

**TABLE S1. Genome size measurements of native American hawkweeds**

Species	Accession	2n	Average 2C [pg]	2C range [pg]
<i>H. albiflorum</i>	H908_1		7.517	7.515–7.521
	H908_2		7.542	7.493–7.591
	H908_3		7.558	7.537–7.580
	<b>H908 (all)</b>		<b>7.539</b>	<b>7.493–7.591</b>
<i>H. canadense</i>	<b>canad</b>		<b>12.332</b>	–
<i>H. carneum</i>	H.carneum.1		9.515	9.416–9.606
	H.carneum.2		9.533	9.432–9.584
	H.carneum.3		9.531	9.454–9.595
	<b>H. carneum (all)</b>		<b>9.526</b>	<b>9.416–9.606</b>
<i>H. guatemalense</i>	GUA/2 + Z	18	9.227	9.193–9.253
	GUA/3 + Z		9.209	9.188–9.231
	GUA/4 + Z		9.217	9.160–9.269
	GUA/5 + Z	18	9.262	9.193–9.318
	GUA/6 + Z		9.248	9.236–9.264
	<b>GUA (all)</b>		<b>9.233</b>	<b>9.160–9.318</b>
<i>H. mexicanum</i>	<b>H903 (8 plants)</b>		<b>10.14</b>	<b>10.09–10.23</b>
<i>H. scabrum</i>	1002/2 + Z	18	9.922	9.861–9.959
	1002/4 + Z		9.942	9.926–9.959
	<b>1002 (all)</b>		<b>9.932</b>	<b>9.861–9.959</b>

Accession: several plants from the same population per species, individual measurements and average for the population (3 measurements, if not indicated otherwise); 2n – chromosome counts ( $2n = 2x = 18$ ). The accession of *H. canadense* is triploid according to its genome size (one measurement only).