Table S43: Identified repeat families in the *Nasonia* genome. Repeat families are based on the Repbase classification using RepeatMasker 3.25 and manual curation. Total number of repeats, total length in assembly, and percentages are shown. 'Novel' families have less than 80% homology to known elements, while 'Novel tandem' indicates a similar prediction that also has a tandem repeat content greater than 15%.

Repeat Class	Repeat family	Number of repeats in assembly	Percent of total repeats	Total length of repeat in assembly (bp)	Percent of total repeat length
DNA Transposons	Chapaev3-1_NVi	701	0.2	153239	0.3
	NAUT1_NVi	2297	0.7	292621	0.6
	NAVIHAT1	53	0.0	12105	0.0
	NAVIMAR1	48	0.0	6079	0.0
	NAVIMARN1	1042	0.3	266510	0.5
	Transib1_NVi	659	0.2	85680	0.2
	DNA Novel	1382	0.4	290838	0.6
Retroposons (LINE-like)	LINER1	17389	5.4	2544361	5.2
	NAVIRTE1	400	0.1	128393	0.3
	PENEL1_NVi	660	0.2	73042	0.1
Retrotransposons (LTR)	BEL1-NVi_LTR	79	0.0	17829	0.0
	Copia12-NVi_I	589	0.2	118215	0.2
	Copia13-NVi_I	180	0.1	21888	0.0
	Copia13-NVi_LTR	227	0.1	41076	0.1
	Copia17-NVi_I	178	0.1	57633	0.1
	Copia3-NVi_LTR	5	0.0	745	0.0
	Copia4-NVi_LTR	1149	0.4	284878	0.6
	Copia6-NVi_LTR	4	0.0	911	0.0
	Copia9-NVi_LTR	31	0.0	9696	0.0
	Gypsy1-NVi_I	268	0.1	118821	0.2
	Gypsy11-NVi_I	53	0.0	9401	0.0
	Gypsy14-NVi_I	226	0.1	50919	0.1

	Gypsy14-NVi_LTR	56	0.0	7856	0.0
	Gypsy3-NVi_I	149	0.0	61921	0.1
	Gypsy5-NVi_I	312	0.1	48645	0.1
	Gypsy5-NVi_LTR	85	0.0	9631	0.0
	Gypsy6-NVi_LTR	312	0.1	30500	0.1
	Gypsy7-NVi_I	70	0.0	14823	0.0
	Gypsy7-NVi_LTR	223	0.1	53596	0.1
	Gypsy8-NVi_I	23	0.0	5035	0.0
	LTR Novel	11202	3.5	3850924	7.8
Retroposon/Retrotransposon		1421	0.4	383807	0.8
Novel Interspersed		111295	34.3	16311505	33.1
Low Complexity	T-rich	116	0.0	11473	0.0
	GC-rich	3593	1.1	103438	0.2
	AT-rich	55187	17.0	6494698	13.2
Novel Tandem Repeats	Novel Tandem	5062	1.6	4328844	8.8
Satellites	HSATII	4	0.0	540	0.0
	NVBRP5	1920	0.6	1170737	2.4
	NVBRP3	1591	0.5	2441680	5.0
	BRP2_NV	7562	2.3	4337105	8.8
Simple Repeats	(TTTA)n	186	0.1	33286	0.1
	(TTAGGC)n	7	0.0	816	0.0
	(TTAAG)n	7	0.0	216	0.0
	(TTAAA)n	76	0.0	4161	0.0
	(TTAA)n	61	0.0	4434	0.0
	(TTA)n	260	0.1	52344	0.1
	(TGGGGG)n	14	0.0	888	0.0
	(TGGA)n	13	0.0	494	0.0
	(TGG)n	328	0.1	16956	0.0
	(TGAG)n	28	0.0	1198	0.0
	(TGAA)n	26	0.0	1045	0.0
	(TG)n	214	0.1	22539	0.0
	(TC)n	2130	0.7	169205	0.3

(TATATG)n	53	0.0	20610	0.0
(TATAA)n	189	0.1	10980	0.0
(TAGG)n	7	0.0	200	0.0
(TAGA)n	98	0.0	3341	0.0
(TAG)n	286	0.1	12540	0.0
(TAATG)n	8	0.0	1059	0.0
(TAAG)n	16	0.0	481	0.0
(TAAAAA)n	419	0.1	28351	0.1
(TAAAA)n	214	0.1	11728	0.0
(TAAA)n	1201	0.4	83393	0.2
(TAA)n	1953	0.6	96461	0.2
(TA)n	13633	4.2	800803	1.6
(GGGGA)n	46	0.0	3751	0.0
(GGGAGA)n	366	0.1	19293	0.0
(GGGAA)n	20	0.0	2124	0.0
(GGGA)n	109	0.0	5990	0.0
(GGAGAA)n	286	0.1	21990	0.0
(GGAGA)n	87	0.0	6662	0.0
(GGAAA)n	68	0.0	8283	0.0
(GGAA)n	149	0.0	8182	0.0
(GGA)n	819	0.3	35255	0.1
(GAGAA)n	211	0.1	19180	0.0
(GAAAA)n	283	0.1	23567	0.0
(GAAA)n	356	0.1	23687	0.0
(GAA)n	1803	0.6	82172	0.2
(GA)n	48807	15.0	2508287	5.1
(G)n	196	0.1	6890	0.0
(CTTTA)n	11	0.0	578	0.0
(CTTAT)n	4	0.0	144	0.0
(CTATT)n	32	0.0	871	0.0
(CTATA)n	18	0.0	857	0.0
(CTACT)n	8	0.0	237	0.0
(CTAAT)n	117	0.0	3086	0.0

(CTAAA)n	2	0.0	178	0.0
(CTAA)n	9	0.0	266	0.0
(CGTAG)n	1	0.0	38	0.0
(CGGT)n	7	0.0	179	0.0
(CGGGGG)n	9	0.0	716	0.0
(CGGG)n	7	0.0	266	0.0
(CGGAG)n	4	0.0	181	0.0
(CGGAA)n	3	0.0	122	0.0
(CGGA)n	69	0.0	1882	0.0
(CGG)n	1405	0.4	51682	0.1
(CGAT)n	23	0.0	689	0.0
(CGAGT)n	9	0.0	203	0.0
(CGAGG)n	4	0.0	114	0.0
(CGAGA)n	2	0.0	64	0.0
(CGAG)n	186	0.1	5510	0.0
(CGACG)n	5	0.0	110	0.0
(CGAAT)n	1	0.0	175	0.0
(CGAAG)n	1	0.0	92	0.0
(CGAAA)n	5	0.0	435	0.0
(CGAA)n	53	0.0	1929	0.0
(CGA)n	1420	0.4	53393	0.1
(CG)n	320	0.1	8121	0.0
(CCTAT)n	2	0.0	40	0.0
(CCTAA)n	15	0.0	393	0.0
(CCGTA)n	1	0.0	50	0.0
(CCGG)n	3	0.0	108	0.0
(CCGCG)n	5	0.0	105	0.0
(CCGAG)n	7	0.0	213	0.0
(CCCGAA)n	12	0.0	1154	0.0
(CCCCG)n	1	0.0	19	0.0
(CCCCAG)n	19	0.0	1563	0.0
(CCCCAA)n	2	0.0	118	0.0
(CCCA)n	3	0.0	89	0.0

(CCAA)n	3	0.0	74	0.0
(CATTT)n	21	0.0	875	0.0
(CATTC)n	1	0.0	24	0.0
(CATTA)n	79	0.0	9793	0.0
(CATGC)n	15	0.0	1308	0.0
(CATG)n	2	0.0	44	0.0
(CATCT)n	4	0.0	260	0.0
(CATCG)n	5	0.0	108	0.0
(CATCC)n	1	0.0	25	0.0
(CATATA)n	256	0.1	12139	0.0
(CATAT)n	3	0.0	175	0.0
(CATAG)n	22	0.0	1010	0.0
(CATAC)n	10	0.0	644	0.0
(CATAA)n	4	0.0	114	0.0
(CATA)n	379	0.1	19196	0.0
(CAT)n	645	0.2	29928	0.1
(CAGTT)n	1	0.0	100	0.0
(CAGTC)n	1	0.0	28	0.0
(CAGTA)n	3	0.0	197	0.0
(CAGT)n	16	0.0	404	0.0
(CAGGC)n	1	0.0	29	0.0
(CAGGA)n	1	0.0	72	0.0
(CAGG)n	28	0.0	786	0.0
(CAGCT)n	2	0.0	41	0.0
(CAGCG)n	1	0.0	19	0.0
(CAGCC)n	2	0.0	56	0.0
(CAGC)n	10	0.0	272	0.0
(CAGAT)n	2	0.0	54	0.0
(CAGAGA)n	53	0.0	4245	0.0
(CAGAG)n	20	0.0	843	0.0
(CAGAA)n	2	0.0	59	0.0
(CAGA)n	45	0.0	1656	0.0
(CAG)n	3759	1.2	147619	0.3

(CACTT)n	4	0.0	158	0.0
(CACTG)n	2	0.0	46	0.0
(CACTA)n	1	0.0	23	0.0
(CACGA)n	1	0.0	23	0.0
(CACG)n	158	0.0	6712	0.0
(CACCT)n	1	0.0	28	0.0
(CACCC)n	4	0.0	104	0.0
(CACCAT)n	65	0.0	3554	0.0
(CACAT)n	1	0.0	47	0.0
(CACAG)n	7	0.0	430	0.0
(CAATT)n	11	0.0	647	0.0
(CAATC)n	1	0.0	64	0.0
(CAATA)n	5	0.0	151	0.0
(CAAT)n	33	0.0	1206	0.0
(CAAGT)n	1	0.0	25	0.0
(CAAGC)n	22	0.0	433	0.0
(CAAGA)n	4	0.0	85	0.0
(CAAG)n	19	0.0	594	0.0
(CAACT)n	2	0.0	62	0.0
(CAACG)n	3	0.0	258	0.0
(CAAAT)n	7	0.0	174	0.0
(CAAAG)n	7	0.0	239	0.0
(CAAAC)n	1	0.0	83	0.0
(CAAAAA)n	106	0.0	8654	0.0
(CAAAA)n	24	0.0	1172	0.0
(CAAA)n	45	0.0	1742	0.0
(CAA)n	684	0.2	34388	0.1
(CA)n	9656	3.0	325115	0.7
(AGGGGG)n	85	0.0	4809	0.0
(A)n	1696	0.5	56036	0.1
Total	**324,694**		**49, 219, 709**	