Table S1: Slow feathering (SF) and fast feathering (FF) turkey samples.

Line	Animal ID	Phenotype	Sex	Mean sequence coverage
H	MG-WUR-121	FF	Female	11.23X
H	MG-WUR-122	FF	Female	9.13X
H	MG-WUR-123	FF	Female	12.43X
H	MG-WUR-124	SF	Female	4.32X
H	MG-WUR-125	SF	Female	16.15X
H	MG-WUR-126	SF	Female	11.54X
H	MG-WUR-127	SF	Female	10.57X
H	MG-WUR-128	FF	Female	17.62X
H	MG-WUR-129	SF	Female	11.79X
H	MG-WUR-130	SF	Female	8.3X
H	MG-WUR-131	SF	Female	6.54X
H	MG-WUR-132	SF	Female	8.93X
H	MG-WUR-133	SF	Female	20.96X
H	MG-WUR-134	SF	Female	9.41X
H	MG-WUR-135	SF	Female	10.68X
H	MG-WUR-136	SF	Female	15.38X
H	MG-WUR-137	FF	Female	2.1X
H	MG-WUR-138	FF	Female	14.14X
H	MG-WUR-139	FF	Female	8.37X
H	MG-WUR-140	FF	Female	11.04X
H	MG-WUR-141	FF	Female	13.21X
H	MG-WUR-142	FF	Female	13.98X
H	MG-WUR-143	FF	Female	8.31X
H	MG-WUR-144	FF	Female	10.89X

Table S2: Variants per type.

Class	Total
SNP	6,595,059
MNP	181,337
INS	737,001
DEL	460,169
MIXED	162,647
Total	**8,136,213**

Table S3: Variant effects per type and region.

Type	Count	Percent
3 prime UTR variant	294,003	0.893%
5 prime UTR premature start codon gain variant	13,260	0.04%
5 prime UTR variant	84,860	0.258%
bidirectional gene fusion	16	0%
conservative inframe deletion	523	0.002%
conservative inframe insertion	337	0.001%
disruptive inframe deletion	299	0.001%
disruptive inframe insertion	189	0.001%
downstream gene variant	3,536,804	10.739%
frameshift variant	3,435	0.01%
gene fusion	40	0%
initiator codon variant	21	0%
intergenic region	3,914,527	11.886%
intragenic variant	819,407	2.488%
intron variant	10,462,820	31.77%
missense variant	80,888	0.246%
non coding transcript exon variant	365,873	1.111%
non coding transcript variant	9,645,839	29.289%
splice acceptor variant	1,563	0.005%
splice donor variant	1,721	0.005%
splice region variant	47,083	0.143%
start lost	368	0.001%
stop gained	790	0.002%
stop lost	160	0%
stop retained variant	97	0%
synonymous variant	140,703	0.427%
upstream gene variant	3,517,777	10.681%

Table S4: Effect of coding SNPs. The missense / silent ratio: 0.545.

Type	Count	Percent
MISSENSE	76,603	35.184%
NONSENSE	691	0.317%
SILENT	140,426	64.498%

Table S5: List of top 100 significant polymorphisms.

Chromosome	Pos	Ref. allele	SF carrier freq.	FF carrier freq	Alt. allele	P-val	Protein altering
ChrZ	8857275	T	1	0.09091	C	4.12E-11	NO
ChrZ	9185457	T	0	0.9091	G	4.12E-11	NO
ChrZ	8642592	T	1	0.1364	C	3.71E-10	NO
ChrZ	9019282	A	0	0.8636	G	3.71E-10	NO
ChrZ	9040199	A	0	0.8636	G	3.71E-10	NO
ChrZ	9040239	T	0	0.8636	A	3.71E-10	NO
ChrZ	8707888	G	0	0.8333	T	1.27E-09	NO
ChrZ	8964132	G	1	0.1667	A	1.27E-09	NO
ChrZ	8964152	A	1	0.1667	G	1.27E-09	NO
ChrZ	9011850	G	0	0.8333	A	1.27E-09	NO
ChrZ	8092917	C	1	0.1364	T	2.19E-09	NO
ChrZ	9007699	T	1	0.1364	C	2.19E-09	NO
ChrZ	**9426018**	**GT**	**1**	**0.1818**	**GTTGGTT**	**2.60E-09**	**YES (PRLR)**
ChrZ	8342756	A	1	0.1818	T	2.60E-09	NO
ChrZ	8351160	C	0	0.8182	T	2.60E-09	NO
ChrZ	8390359	AG	0	0.8182	AGG	2.60E-09	NO
ChrZ	8448741	T	0	0.8182	C	2.60E-09	NO
ChrZ	8735559	A	1	0.1818	C	2.60E-09	NO
ChrZ	8824038	G	0	0.8182	A	2.60E-09	NO
ChrZ	8824824	C	1	0.1818	T	2.60E-09	NO
ChrZ	8831283	C	0	0.8182	T	2.60E-09	NO
ChrZ	8838674	A	0	0.8182	G	2.60E-09	NO
ChrZ	8851245	A	1	0.1818	C	2.60E-09	NO
ChrZ	8852149	A	1	0.1818	G	2.60E-09	NO
ChrZ	8856691	A	1	0.1818	G	2.60E-09	NO
ChrZ	8857364	C	0	0.8182	A	2.60E-09	NO
ChrZ	8953215	A	1	0.1818	G	2.60E-09	NO
ChrZ	8957954	T	0	0.8182	A	2.60E-09	NO
ChrZ	8962958	C	1	0.1818	T	2.60E-09	NO
ChrZ	8965325	T	1	0.1818	A	2.60E-09	NO
ChrZ	8973222	C	1	0.1818	A	2.60E-09	NO
ChrZ	8978769	T	0	0.8182	C	2.60E-09	NO
ChrZ	8981361	A	0	0.8182	G	2.60E-09	NO
ChrZ	8983221	A	1	0.1818	G	2.60E-09	NO
ChrZ	8985961	G	1	0.1818	A	2.60E-09	NO
ChrZ	8991818	G	1	0.1818	T	2.60E-09	NO
ChrZ	8993640	G	0	0.8182	A	2.60E-09	NO
ChrZ	8997377	G	0	0.8182	A	2.60E-09	NO
ChrZ	8997673	C	0	0.8182	G	2.60E-09	NO
ChrZ	9000514	G	1	0.1818	A	2.60E-09	NO
ChrZ	9000640	CTTTTTTTTC	0	0.8182	CTTTTTTTC	2.60E-09	NO
ChrZ	9001463	G	0	0.8182	A	2.60E-09	NO
ChrZ	9001604	T	1	0.1818	C	2.60E-09	NO
ChrZ	9001884	T	0	0.8182	C	2.60E-09	NO
ChrZ	9002293	A	0	0.8182	G	2.60E-09	NO
ChrZ	9002479	T	0	0.8182	C	2.60E-09	NO
ChrZ	9002550	T	1	0.1818	C	2.60E-09	NO
ChrZ	9003502	A	0	0.8182	T	2.60E-09	YES (ADAMTS12)
ChrZ	9005712	G	1	0.1818	A	2.60E-09	NO
ChrZ	9006017	T	1	0.1818	C	2.60E-09	NO
ChrZ	9008586	A	1	0.1818	G	2.60E-09	NO
ChrZ	9008937	C	1	0.1818	T	2.60E-09	NO
ChrZ	9009057	C	1	0.1818	T	2.60E-09	NO
ChrZ	9011233	TT	0	0.8182	TGT	2.60E-09	NO
ChrZ	9012253	G	0	0.8182	A	2.60E-09	NO
ChrZ	9012757	A	0	0.8182	G	2.60E-09	NO
ChrZ	9014146	A	0	0.8182	C	2.60E-09	NO
ChrZ	9014751	G	0	0.8182	A	2.60E-09	NO
ChrZ	9017562	C	0	0.8182	T	2.60E-09	NO
ChrZ	9017679	A	0	0.8182	G	2.60E-09	NO
ChrZ	9017967	T	0	0.8182	C	2.60E-09	NO
ChrZ	9018427	A	0	0.8182	G	2.60E-09	NO
ChrZ	9021484	A	0	0.8182	G	2.60E-09	NO
ChrZ	9022805	G	0	0.8182	A	2.60E-09	NO

ChrZ	9024002	A	0	0.8182	G	2.60E-09	NO
ChrZ	9024415	ATTTTTTTTG	0	0.8182	ATTTTTTTG	2.60E-09	NO
ChrZ	9024917	G	1	0.1818	A	2.60E-09	NO
ChrZ	9032079	G	0	0.8182	A	2.60E-09	NO
ChrZ	9032522	AGT	0	0.8182	AGGT	2.60E-09	NO
ChrZ	9044048	C	0	0.8182	T	2.60E-09	NO
ChrZ	9049191	T	0	0.8182	C	2.60E-09	NO
ChrZ	9050159	T	0	0.8182	A	2.60E-09	NO
ChrZ	9050501	G	0	0.8182	A	2.60E-09	NO
ChrZ	9050750	A	0	0.8182	G	2.60E-09	NO
ChrZ	9055326	T	1	0.1818	G	2.60E-09	NO
ChrZ	9055593	G	0	0.8182	C	2.60E-09	NO
ChrZ	9055595	A	0	0.8182	C	2.60E-09	NO
ChrZ	9055839	A	0	0.8182	G	2.60E-09	NO
ChrZ	9057437	G	0	0.8182	A	2.60E-09	NO
ChrZ	9057946	G	1	0.1818	C	2.60E-09	NO
ChrZ	9091728	G	0	0.8182	T	2.60E-09	NO
ChrZ	9095264	C	0	0.8182	T	2.60E-09	NO
ChrZ	9136697	C	0	0.8182	T	2.60E-09	NO
ChrZ	9160481	A	0	0.8182	G	2.60E-09	NO
ChrZ	9181053	T	0	0.8182	C	2.60E-09	NO
ChrZ	9181900	T	1	0.1818	A	2.60E-09	NO
ChrZ	9200910	T	0	0.8182	C	2.60E-09	NO
ChrZ	9790932	T	1	0.1818	C	2.60E-09	NO
ChrZ	9052821	C	0	0.9	A	3.35E-09	NO
ChrZ	8986123	TGTGAG	0.04167	0.8636	TGTGAGTGAG	8.53E-09	NO
ChrZ	8755552	T	1	0.2	C	1.16E-08	NO
ChrZ	8857343	T	0	0.8	C	1.16E-08	NO
ChrZ	8985758	T	0	0.8	C	1.16E-08	NO
ChrZ	9014562	A	0	0.8	G	1.16E-08	NO
ChrZ	9024781	T	0	0.8	C	1.16E-08	NO
ChrZ	9041949	A	0	0.8	G	1.16E-08	NO
ChrZ	9421693	G	1	0.2	A	1.16E-08	NO
ChrZ	8857649	C	0.08333	0.9091	G	1.38E-08	NO
ChrZ	7957723	T	1	0.1818	C	1.42E-08	NO