

	FA	FE	IM	JA	LE	MA	NT	NO	OB	OU	QU	SA
Semen conception rate – 1 <sup>st</sup> AI on heifers	22.6	22.2	39.1	29.2	28.3	26.8	48.2	43.8	58.6	31.3	29.2	31.9
(points loss)	(34.1)	(34.5)	(17.8)	(26.8)	(38.7)	(30.1)	(8.7)	(23.1)	(1.2)	(25.6)	(27.7)	(25.0)
n	914	856	298	403	145	4,002	2,021	157	132	1,039	281	124
Mortality rate of females in 1 <sup>st</sup> year	12.2	10.3	18.5	17.9	NA	12.0	41.2	NA	11.0	19.2	16.4	16.8
n	606	620	761	761		2,858	3,122		209	1,100	170	32

**Supplemental Table S1. Raw technical numbers for affected bulls.** Conception rate is the ratio [number of calving/number of inseminations] and progeny juvenile mortality rate is [number of females that died before 366 days/number of females born].

Breed	Number of bulls with >30 genomic tests	Number of bulls [1:30] tests	Average number of genomic test per bull with $\geq 30$ genomic tests	Average number of genomic test per bull	Maximum number of genomic tests per bull	Number of rearrangements found
Abondance	71	351	91 ± 50	34 ± 49	235	1
Aubrac	10	2149	44 ± 18	3 ± 4	87	0
Jersey	50	236	92 ± 62	21 ± 42	287	0
Brown Swiss	119	456	101 ± 112	26 ± 4	879	0
Salers	1	994	44	2 ± 3	44	0
Tarentaise	121	211	60 ± 25	28 ± 30	169	0
Limousine	46	1607	55 ± 40	5 ± 12	202	0
Simmental	67	545	66 ± 44	12 ± 25	224	0
Charolaise	245	4197	147 ± 167	11 ± 51	1420	2
Montbéliarde	1270	2985	374 ± 618	115 ± 378	7141	0
Normande	653	995	216 ± 254	90 ± 190	2081	1
Vosgienne	50	83	82 ± 52	34 ± 49	239	0
Holstein	2635	6687	332 ± 629	98 ± 365	12676	8
Parthenaise	15	1040	53 ± 38	4 ± 8	183	0
Blonde d'Aquitaine	118	3015	95 ± 83	7 ± 24	417	0

**Supplemental Table S2. Number of eligible bull cohorts per breed.**

IR	Breakpoints	Number of genotyped progeny	Distance between markers considered (bp) ± 10%	LD breakpoint regions	LD in affected chromosome	Percentile in the non-affected chromosomes
t(5;28)	5:74,392,480	2,388	729,336	0.989	65	71
	28:2,572,390		222,160	1.000	99	97
t(1;11)	1:128,820,480	385	755,342	0.974	24	28
	11:77,103,600		170,519	0.995	54	55
t(19;23)	19:56,469,708	463	160,471	0.996	34	21
	23:9,681,314		482,602	1.000	87	82
t(3;8)	3:69,934,840	403	452,802	0.980	29	28
	3:71,854,170		835,682	0.950	9	10
	8:23,449,820		635,054	0.990	65	75
Ins inv (8;4)	4:65,642,810	12,600	18,908,818	0.703	85	82
	4:76,557,790		593,292	0.978	18	31
	8:37,638,710		608,545	0.995	99	98

**Supplemental Table S3. Analysis of linkage disequilibrium around breakpoints.** LD is calculated among the descendants of male ancestors which produced mutant sperm responsible for five IR.

IR	Breakpoint	Repeated element
t(1;11)	1:128,820,473	-
	11:77,103,578	LTR (MLT1E3)
t(2;22)	2:60,476,739	LINE (L1_Art)
	22	
t(3;8)	3:69,934,841	
	3:71,854,170	LINE (BovB)
	8:23,449,818	-
Inv ins(4;8)	4:65,642,811	-
	4:76,557,774	LINE (BovB)
	8:37,638,713	-
t(5;28)	5:74,392,477	LTR (LTR16E2)
	28:2,572,389	-
t(19;23)	19:56,469,708	-
	23:9,681,291	LINE (L1MEg)
t(24;29),-der29	24:58,418,701	-
	29:3,257,559	-

**Supplemental Table S4. Analysis of repeated elements including a breakpoint.** In 6 bull, one of the breakpoint was located in repeated element.