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Supplemental Data

Mutations in *IL36RN/IL1F5* Are Associated with the

Severe Episodic Inflammatory Skin Disease

Known as Generalized Pustular Psoriasis

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Table S1. Summary Statistics for Exome Sequencing - Mapping and Coverage

Sequenced Exomes	GPP-01 II:5	GPP-02 II:1	GPP-03II-2	GPP-04 I:1	GPP-05 I:1
Uniquely mapped reads	68594921	62009656	65314156	65646601	69407301
Uniquely mapped to target +/- 150bp reads	55198407	49208880	52015608	52627576	55268375
Uniquely mapped to target reads	48215586	42753343	45238186	46191914	48396089
CCDS bases with coverage >1	33260912	33449940	33362220	33361093	33494779
CCDS bases with coverage >5	31312830	31533617	31431865	31514504	31787327
CCDS bases with coverage >10	29670758	29801616	29772801	29904282	30254958
CCDS bases with coverage >20	26782011	26684328	26794008	27052242	27593347
Mean coverage	65.06	57.86	61.16	62.63	65.71

Total number of mapped reads and resulting coverage of the CCDS exome.

Table S2. Summary Statistics for Exome Sequencing - Variant Calling

Variant type	GPP-01 II:5		GPP-02 II:1		GPP-03 II:2		GPP-04 I:1		GPP-05 I:1	
	known	novel	known	novel	known	novel	known	novel	known	novel
All variants	22758	370	22678	275	22731	251	23120	281	22679	270
heterozygous	13665	357	13602	270	14234	248	14124	273	14037	266
homozygous	9093	13	9076	5	8497	3	8996	8	8642	4
Indels	16	531	365	8	358	7	362	9	356	11
heterozygous	14	277	164	7	167	7	154	8	167	11
homozygous	2	254	201	1	191	0	208	1	189	0
3n indels	179	8	177	8	173	3	172	4	176	4
heterozygous	102	8	102	7	110	3	98	4	103	4
homozygous	77	0	75	1	63	0	74	0	73	0
Non 3n indels	196	10	188	3	185	4	190	5	180	7
heterozygous	65	8	62	2	57	4	56	4	64	7
homozygous	131	2	126	1	128	0	134	1	116	0
Snvs	19836	314	19752	225	19844	228	20203	243	19808	227
heterozygous	11984	306	11925	222	12511	226	12414	237	12370	225
homozygous	7852	8	7827	3	7333	2	7789	6	7438	2
Synonymous_snvs	10238	108	10186	68	10267	78	10465	79	10279	75
heterozygous	6135	105	6033	66	6407	78	6364	77	6334	74
homozygous	4103	3	4153	2	3860	0	4101	2	3945	1
Nonsynonymous_snvs	9598	206	9566	157	9577	150	9738	164	9529	152
heterozygous	5849	201	5892	156	6104	148	6050	160	6036	151
homozygous	3749	5	3674	1	3473	2	3688	4	3493	1
Splice site (10bp)	2547	38	2561	42	2529	16	2555	29	2515	32
heterozygous	1514	35	1513	41	1556	15	1556	28	1500	30
homozygous	1033	3	1048	1	973	1	999	1	1015	2
Transition:Transversion ratio	3.04	3.32	3.07	3.06	3.06	2.87	3.06	2.91	3.14	2.8
heterozygous	3.12	3.36	3.09	3.06	3.12	2.83	3.05	2.82	3.15	2.81
homozygous	2.93	2.33	3.03	3	2.97	n/a	3.07	n/a	3.13	2

Numbers of variants of different classes identified by exome sequencing in the five sequenced cases.

Table S3. Primer Sequences Used for Amplification and Sanger Sequencing of IL36RN

ID	Sequence 5' to 3'
IL1F5-EX1-F	gctccgtggaggctgttc
IL1F5-EX1-R	cacaatttcccagctgcaat
IL1F5-EX2-F	ggagacaaggctgtgctgtt
IL1F5-EX2-R	gcttagagcctggtttgtgc
IL1F5-EX3-F	ctgctgagaagcctcccttc
IL1F5-EX3-R	caaagctgcatcaacagaa
IL1F5-EX4-F	ttctgttgatggcagctttg
IL1F5-EX4-R	ggtcaggtgccactaagtc