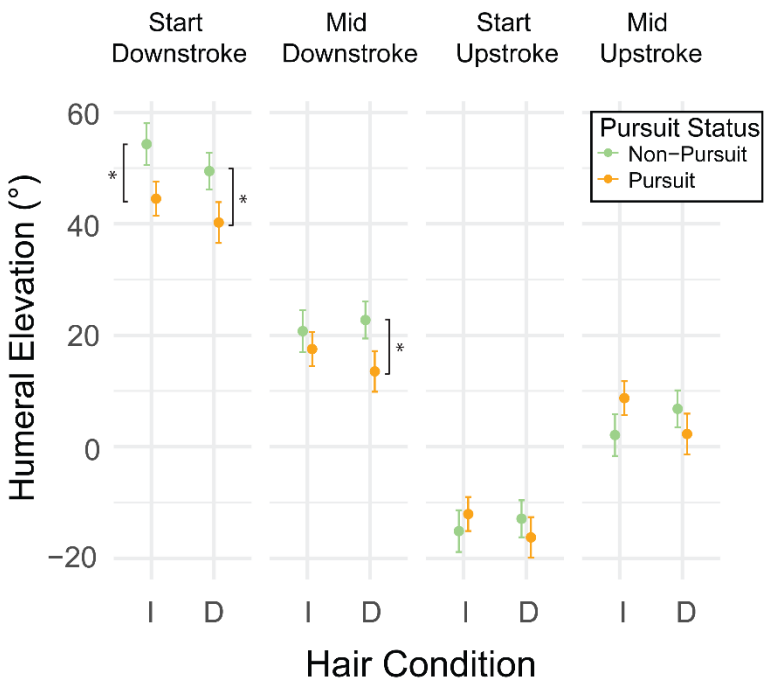


Supplementary Figure 3.1: Estimated marginal means and standard errors humeral elevation by hair and pursuit status. Values are separated by hair condition on the horizontal axis (I=intact, D=depilated) and by pursuit status within that (non-pursuit left in green, pursuit right in orange), based on best-fit linear model. Significant differences at α=0.05 indicated by *. Differences between pursuit categories within hair condition indicated by vertical bars.

Supplementary Table 3.1: Linear mixed-effects models tested for each response variable. Random effects of individual and trial included unless boundary fit is singular due to near-zero standard deviation of random effect. Best-fit model chosen in bold.

Fixed effects	Random effects	logLik	AICc
Humeral elevation			
Timepoint*Condition*Pursuit	**Individual, Trial**	**-12377.19**	**24792.38**
Timepoint*Condition	Individual, Trial	-12429.05	24880.10
Timepoint*Pursuit	Individual, Trial	-12401.19	24824.37
Timepoint	Individual, Trial	-12436.64	24887.29
Humeral protraction			
Timepoint*Condition*Pursuit	**Individual, Trial**	**-12266.71**	**24571.41**
Timepoint*Condition	Individual, Trial	-12297.38	24616.77
Timepoint*Pursuit	Individual, Trial	-12284.70	24591.40
Timepoint	Individual, Trial	-12304.20	24622.41
Elbow extension			
Timepoint*Condition*Pursuit	**Trial**	**-12130.58**	**24299.16**
Timepoint*Condition	Individual, Trial	-12179.58	24381.17
Timepoint*Pursuit	Trial	-12166.70	24353.40
Timepoint	Individual, Trial	-12193.60	24401.20
Wrist Extension			
Timepoint*Condition*Pursuit	**Individual, Trial**	**-11103.94**	**22245.87**
Timepoint*Condition	Individual, Trial	-11165.51	22353.01
Timepoint*Pursuit	Individual, Trial	-11139.65	22301.30
Timepoint	Individual, Trial	-11180.90	22375.80
Wing Area			
Timepoint*Condition*Pursuit	**Individual, Trial**	**-8308.39**	**16655.03**
Timepoint*Condition	Individual, Trial	-8324.36	16670.82
Timepoint*Pursuit	Trial	-8325.64	16671.36
Timepoint	Individual, Trial	-8332.30	16678.64
Speed			
Condition*Pursuit	Trial	-396.89	805.99
Condition	**Trial**	**-396.39**	**800.88**
Pursuit	Trial	-397.05	802.20
Wingbeat frequency			
Condition*Pursuit	Individual, Trial	-907.56	1829.34
Condition	Individual, Trial	-910.59	1831.33
Pursuit	**Individual, Trial**	**-908.47**	**1827.10**
Wingbeat amplitude			
Condition*Pursuit	Individual, Trial	-709.38	1433.04
Condition	Individual, Trial	-709.95	1430.04
Pursuit	**Individual, Trial**	**-709.26**	**1428.68**
Turn rate			
Condition*Pursuit	Individual, Trial	-4470.66	8953.37
Condition	**Individual**	**-4472.84**	**8953.70**
Pursuit	Individual, Trial	-4473.68	8955.39
Turn radius			
Condition*Pursuit	Individual, Trial	-3707.83	7429.73
Condition	**Individual, Trial**	**-3709.66**	**7429.36**
Pursuit	Individual, Trial	-3714.82	7439.68

Supplementary Table 3.4: Pairwise contrasts between the intact and depilated conditions within pursuit categories at four selected timepoints. Values are estimated marginal means, standard error (SE), degrees of freedom (df), t-ratio, and p-values calculated using emmeans in R from the best-fit generalized linear mixed-effects model. Significance indicated by bolding and at alpha levels given as follows: p≤0.01, **; p≤0.05, *. Bonferroni correction applied to account for multiple pairwise comparisons.

Timepoint	Intact	Depilated	SE	df	t-ratio	p-value
Humeral elevation (°): non-pursuit						
Up-down	54	50	3.53	49.8	1.370	0.1770
Mid-down	21	23	3.53	49.8	-0.565	0.5750
Down-up	-15	-13	3.53	49.4	-0.630	0.5320
Mid-up	2	7	3.53	49.8	-1.331	0.1890
Humeral elevation (°): pursuit						
Up-down	45	40	3.44	49.6	1.240	0.2210
Mid-down	18	14	3.43	49.1	1.168	0.2480
Down-up	-12	-16	3.42	48.5	1.226	0.2260
Mid-up	9	2	3.42	48.4	1.881	0.0660
Humeral protraction (°): non-pursuit						
Up-down	148	145	4.06	44.3	0.819	0.4170
Mid-down	129	128	4.06	44.2	0.244	0.8090
Down-up	115	116	4.05	44.0	-0.255	0.8000
Mid-up	130	130	4.06	44.3	0.819	0.9410
Humeral protraction (°): pursuit						
Up-down	139	134	3.98	44.9	1.125	0.2660
Mid-down	126	120	3.98	44.6	1.441	0.1570
Down-up	116	112	3.97	44.3	1.261	0.2140
Mid-up	**128**	**120**	3.97	44.2	2.010	0.0510 *
Elbow extension (°): non-pursuit						
Up-down	99	98	2.71	63.0	0.259	0.7960
Mid-down	114	113	2.70	62.9	0.128	0.8990
Down-up	104	107	2.70	62.4	-1.092	0.2790
Mid-up	**73**	**81**	2.71	63.1	-3.132	0.0030 **
Elbow extension (°): pursuit						
Up-down	102	100	2.73	64.6	0.684	0.4970
Mid-down	115	110	2.72	63.4	1.861	0.0670
Down-up	108	105	2.71	62.3	1.251	0.2160
Mid-up	**84**	**90**	2.71	61.7	-1.977	0.0530 *
Wrist extension (°): non-pursuit						
Up-down	123	126	2.61	46.0	-1.242	0.2210
Mid-down	138	141	2.61	45.9	-1.012	0.3170
Down-up	142	143	2.60	45.7	-0.581	0.5640
Mid-up	**117**	**124**	2.61	46.0	-2.351	0.0230 *
Wrist extension (°): pursuit						
Up-down	129	127	2.53	45.0	0.791	0.4330
Mid-down	**139**	**134**	2.52	44.6	2.242	0.0300 *
Down-up	140	136	2.52	44.2	1.705	0.0950

Mid-up	122	124	2.52	44.1	-0.874	0.3870
Wing area (cm^2): non-pursuit						
Up-down	29.7	31.3	1.04	46.2	-1.484	0.1450
Mid-down	34.4	34.9	1.04	46.2	-0.427	0.6710
Down-up	35.5	35.4	1.04	45.9	0.025	0.9800
Mid-up	29.1	29.5	1.04	46.2	-0.336	0.7380
Wing area (cm^2): pursuit						
Up-down	30.2	29.4	1.03	47.1	0.735	0.4660
Mid-down	**34.9**	**32.3**	1.02	46.7	2.665	0.0110 *
Down-up	**34.6**	**31.6**	1.02	46.3	3.013	0.0040 **
Mid-up	28.5	27.0	1.02	46.1	1.441	0.1560

Supplementary Table 3.5: Pairwise contrasts between the pursuit and non-pursuit categories within hair conditions at four select timepoints. Estimated marginal means can be found in Supp. Table 3. Values are contrast estimates within hair conditions ± standard error (SE), degrees of freedom (df), t-ratio, and p-values calculated using emmeans in R from the best-fit linear mixed-effects model. Significance indicated by bolding and at alpha levels given as follows: $p \leq 0.01$, **; $p \leq 0.05$, *. Bonferroni correction applied to account for multiple pairwise comparisons.

Timepoint	Intact contrast	df	t-ratio	p-value	Depilated contrast	df	t-ratio	p-value
Humeral elevation (°): non-pursuit - pursuit								
Up-down	**9.80±4.69**	22.7	2.088	0.0480 *	**9.23±4.58**	37.6	2.016	0.0510 *
Mid-down	3.22±4.69	22.6	0.686	0.5000	**9.22±4.58**	37.6	2.015	0.0510 *
Down-up	-3.07±4.69	22.6	-0.655	0.5190	3.35±4.56	37.1	0.734	0.4680
Mid-up	-6.62±4.69	22.7	-1.412	0.1720	4.51±4.57	37.0	0.988	0.3300
Humeral protraction (°): non-pursuit - pursuit								
Up-down	9.28±5.32	17.4	1.744	0.0990	**10.44±5.21**	32.0	2.004	0.0540 *
Mid-down	3.23±5.32	17.3	0.608	0.5510	7.98±5.21	32.0	1.532	0.1350
Down-up	-1.36±5.32	17.3	-0.255	0.8020	4.68±5.20	31.7	0.901	0.3750
Mid-up	2.15±5.32	17.4	0.404	0.6910	9.83±5.20	31.6	1.890	0.0680
Elbow extension (°): non-pursuit - pursuit								
Up-down	-2.88±2.79	11.1	-1.030	0.3250	-1.71±2.94	44.8	-0.580	0.5630
Mid-down	-1.12±2.78	11.0	-0.400	0.6960	3.60±2.93	44.6	1.230	0.2260
Down-up	-3.85±2.78	11.0	-1.380	0.1940	2.48±2.92	43.6	0.850	0.3990
Mid-up	**-11.71±2.79**	11.1	-4.190	0.0010 **	**-8.59±2.92**	43.2	-2.950	0.0050 **
Wrist extension (°): non-pursuit – pursuit								
Up-down	-6.27±3.68	34.8	-1.704	0.0970	-1.03±3.53	41.6	-0.291	0.7720
Mid-down	-1.00±3.67	34.6	-0.273	0.7860	**7.29±3.53**	41.5	2.065	0.0450 *
Down-up	1.98±3.67	34.6	0.538	0.5940	**7.78±3.52**	41.2	2.208	0.0330 *
Mid-up	-4.47±3.68	34.8	-1.215	0.2330	-0.53±3.52	41.2	-0.151	0.8800
Wing area (cm^2): non-pursuit - pursuit								
Up-down	-0.44±1.34	16.2	-0.327	0.7480	1.87±1.32	32.3	1.418	0.1660
Mid-down	-0.48±1.34	16.1	-0.361	0.7230	**2.70±1.32**	32.1	2.047	0.0490 *
Down-up	0.83±1.34	16.1	0.619	0.5440	**3.88±1.31**	31.8	2.954	0.0060 **
Mid-up	0.67±1.34	16.2	0.500	0.6240	2.49±1.31	31.7	1.896	0.0670

Supplementary Table 4.1: All pairwise comparisons between hair conditions (I=intact, F=fully-depilated, H=half-depilated) for each within-wingbeat timepoint (DWUP=down-upstroke transition, MDDW=mid-downstroke, MDUP=mid-upstroke, UPDW=up-downstroke transition). Degrees of freedom for all comparisons = 364. Values are estimated marginal means ± standard error (SE), test comparing hair conditions (I=intact, F=full, H=half), degrees of freedom (df), t-ratio, and p-values calculated using *emmeans* in R from the best-fit linear mixed-effects model. Estimate ± SE column represents contrast estimates from pairwise comparison ± cluster-robust CR2 standard error values. Tukey correction applied to account for multiple pairwise comparisons.

Variable	Contrast	Time	Estimate	SE	t-ratio	p-value
Elbow Asymmetry (cm)	I - F	DWUP	0.126	0.132	0.951	0.609
	I - H	DWUP	-0.364	0.309	-1.178	0.467
	F - H	DWUP	-0.489	0.292	-1.674	0.217
	I - F	MDDW	0.039	0.165	0.235	0.970
	I - H	MDDW	-0.391	0.469	-0.834	0.682
	F - H	MDDW	-0.430	0.461	-0.932	0.620
	I - F	MDUP	0.313	0.150	2.091	0.093
	I - H	MDUP	-0.511	0.446	-1.146	0.486
	F - H	MDUP	-0.824	0.423	-1.949	0.127
	I - F	UPDW	0.050	0.166	0.298	0.952
	I - H	UPDW	-0.567	0.509	-1.113	0.506
	F - H	UPDW	-0.616	0.495	-1.245	0.428
Shoulder Asymmetry (cm)	I - F	DWUP	0.100	0.096	1.037	0.554
	I - H	DWUP	-0.349	0.408	-0.856	0.668
	F - H	DWUP	-0.449	0.406	-1.106	0.511
	I - F	MDDW	0.070	0.121	0.578	0.832
	I - H	MDDW	-0.413	0.465	-0.888	0.648
	F - H	MDDW	-0.483	0.464	-1.041	0.551
	I - F	MDUP	0.226	0.089	2.546	0.030
	I - H	MDUP	-0.378	0.397	-0.952	0.608
	F - H	MDUP	-0.605	0.397	-1.523	0.281

Variable	Contrast	Time	Estimate	SE	t-ratio	p-value
	I - F	UPDW	0.116	0.086	1.344	0.372
	I - H	UPDW	-0.390	0.363	-1.074	0.531
	F - H	UPDW	-0.505	0.361	-1.399	0.343
Wingtip Asymmetry (cm)	I - F	DWUP	-0.185	0.423	-0.437	0.900
	I - H	DWUP	-1.192	0.961	-1.240	0.430
	F - H	DWUP	-1.007	0.923	-1.091	0.520
	I - F	MDDW	-0.330	0.703	-0.469	0.886
	I - H	MDDW	-1.327	1.329	-0.998	0.578
	F - H	MDDW	-0.997	1.388	-0.718	0.753
	I - F	MDUP	0.304	0.450	0.676	0.777
	I - H	MDUP	-1.712	1.319	-1.299	0.397
	F - H	MDUP	-2.017	1.317	-1.532	0.277
	I - F	UPDW	0.554	0.788	0.703	0.762
	I - H	UPDW	-1.131	1.333	-0.848	0.673
	F - H	UPDW	-1.685	1.229	-1.371	0.357
Fifth Digit Asymmetry (cm)	I - F	DWUP	0.155	0.232	0.667	0.783
	I - H	DWUP	-0.874	0.669	-1.307	0.392
	F - H	DWUP	-1.029	0.633	-1.626	0.236
	I - F	MDDW	-0.198	0.344	-0.577	0.833
	I - H	MDDW	-0.792	0.776	-1.021	0.564
	F - H	MDDW	-0.594	0.786	-0.755	0.731

Variable	Contrast	Time	Estimate	SE	t-ratio	p-value
	I - F	MDUP	0.327	0.239	1.365	0.361
	I - H	MDUP	-1.032	0.594	-1.739	0.192
	F - H	MDUP	-1.359	0.575	-2.364	0.049
	I - F	UPDW	0.284	0.252	1.129	0.497
	I - H	UPDW	-0.746	0.648	-1.152	0.483
	F - H	UPDW	-1.030	0.625	-1.648	0.227
Wrist Asymmetry (cm)	I - F	DWUP	0.110	0.290	0.378	0.924
	I - H	DWUP	-0.420	0.562	-0.748	0.735
	F - H	DWUP	-0.530	0.522	-1.015	0.568
	I - F	MDDW	0.083	0.182	0.454	0.892
	I - H	MDDW	-0.739	0.799	-0.925	0.625
	F - H	MDDW	-0.822	0.781	-1.053	0.544
	I - F	MDUP	0.520	0.203	2.565	0.029
	I - H	MDUP	-0.673	0.697	-0.966	0.599
	F - H	MDUP	-1.193	0.692	-1.725	0.197
	I - F	UPDW	0.826	0.330	2.504	0.034
	I - H	UPDW	-0.409	0.729	-0.562	0.840
	F - H	UPDW	-1.236	0.685	-1.803	0.170
Left Chordwise Extension (cm)	I - F	DWUP	-0.037	0.198	-0.187	0.981
	I - H	DWUP	0.155	0.156	0.998	0.578
	F - H	DWUP	0.192	0.190	1.011	0.571

Variable	Contrast	Time	Estimate	SE	t-ratio	p-value
	I - F	MDDW	-0.057	0.152	-0.376	0.925
	I - H	MDDW	0.177	0.111	1.603	0.246
	F - H	MDDW	0.234	0.115	2.030	0.106
	I - F	MDUP	0.046	0.208	0.222	0.973
	I - H	MDUP	0.174	0.112	1.555	0.267
	F - H	MDUP	0.128	0.204	0.631	0.803
	I - F	UPDW	0.048	0.161	0.300	0.952
	I - H	UPDW	0.332	0.148	2.234	0.067
	F - H	UPDW	0.283	0.129	2.192	0.074
Right Chordwise Extension (cm)	I - F	DWUP	0.029	0.145	0.200	0.978
	I - H	DWUP	0.266	0.133	1.995	0.115
	F - H	DWUP	0.237	0.132	1.791	0.174
	I - F	MDDW	0.083	0.163	0.508	0.868
	I - H	MDDW	0.307	0.100	3.073	0.006
	F - H	MDDW	0.224	0.152	1.470	0.306
	I - F	MDUP	-0.065	0.232	-0.280	0.958
	I - H	MDUP	-0.048	0.192	-0.248	0.967
	F - H	MDUP	0.017	0.229	0.076	0.997
	I - F	UPDW	0.048	0.218	0.220	0.974
	I - H	UPDW	0.174	0.126	1.381	0.352
	F - H	UPDW	0.126	0.226	0.558	0.842

Variable	Contrast	Time	Estimate	SE	t-ratio	p-value
Left Elbow Extension (º)	I - F	DWUP	0.067	0.204	0.328	0.943
	I - H	DWUP	0.177	0.214	0.826	0.687
	F - H	DWUP	0.110	0.282	0.391	0.919
	I - F	MDDW	0.142	0.185	0.767	0.723
	I - H	MDDW	0.180	0.189	0.953	0.607
	F - H	MDDW	0.038	0.237	0.159	0.986
	I - F	MDUP	0.010	0.176	0.056	0.998
	I - H	MDUP	0.110	0.150	0.731	0.745
	F - H	MDUP	0.100	0.217	0.462	0.889
	I - F	UPDW	0.166	0.107	1.548	0.270
	I - H	UPDW	0.152	0.127	1.191	0.459
	F - H	UPDW	-0.014	0.148	-0.097	0.995
Right Elbow Extension (º)	I - F	DWUP	0.216	0.103	2.103	0.091
	I - H	DWUP	0.278	0.128	2.170	0.078
	F - H	DWUP	0.061	0.151	0.407	0.913
	I - F	MDDW	0.099	0.142	0.697	0.765
	I - H	MDDW	0.067	0.112	0.599	0.821
	F - H	MDDW	-0.032	0.109	-0.294	0.954
	I - F	MDUP	0.168	0.090	1.879	0.146
	I - H	MDUP	0.203	0.137	1.486	0.299
	F - H	MDUP	0.035	0.140	0.248	0.967

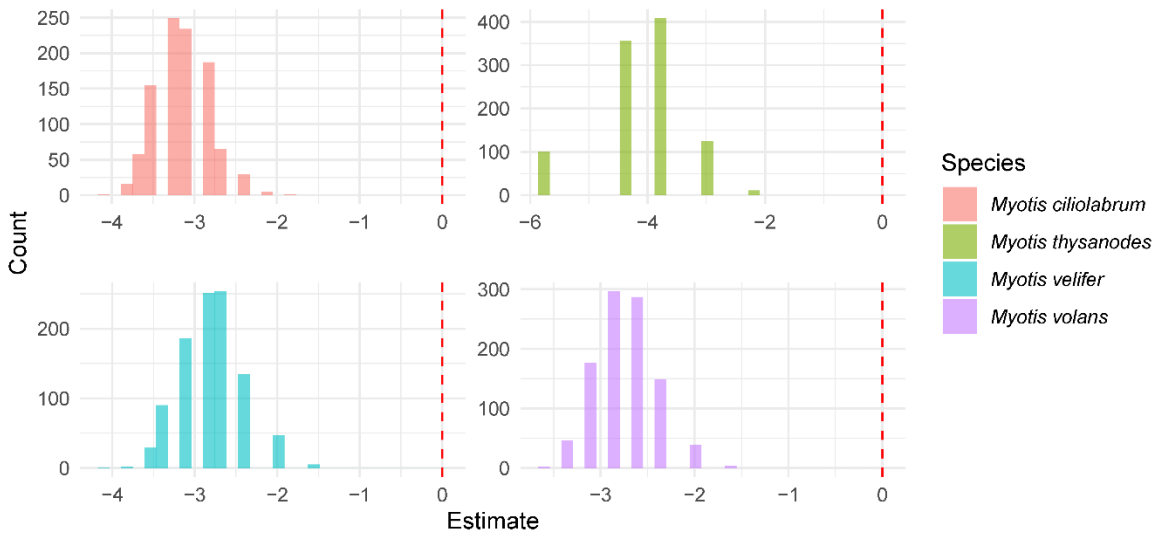
Variable	Contrast	Time	Estimate	SE	t-ratio	p-value
	I - F	UPDW	-0.004	0.118	-0.031	0.999
	I - H	UPDW	0.144	0.070	2.064	0.099
	F - H	UPDW	0.148	0.113	1.311	0.390
Left Wingspan Extension (cm)	I - F	DWUP	0.343	0.552	0.621	0.809
	I - H	DWUP	0.556	0.410	1.358	0.364
	F - H	DWUP	0.214	0.438	0.488	0.877
	I - F	MDDW	0.367	0.487	0.754	0.732
	I - H	MDDW	0.723	0.391	1.848	0.156
	F - H	MDDW	0.356	0.390	0.912	0.633
	I - F	MDUP	-0.073	0.519	-0.141	0.989
	I - H	MDUP	0.680	0.445	1.526	0.280
	F - H	MDUP	0.753	0.448	1.683	0.213
	I - F	UPDW	0.279	0.489	0.570	0.836
	I - H	UPDW	1.099	0.313	3.512	0.001
	F - H	UPDW	0.820	0.386	2.126	0.086
Right Wingspan Extension (cm)	I - F	DWUP	0.695	0.424	1.638	0.231
	I - H	DWUP	1.273	0.306	4.164	0
	F - H	DWUP	0.578	0.402	1.436	0.323
	I - F	MDDW	0.382	0.348	1.098	0.516
	I - H	MDDW	1.218	0.416	2.929	0.010
	F - H	MDDW	0.835	0.396	2.110	0.089

Variable	Contrast	Time	Estimate	SE	t-ratio	p-value
	I - F	MDUP	0.140	0.369	0.380	0.923
	I - H	MDUP	0.833	0.483	1.726	0.197
	F - H	MDUP	0.693	0.419	1.654	0.224
	I - F	UPDW	0.657	0.320	2.052	0.101
	I - H	UPDW	1.085	0.331	3.278	0.003
	F - H	UPDW	0.428	0.171	2.506	0.034
Left Wing Area (cm^2)	I - F	DWUP	1.445	2.422	0.597	0.822
	I - H	DWUP	1.948	2.795	0.697	0.765
	F - H	DWUP	0.503	2.360	0.213	0.975
	I - F	MDDW	1.497	2.333	0.642	0.797
	I - H	MDDW	2.517	3.039	0.828	0.686
	F - H	MDDW	1.019	2.021	0.504	0.869
	I - F	MDUP	0.241	2.036	0.118	0.992
	I - H	MDUP	1.860	2.720	0.684	0.773
	F - H	MDUP	1.619	2.661	0.608	0.816
	I - F	UPDW	1.817	1.974	0.920	0.628
	I - H	UPDW	4.540	2.927	1.551	0.269
	F - H	UPDW	2.723	2.356	1.156	0.481
Right Wing Area (cm^2)	I - F	DWUP	3.249	1.869	1.738	0.193
	I - H	DWUP	5.038	2.505	2.012	0.111
	F - H	DWUP	1.790	2.069	0.865	0.663

Variable	Contrast	Time	Estimate	SE	t-ratio	p-value
	I - F	MDDW	3.280	1.645	1.993	0.115
	I - H	MDDW	5.147	2.640	1.950	0.126
	F - H	MDDW	1.868	2.170	0.861	0.665
	I - F	MDUP	0.215	1.574	0.136	0.990
	I - H	MDUP	1.109	2.898	0.383	0.923
	F - H	MDUP	0.894	2.559	0.349	0.935
	I - F	UPDW	3.135	1.645	1.906	0.138
	I - H	UPDW	3.900	2.102	1.855	0.153
	F - H	UPDW	0.765	1.613	0.474	0.884

Supplementary Table 4.2: Pairwise contrasts between the intact, fully-depilated, and half-depilated conditions for the range in anteroposterior axis motion. Estimates reflect the difference between the paired conditions, along with the standard error values (SE), t-ratios, and p-values calculated using *emmeans* in R with a linear mixed-effects model, adjusted for multiple comparisons using Tukey correction; degrees of freedom = 91 for all comparisons. Significance at $p \leq 0.05$ indicated by *.

Contrast	Estimate	SE	t-ratio	p-value
Intact - Full	-0.1778	0.4920	-0.3614	0.9306
Intact - Half	1.1445	0.3996	2.8640	0.0142 *
Full - Half	1.3223	0.5187	2.5495	0.0331 *



Supplementary Figure 5.1: Distribution of fixed effect estimates for sensitivity analysis. Subset of data includes all species which included drop trials except for Myotis ciliolabrum, the species with the highest number of drops. Represents results from 1000 iterations of ≤5 trials per individual per species, randomly sampled. See Supplementary Table A for proportion of fixed effect estimates that were significant.

Supplementary Table 5.1: Wing areas and masses from one voucher specimen per species collected from the field site in Portal, AZ, USA.

Species	Wing area (cm^2)	Mass (g)
Corynorhinus townsendii	34.5	10.0
Myotis ciliolabrum	21.5	3.5
Myotis thysanodes	25.7	6.0
Myotis velifer	38.1	8.1
Myotis volans	29.0	6.5

Supplementary Table 5.2: Means and standard deviations of estimates from models of first interaction contact point by species across 1000 iterations with data subsetted to up to five randomly-selected trials per individual. Significance proportion represents the proportion of models resulting in a significant difference between a given species and the reference level of *Corynorhinus townsendii*.

Species	Mean estimate	SD estimate	Significance proportion
M. ciliolabrum	-3.135	0.32	0.994
M. thysanodes	-4.081	0.75	0.989
M. velifer	-2.814	0.38	0.813
M. volans	-2.760	0.32	0.808

Supplementary Table 5.6: Estimated marginal means from generalized linear mixed-effects model. Response variable is binomially-distributed first interaction contact point, predictor variable is species, with reference level of 'tail'. Probability values are back-transformed from logit scale.

Species	Predicted probability of wing-first interaction	SE	Confidence interval lower bound	Confidence interval upper bound
C. townsendii	0.98	0.026	0.76	1.0
M. ciliolabrum	0.55	0.068	0.41	0.67
M. thysanodes	0.32	0.113	0.15	0.57
M. velifer	0.62	0.074	0.46	0.75
M. volans	0.58	0.087	0.40	0.74

Supplementary Table 5.7: Pairwise contrasts between species' first interaction contact point. t-ratios and p-values calculated from predicted probability values produced by a generalized linear model with first interaction contact point as the response variable, species as the predictor variable. Produced using Firth's bias-Reduced penalized-likelihood logistic regression with respect to the reference level of 'tail'. Significance at alpha levels given as follows: $p<0.01$, ***; $p<0.05$, **; $p<0.10$, *.

Contrast	Odds ratio	SE	t-ratio	p-value
Myotis ciliolabrum / Corynorhinus townsendii	0.023	0.033	-2.604	0.074*
Myotis thysanodes / Corynorhinus townsendii	0.009	0.014	-3.100	0.019**
Myotis velifer / Corynorhinus townsendii	0.030	0.044	-2.392	0.123
Myotis volans / Corynorhinus townsendii	0.026	0.038	-2.484	0.099*
Myotis ciliolabrum / Myotis thysanodes	2.518	1.480	1.575	0.515
Myotis ciliolabrum / Myotis velifer	0.750	0.312	-0.692	0.958
Myotis ciliolabrum / Myotis volans	0.879	0.396	-0.287	0.999
Myotis thysanodes / Myotis velifer	0.298	0.180	-1.999	0.271
Myotis thysanodes / Myotis volans	0.349	0.220	-1.671	0.455
Myotis velifer / Myotis volans	1.172	0.558	0.333	0.997

Supplementary Table 5.8: Generalized linear mixed-effects model output with binomially-distributed success/failure as the response variable, number of contact points as the predictor, and individual as a random effect. Number of observations = 134. Significance at alpha levels given as follows: $p<0.01$, ***; $p<0.05$, **; $p<0.10$, *.

	Estimate	SE	z-value	p-value
Intercept	-6.071	1.524	-3.99	<0.001 ***
Number of contacts	3.617	0.769	4.71	<0.001 ***

Supplementary Table 5.9: Generalized linear mixed-effects model output with binomially-distributed success/failure as the response variable and number of contact points as the predictor. Data subsetted to include trials from all species except *Myotis ciliolabrum*. Number of observations = 89, number of individuals = 13. When fitting a model with individual as a random effect, the boundary fit was singular with standard deviation of variance due to individual equal to 0.0000000103, and the model's AIC value was 39.3. When fitting without individual as a random effect, boundary fit was no longer singular and model AIC value was 37.31. Significance at alpha levels given as follows: p<0.01, ***; p<0.05, **; p<0.10, *.

	Estimate	SE	z-value	p-value
Intercept	-5.85	2.10	-2.79	0.005 ***
Number of contacts	3.78	1.08	3.51	0.001 ***

Supplementary Table 5.10: Generalized linear mixed-effects model output with binomially-distributed success/failure as the response variable, number of contact points as the predictor, and individual as a random effect. Data subsetted to include only trials from *Myotis ciliolabrum*. Number of observations = 45, number of individuals = 6. Significance at alpha levels given as follows: p<0.01, ***; p<0.05, **; p<0.10, *.

	Estimate	SE	z-value	p-value
Intercept	-6.73	2.36	-2.85	0.004 ***
Number of contacts	3.52	1.12	3.14	0.002 ***

Supplementary Table 5.11: Estimated marginal means from a generalized linear mixed-effects model. Response variable is moth handling time (units of seconds), predictor variable is species, with random effect of individual.

Species	Predicted moth handling time	SE	Confidence interval lower bound	Confidence interval upper bound
C. townsendii	0.44	0.0761	0.26	0.61
M. ciliolabrum	0.40	0.0675	0.24	0.55
M. thysanodes	0.45	0.114	0.16	0.74
M. velifer	0.38	0.0703	0.21	0.54
M. volans	0.34	0.0783	0.16	0.52

Supplementary Table 5.12: Pairwise contrasts of moth handling time between species. Estimates and p-values calculated from predicted probability values produced by a generalized linear mixed-effects model with moth handling time as the response variable and species as the predictor variable with individual as a random effect.

Contrast	Estimate	SE	t-ratio	p-value
Corynorhinus townsendii / Myotis ciliolabrum	0.041	0.102	-0.366	0.448
Corynorhinus townsendii / Myotis thysanodes	-0.0097	0.137	-0.659	0.639
Corynorhinus townsendii / Myotis velifer	0.062	0.104	-0.358	0.483
Corynorhinus townsendii / Myotis volans	0.10	0.109	-0.349	0.549
Myotis ciliolabrum / Myotis thysanodes	-0.051	0.133	-0.685	0.584
Myotis ciliolabrum / Myotis velifer	0.021	0.0975	-0.374	0.417
Myotis ciliolabrum / Myotis volans	0.059	0.103	-0.366	0.484
Myotis thysanodes / Myotis velifer	0.072	0.134	-0.572	0.716
Myotis thysanodes / Myotis volans	0.11	0.139	-0.554	0.773
Myotis velifer / Myotis volans	0.037	0.105	-0.402	0.477

Supplementary Table 5.14: Generalized linear model output with a response variable of success/failure, a predictor variable of first interaction contact point, and individual as a random effect. Estimates and p-values with respect to the reference level of ‘wing’. Estimates reported on the logit scale; dataset comprises 170 observations. Significance at alpha levels given as follows: $p<0.01$, ***; $p<0.05$, **; $p<0.10$, *.

	Estimate	SE	z value	p-value
Intercept	0.8216	0.2411	3.408	0.0007***
Tail	-0.7325	0.3430	-2.135	0.0327**

Supplementary Table 5.15: Estimated marginal means from generalized linear model. Response variable is binomially-distributed success/failure, predictor variable is species. Probability values are back-transformed from logit scale. See Supplementary Table 5.18 for model output.

Species	Predicted probability of success	SE	Confidence interval lower bound	Confidence interval upper bound
C. townsendii	0.923	0.052	0.74	0.98
M. ciliolabrum	0.547	0.068	0.41	0.68
M. thysanodes	0.647	0.116	0.40	0.83
M. velifer	0.581	0.075	0.43	0.72
M. volans	0.581	0.089	0.40	0.74

Supplementary Table 5.16: Generalized linear mixed-effects model output with insect handling time as the response variable, species as the predictor, and individual as a random effect. Number of observations = 108. Significance at alpha levels given as follows: p<0.01, ***; p<0.05, **; p<0.10, *.

	Estimate	SE	t-value	p-value
Intercept	0.4376	0.073	6.023	<0.001 ***
M. ciliolabrum	-0.0409	0.097	-0.421	0.681
M. thysanodes	0.0107	0.135	0.071	0.945
M. velifer	-0.0623	0.100	-0.621	0.547
M. volans	-0.0998	0.106	-0.943	0.366

Supplementary Table 5.17: Generalized linear model output using Firth's bias-Reduced penalized-likelihood logistic regression with a response variable of first interaction contact point and a predictor variable of species. Estimates and p-values with respect to the reference level of 'tail'. Estimates reported on the logit scale. Significance at alpha levels given as follows: p<0.01, ***; p<0.05, **; p<0.10, *.

	Estimate	**SE**	**χ^2 value**	**p-value**
Intercept	3.9703	1.427	32.450	<0.001***
M. ciliolabrum	-3.7846	1.453	20.742	<0.001***
M. thysanodes	-4.7079	1.519	25.181	<0.001***
M. velifer	-3.4965	1.461	15.366	<0.001***
M. volans	-3.6552	1.472	16.099	<0.001***

Supplementary Table 5.18: Generalized linear model output with a response variable of success/failure and a predictor variable of species. Estimates and p-values with respect to the reference level of *Corynorhinus townsendii*. Estimates reported on the logit scale; dataset comprises 170 observations. When fitting a model with individual as a random effect, the boundary fit was singular with standard deviation of variance due to individual equal to 0, and model AIC value of 221.8. When fitting without individual as a random effect, boundary fit was no longer singular and the model's AIC value was 219.8. Significance at alpha levels given as follows: p<0.01, ***; p<0.05, **; p<0.10, *.

	Estimate	**SE**	**z value**	**p-value**
Intercept	2.485	0.736	3.376	0.0007 ***
M. ciliolabrum	-2.300	0.786	-2.921	0.0035 ***
M. thysanodes	-1.879	0.894	-2.102	0.0360 **
M. velifer	-2.156	0.798	-2.701	0.0069 ***
M. volans	-2.160	0.821	-2.630	0.0085 ***

Supplementary Table 5.19: Raw proportions and counts of success, miss, and drop interaction outcomes by species.

Species	Outcome	Count	Proportion
Corynorhinus townsendii	Miss	2	0.077
Corynorhinus townsendii	Success	24	0.923
Myotis ciliolabrum	Drop	16	0.302
Myotis ciliolabrum	Miss	8	0.151
Myotis ciliolabrum	Success	29	0.547
Myotis thysanodes	Drop	3	0.167
Myotis thysanodes	Miss	4	0.222
Myotis thysanodes	Success	11	0.611
Myotis velifer	Drop	5	0.116
Myotis velifer	Miss	13	0.302
Myotis velifer	Success	25	0.581

Myotis volans	Drop	4	0.129
Myotis volans	Miss	9	0.290
Myotis volans	Success	18	0.581