

Table S1.

chromosome	start	end	min_length	max_length	n_variants	Sanger_validated	DMC1_elated	H3K4me3_related	DMC1_B6	DMC1_BP	DMC1_P8	DMC1_PWD	DMC1_Prdm9_KO	PRDM9_origin	SVO11_B6	H3K36me3_B6	variants_coords	variants_B6	variants_PWD	left_nonconv_coord	right_nonconv_coord	left_nonconv_B6	left_nonconv_PWD	right_nonconv_B6	right_nonconv_PWD
chr1	13845860	13845929	70	277	3	T	T	T	T	T	T	T	T	F	T	71; 13845929	TTT; C; G	TTTT; T; A	13845847	13846125	C	T	C	T	
chr1	46907980	46907980	1	419	1	T	T	T	T	T	T	T	T	F	T	46907980	G	A	46907905	46908325	CTT	---	C	T	
chr1	59359320	59359321	2	692	1	T	T	T	T	T	T	T	T	F	T	59359320	TG	GT	59358707	59359400	G	A	C	T	
chr1	61872329	61872329	1	69	1	n.d.	T	T	T	T	T	T	T	F	T	61872329	G; C	A; C	61872313	61872383	G	T	T	C	
chr1	63879266	63879271	6	117	2	n.d.	T	T	T	T	T	T	T	F	T	56; 63879271	A; G; C	A; G	63879207	63879325	G	A	A	C	
chr1	67960742	67963400	2659	3966	8	T	T	T	T	T	T	T	T	F	T	20; 67963400	A; G; A; C; T	A; G; A; G; T; A	67960131	67964098	A	-----	3CCGAG		
chr1	128517316	128517318	3	985	2	n.d.	T	T	T	T	T	T	T	F	T	5; 128517318	C; G	T; T	128517205	128518191	G	A	T	A	
chr1	137135844	137135844	1	141	1	n.d.	T	T	T	T	T	T	T	F	T	7; 137135844	G	C	137135739	137135881	A	G	C	T	
chr1	165896307	165896311	5	680	2	T	T	T	T	T	T	T	T	F	T	7; 165896311	C; G	T; A	165895698	165896379	C	T	A	C	
chr1	183578162	183578162	1	542	1	T	T	T	T	T	T	T	T	F	T	183578162	G	T	183577957	183578500	C	G	T	C	
chr2	3736957	3736957	1	57	1	n.d.	T	T	T	T	T	T	T	F	T	3736957	G	T	3736938	3736996	T	C	G	A	
chr2	5040747	5040747	1	133	1	n.d.	T	T	T	T	T	T	T	F	T	5040747	G	A	5040687	5040821	AAA	---	C	T	
chr2	10336587	10336592	6	264	2	T	T	T	T	T	T	T	T	F	T	87; 10336592	T; C	G; T	10336480	10336745	T	A	A	T	
chr2	11688991	11689010	20	549	3	T	T	T	T	T	T	T	T	F	T	07; 11689010	C; G; G	A; A; A	11688523	11689073	A	-	C	T	
chr2	13697711	13697711	1	431	1	T	T	T	T	T	T	T	T	F	T	13697711	A	G	13697334	13697766	AC	--	T	G	
chr2	28188305	28188305	1	361	1	T	T	T	T	T	T	T	T	F	T	28188305	G	A	28188155	28188517	A	A	G	A	
chr2	32226478	32226493	16	147	2	n.d.	T	T	T	T	T	T	T	F	T	78; 32226493	C; A	A; C	32226396	32226544	C	G	A	G	
chr2	58517611	58517618	8	270	2	T	T	T	T	T	T	T	T	F	T	11; 58517618	G; C	A; T	58517431	58517702	G	A	GTAGC	-----	
chr2	61489637	61489637	1	643	1	T	T	T	T	T	T	T	T	F	T	61489637	C	G	61489162	61489806	-----	3TGTGT	T	-	
chr2	72241857	72241857	1	462	1	T	T	T	T	T	T	T	T	F	T	72241857	C	A	72241474	72241937	G	A	T	A	
chr2	74937052	74937064	13	384	2	T	T	T	T	T	T	T	T	F	T	52; 74937064	G; C	A; T	74936895	74937280	C	T	C	A	
chr2	78357403	78357403	1	50	1	n.d.	T	T	T	T	T	T	T	F	T	78357403	C	G	78357374	78357425	G	A	G	A	
chr2	79679676	79679676	1	330	1	T	T	T	T	T	T	T	T	F	T	79679676	G	A	79679609	79679940	A	G	A	T	
chr2	85528071	85528071	1	131	1	n.d.	T	T	T	T	T	T	T	F	T	85528071	C	T	85528033	85528165	C	T	C	T	
chr2	96760589	96760589	1	169	1	T	T	T	T	T	T	T	T	F	T	96760589	C	T	96760507	96760767	G	A	C	G	
chr2	116516318	116516318	1	126	1	n.d.	T	T	T	T	T	T	T	F	T	116516318	T	G	116516266	116516393	A	G	A	G	
chr2	135984537	135984537	1	46	1	n.d.	T	T	T	T	T	T	T	F	T	135984537	T	C	135984527	135984574	G	A	T	C	
chr2	147805390	147805390	1	383	1	T	T	T	T	T	T	T	T	F	T	147805390	C	T	147805306	147805690	G	A	C	T	
chr2	150590002	150590002	1	687	1	T	T	T	T	T	T	T	T	F	T	150590002	C	T	150589924	150590612	-	C	C	A	
chr2	166617293	166617524	232	370	1	T	T	T	T	T	T	T	T	F	T	3; 166617524	ncC*; ncC*; G	ncT*; ncT*; A	166617226	166617597	G	A	G	A	
chr3	16828944	16828944	1	267	1	T	T	T	T	T	T	T	T	F	T	16828944	C	T	16828894	16829162	A	G	G	T	
chr3	22128566	22128566	1	378	1	T	T	T	T	T	T	T	T	F	T	22128566	G	A	22128341	22128720	T	C	T	C	
chr3	36830205	36830205	1	492	1	T	T	T	T	T	T	T	T	F	T	36830205	G	A	36829989	36830482	-	T	G	T	
chr3	51188409	51188409	1	182	1	T	T	T	T	T	T	T	T	F	T	51188409	T	C	51188366	51188549	T	A	AAAA	-----	
chr3	65603278	65603278	1	662	1	T	T	T	T	T	T	T	T	F	T	65603278	C	G	65602922	65603585	G	A	-	-	
chr3	65655136	65655136	1	466	1	T	T	T	T	T	T	T	T	F	T	65655136	C	G	65654711	65655178	C	T	G	T	
chr3	69739785	69739785	1	232	1	n.d.	T	T	T	T	T	T	T	F	T	69739785	G	T	69739758	69739991	A	G	A	T	
chr3	85792585	85792585	1	138	1	n.d.	T	T	T	T	T	T	T	F	T	85792585	G	A	85792540	85792679	G	T	C	A	
chr3	95869211	95869211	1	36	1	n.d.	T	T	T	T	T	T	T	F	T	95869211	G	A	95869199	95869236	C	T	G	A	
chr3	107617094	107617095	2	185	1	T	T	T	T	T	T	T	T	F	T	107617094	CG	TA	107616928	107617114	G	A	A	C	
chr3	130702831	130702831	1	177	1	T	T	T	T	T	T	T	T	F	T	130702831	C	T	130702792	130702970	A	C	A	G	
chr3	136064382	136064385	4	622	1	T	T	T	T	T	T	T	T	F	T	3; 136064385	G; C	A; T	136063966	136064589	G	A	GGA	ATT	
chr4	6396524	6396541	18	399	2	T	T	T	T	T	T	T	T	F	T	524; 6396541	C; T	T; C	6396368	6396768	C	T	GGA	T	
chr4	10936243	10936243	1	448	1	T	T	T	T	T	T	T	T	F	T	10936243	C	T	10935986	10936435	--	GT	G	A	
chr4	49528333	49528367	35	225	3	T	T	T	T	T	T	T	T	F	T	35; 49528367	C; C; C	T; G; T	49528278	49528504	G	A	C	T	
chr4	59369670	59369670	1	286	1	T	T	T	T	T	T	T	T	F	T	59369670	C	T	59369506	59369793	A	G	T	C	
chr4	83240097	83240097	1	260	1	n.d.	T	T	T	T	T	T	T	F	T	83240097	C	T	83240079	83240340	T	G	A	G	
chr4	92481179	92481179	1	596	1	T	F	F	F	F	F	F	F	no_DMC1	F	F	92481179	T	C	92480956	92481553	A	G	GTGTG	-----
chr4	125451332	125451332	1	661	1	T	T	T	T	T	T	T	T	F	T	125451332	C	T	125451295	125451957	A	T	C	-----	
chr4	142990293	142990308	16	364	2	n.d.	T	T	T	T	T	T	T	F	T	3; 142990308	--; C	CT; T	142990122	142990487	A	C	G	A	
chr5	6242093	6242323	231	407	2	T	T	T	T	T	T	T	T	F	T	093; 6242323	C; C	T; G	6242023	6242431	AT	GG	A	C	
chr5	20789067	20789067	1	115	1	n.d.	T	T	T	T	T	T	T	F	T	20789067	C	T	20789051	20789167	C	T	-	G	
chr5	27852657	27852657	1	338	1	T	T	T	T	T	T	T	T	F	T	27852657	G	T	27852582	27852921	-----	GAGGG	T	-	
chr5	51691842	51691842	1	92	1	n.d.	T	T	T	T	T	T	T	F	T	51691842	A	G	51691831	51691924	G	A	-	-	
chr5	55484917	55484946	30	278	2	T	T	T	T	T	T	T	T	F	T	17; 55484946	C; C	T; G	55484708	55484987	C	A	CCCCCT	-----	
chr5	90775650	90775650	1	61	1	n.d.	T	T	T	T	T	T	T	F	T	90775650	G	A	90775609	90775671	A	G	C	A	
chr5	96571457	96571457	1	94	1	n.d.	T	T	T	T	T	T	T	F	T	96571457	G	T	96571409	96571504	C	T	G	A	
chr5	102062273	102062273	1	190	1	T	T	T	T	T	T	T	T	F	T	102062273	G	A	102062209	102062400	C	T	A	-	
chr5	104084656	104084656	1	340	1	T	T	T	T	T	T	T	T	F	T	104084656	T	A	104084370	104084711	G	A	-----	CTAGG	
chr5	108572496	108572496	1	441	1	T	T	T	T	T	T	T	T	F	T	108572496	G	A	108572066	108572508	C	T	T	CC	
chr5	117528325	117528325	1	380	1	T	T	T	T	T	T	T	T	F	T	117528325	G	A	117528280	117528661	G	A	C	T	
chr5	119304743	119304775	33	110	2	n.d.	T	T	T	T	T	T	T	F	T	3; 119304775	A; C	G; T	119304692	119304803	C	T	G	-	
chr5	125695123	125695137	15	211	2	T	T	T	T	T	T	T	T	F	T	3; 125695137	T; C	C; A	125695019	125695231	A	-	T	C	
chr5	141144023	141144023	1	246	1	n.d.	T	T	T	T	T	T	T	F	T	141144023	T	C	141143846	141144093	G	A	G	A	
chr5	148185214	148185214	1	54	1	T	F	F	F	F	F	F	F	no_DMC1	F	F	148185214	T	C	148185183	148185238	C	-	T	G
chr6	18095110	18095110	1	159	1	n.d.	T	T	T	T	T	T	T	F	T	18095110	C	T	18095046	18095206	C	A	C	G	
chr6	36814629																								