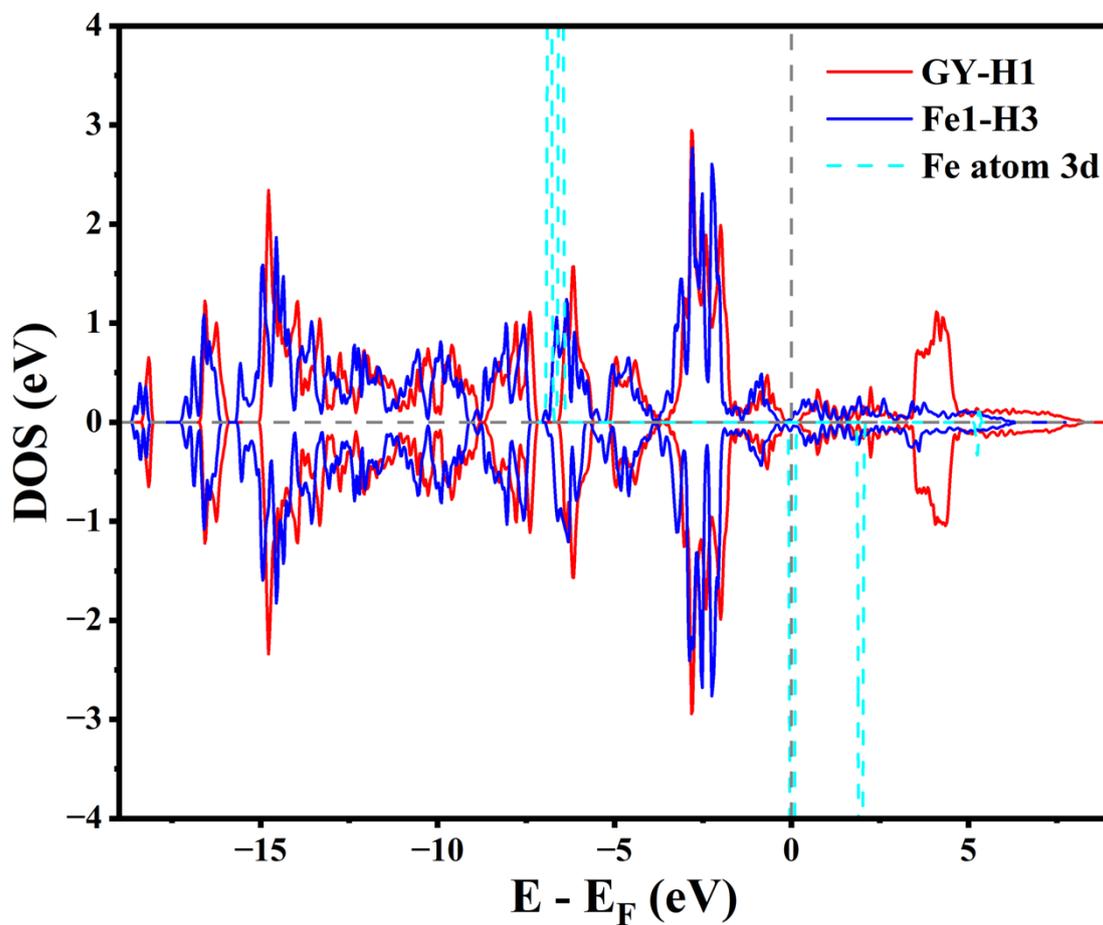


Figure S9. The density of states (DOS) for GY-H1, Fe1-H3, and Fe atom 3d.

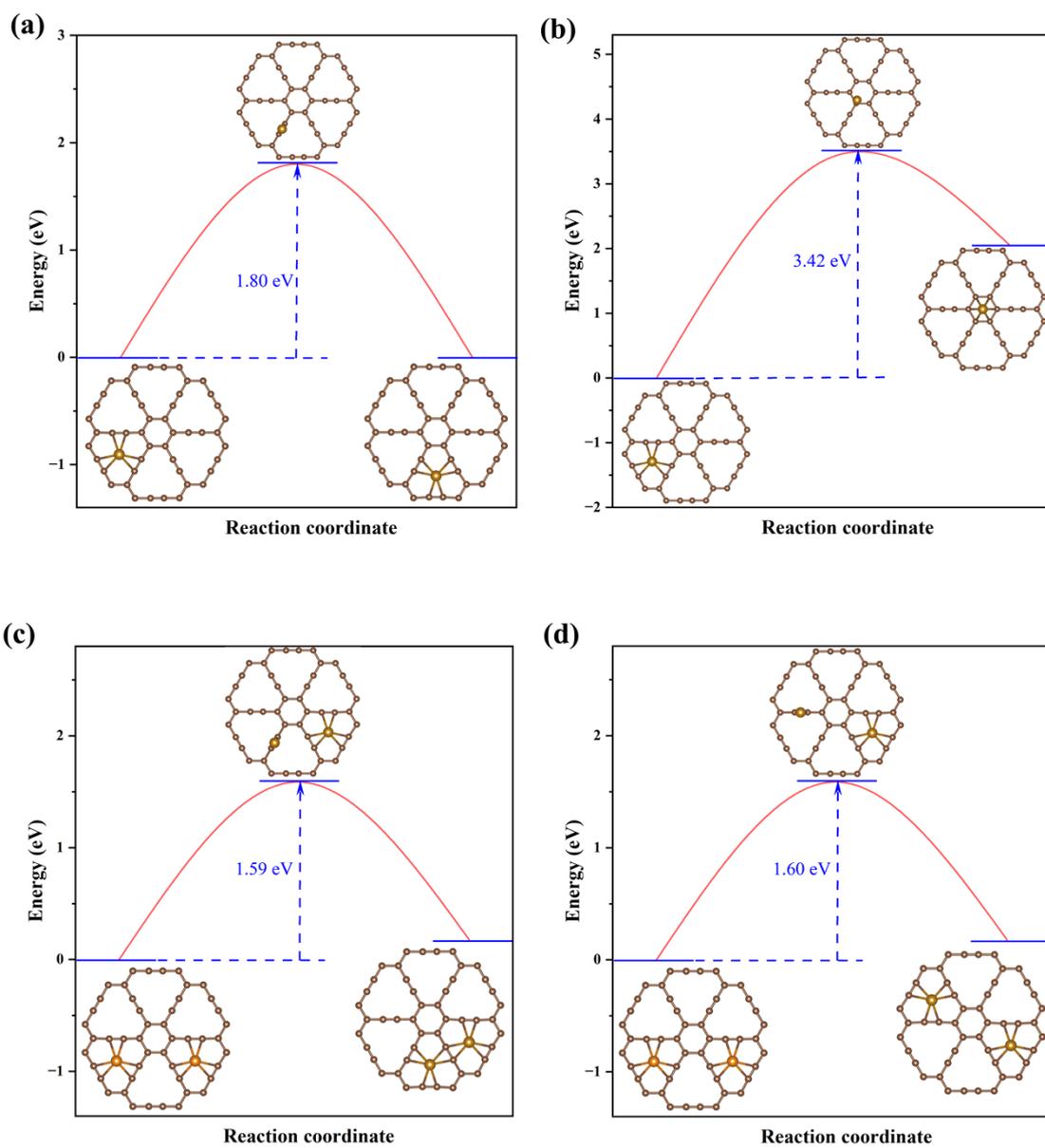


Figure S10. Energy change during Fe atom diffusion process: (a–b) low-loading Fe-GY and (c–d) high-loading Fe-GY.

Table S1. From top to bottom, the values are (in eV): the energies of the three possible configurations of high-loading TM-GY, the energy of GY with an adsorbed TM dimer, and the binding energy and clustering energy of TM atoms for the most stable high-loading TM-GY.

TM	Fe	Co	Ni	Cu	Rh	Pd	Ag	Ir	Pt
$E_{\text{TM1-TM2}}$	-422.72	-419.47	-418.12	-415.98	-418.50	-421.33	-414.97	-424.11	-421.40
$E_{\text{TM1-TM3}}$	-422.91	-419.88	-418.52	-416.36	-418.37	-421.40	-415.03	-424.04	-421.33
$E_{\text{TM1-TM4}}$	-422.85	-420.16	-418.56	-416.42	-418.56	-421.23	-415.07	-424.37	-421.55
$E_{2\text{TM-GY}}$	-421.28	-417.99	-416.62	-414.04	-417.75	-420.23	-415.22	-422.37	-420.24
$E_{\text{b,mono}}$	-1.38	-1.59	-1.94	-1.20	-1.02	-3.78	-0.57	-3.92	-3.42
E_{cluster}	-0.75	-1.08	-0.96	-1.19	-0.41	-0.58	0.05	-1.00	-0.66

References

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