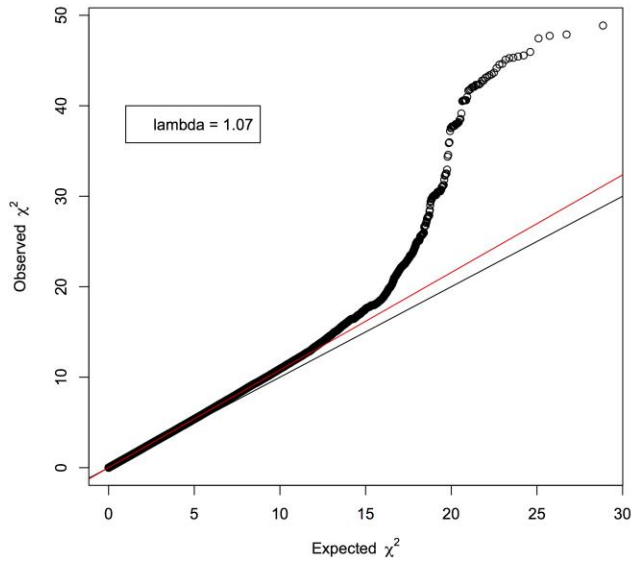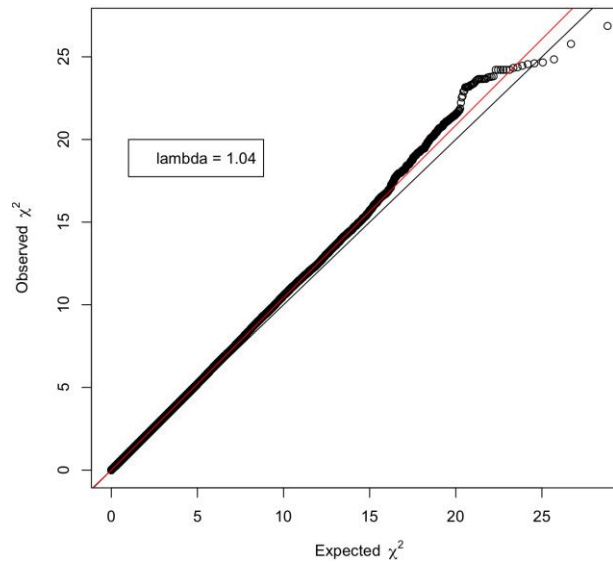**Supplementary Figure 1:** QQ plots of the EoE discovery GWAS (λ1.07), replication GWAS (λ1.04), and meta-analysis (λ1.001)

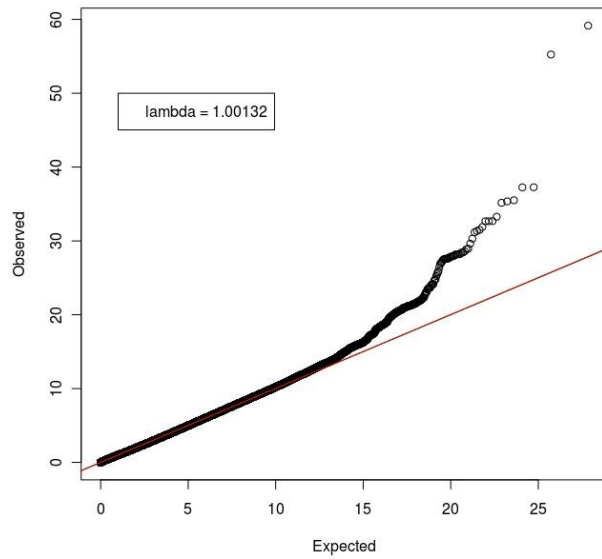**Supplementary Figure 2**: Regional association plot at the TSLP locus on chr5q22.1
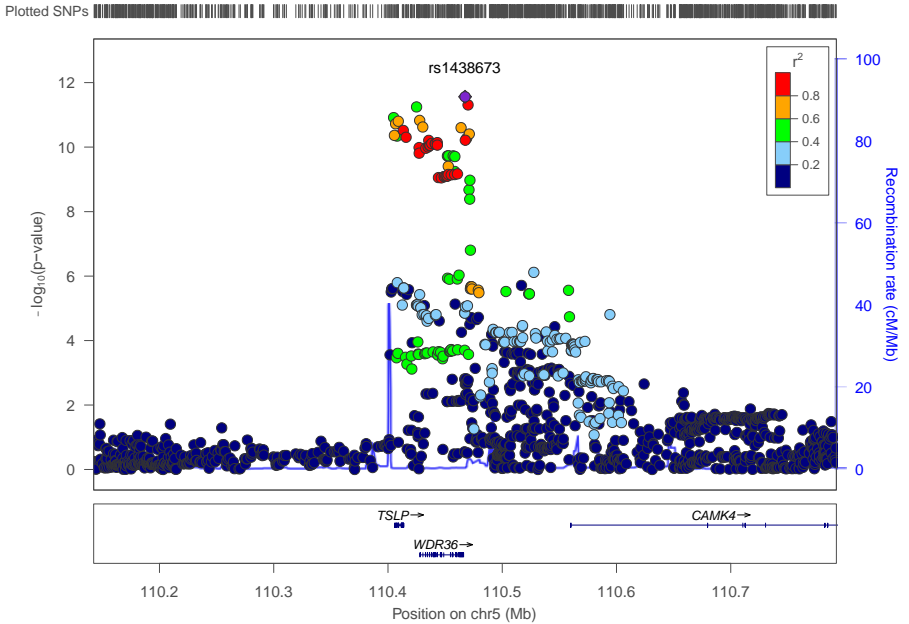
Supplementary Figure 3: Regional association plot at the c11orf30 locus. Independent effects are clearly visible in the LD patterns of the associated variants. Panel A) SNPs in LD with rs55646091 and Panel B) SNPs in LD with rs11236791.

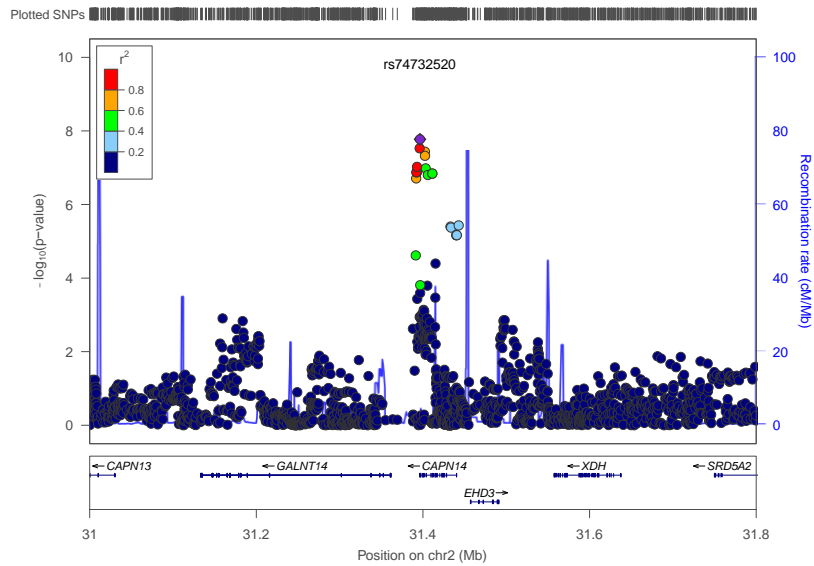**A**   **B**
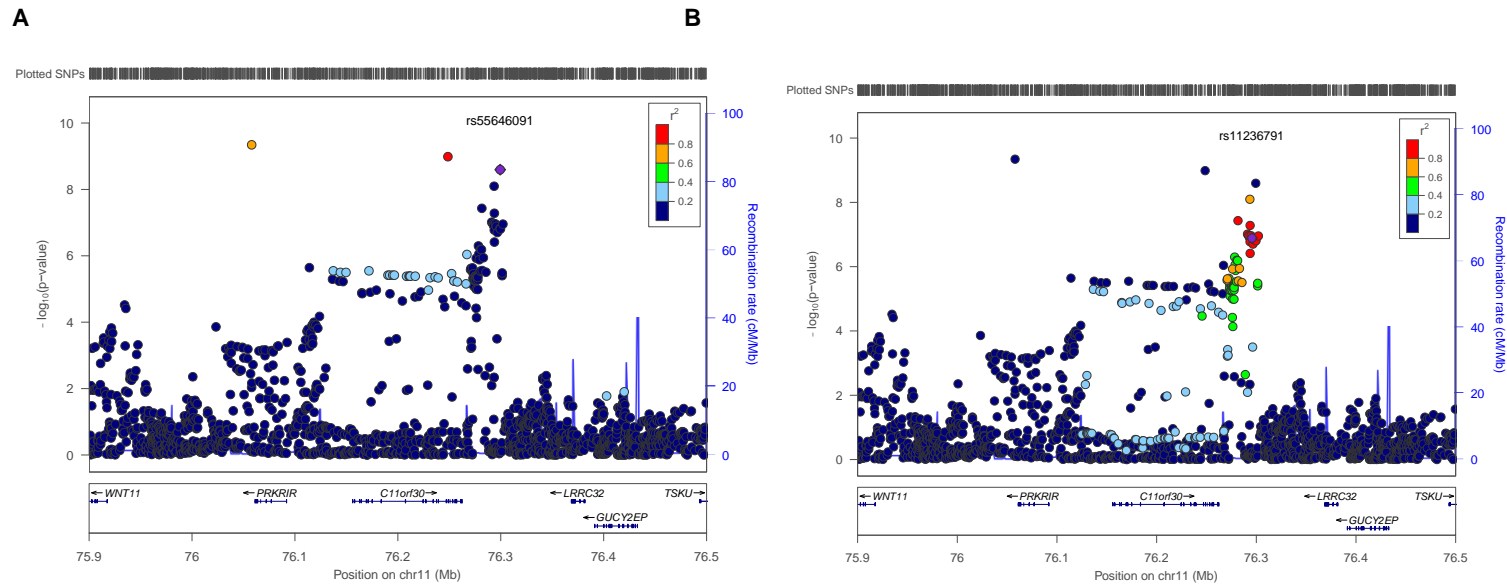
Supplementary Figure 4: Regional association plot at the CAPN14 locus on chr2p23.1
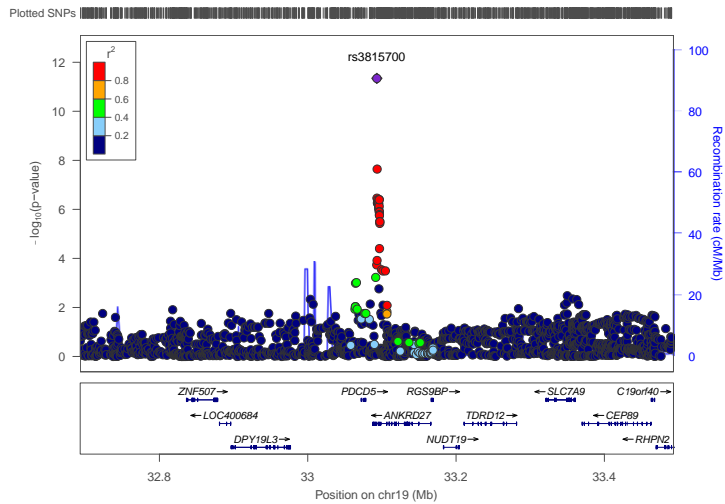
Supplementary Figure 5: Regional association plot at the STAT6 locus on chr12q13.3
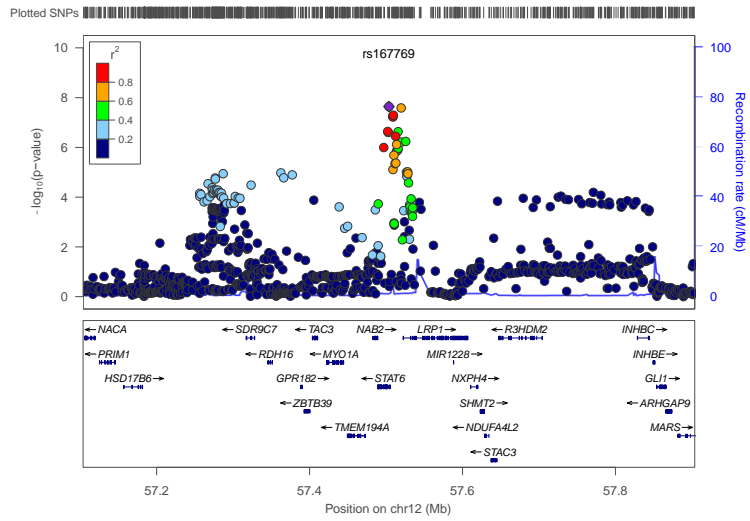
Supplementary Figure 6: Regional association plot at the ANKRD27 locus on chr19q13.11

Supplementary Table 1: Genome-wide significant variants: Discovery, replication and meta-analysis ORs and Pvals *P* values for the discovery analysis are shown in bold if directly genotyped. *P* values for the discovery and replication sets were generated using a missing data likelihood score test as implemented in SNPTEST2. Cutoffs, genome-wide significance ($P < 5 \times 10^{-8}$), MAF ≥ 3%, info scores ≥ 0.8. P_{het}, heterogeneity *P* value for Cochrane's *Q* statistic. OR, odds ratio.

Variant [Effect Allele]	chr:pos hg19	Gene	Discovery				Replication				Meta			
			effect allele MAF	OR	Pval	SE	effect allele MAF	OR	Pval	SE	OR	SE	Pval	P_{het}
rs78464756[G]	chr2:31396059	CAPN14	0.067	1.767	2.96×10^{-8}	0.131	0.079	1.569	5.42×10^{-3}	0.181	1.904	0.111	5.927×10^{-9}	0.333
rs74732520[G]	chr2:31396392	CAPN14	0.067	1.782	1.69×10^{-8}	0.131	0.079	1.561	5.87×10^{-3}	0.182	1.917	0.111	4.166×10^{-9}	0.301
rs143457388[A]	chr2:31402370	CAPN14	0.052	1.858	3.66×10^{-8}	0.149	0.056	1.726	6.36×10^{-4}	0.219	2.215	0.129	6.061×10^{-10}	0.787
rs149864795[A]	chr2:31402407	CAPN14	0.052	1.846	4.74×10^{-8}	0.149	0.057	1.759	4.41×10^{-4}	0.218	2.216	0.128	5.245×10^{-10}	0.861
rs10455025[C]	chr5:110404999	TSLP	0.356	1.537	1.21×10^{-11}	0.067	0.354	1.276	2.76×10^{-3}	0.102	1.511	0.057	4.275×10^{-13}	0.233
rs3806932[G]	chr5:110405675	TSLP	0.444	0.630	4.31×10^{-11}	0.064	0.437	0.720	7.00×10^{-4}	0.100	0.671	0.055	2.706×10^{-13}	0.502
rs3806933[T]	chr5:110406742	TSLP	0.439	0.628	1.88×10^{-11}	0.064	0.418	0.713	1.00×10^{-3}	0.101	0.668	0.055	1.829×10^{-13}	0.419
rs1898671[T]	chr5:110408002	TSLP	0.350	1.514	4.54×10^{-11}	0.068	0.348	1.255	5.01×10^{-3}	0.104	1.499	0.058	2.826×10^{-12}	0.213
rs2289277[G]	chr5:110409067	TSLP	0.437	0.626	1.57×10^{-11}	0.064	0.421	0.724	1.45×10^{-3}	0.101	0.669	0.055	2.336×10^{-13}	0.358
rs10073816[A]	chr5:110413489	TSLP	0.442	0.628	3.03×10^{-11}	0.064	0.434	0.719	6.70×10^{-4}	0.101	0.668	0.055	1.873×10^{-13}	0.488
rs6594497[T]	chr5:110415868	TSLP	0.441	0.631	4.92×10^{-11}	0.064	0.433	0.733	1.16×10^{-3}	0.100	0.674	0.055	5.262×10^{-13}	0.432
rs252716[C]	chr5:110425063	TSLP	0.447	1.545	5.65×10^{-12}	0.065	0.454	1.361	6.65×10^{-4}	0.100	1.516	0.055	4.053×10^{-14}	0.389
rs10050834[T]	chr5:110427328	TSLP	0.452	0.639	1.03×10^{-10}	0.064	0.437	0.749	1.59×10^{-3}	0.101	0.680	0.054	1.418×10^{-12}	0.448
rs7723819[A]	chr5:110427347	TSLP	0.453	0.641	1.54×10^{-10}	0.064	0.441	0.739	1.05×10^{-3}	0.101	0.680	0.054	1.341×10^{-12}	0.524
rs79881201[T]	chr5:110427795	TSLP	0.362	1.536	1.48×10^{-11}	0.067	0.367	1.250	5.45×10^{-3}	0.102	1.495	0.057	1.123×10^{-12}	0.184
rs17623144[G]	chr5:110430488	TSLP	0.360	1.532	2.37×10^{-11}	0.067	0.361	1.261	3.35×10^{-3}	0.103	1.498	0.057	9.369×10^{-13}	0.248
rs1993465[G]	chr5:110433098	TSLP	0.456	0.640	1.08×10^{-10}	0.064	0.444	0.748	1.42×10^{-3}	0.101	0.679	0.055	1.318×10^{-12}	0.462
rs6859041[A]	chr5:110435231	TSLP	0.455	0.639	9.85×10^{-11}	0.064	0.444	0.744	1.39×10^{-3}	0.101	0.679	0.055	1.186×10^{-12}	0.457
rs1379298[C]	chr5:110435726	TSLP	0.455	0.639	6.16×10^{-11}	0.064	0.444	0.752	1.79×10^{-3}	0.101	0.677	0.055	1.005×10^{-12}	0.405
rs10038177[T]	chr5:110436450	TSLP	0.457	0.638	9.00×10^{-11}	0.064	0.445	0.755	2.19×10^{-3}	0.100	0.681	0.054	1.785×10^{-12}	0.389
rs6865932[C]	chr5:110436852	TSLP	0.457	0.638	8.79×10^{-11}	0.064	0.445	0.752	1.90×10^{-3}	0.100	0.680	0.054	1.501×10^{-12}	0.405
chr5:110437826:I[TA]	chr5:110437826	TSLP	0.361	1.539	1.72×10^{-11}	0.066	0.365	1.256	5.71×10^{-3}	0.102	1.492	0.056	1.329×10^{-12}	0.189
chr5:110437828:I[AT]	chr5:110437828	TSLP	0.361	1.539	1.68×10^{-11}	0.067	0.364	1.248	5.68×10^{-3}	0.102	1.493	0.057	1.297×10^{-12}	0.188
rs10045255[G]	chr5:110438357	TSLP	0.458	0.637	7.68×10^{-11}	0.064	0.446	0.765	3.13×10^{-3}	0.100	0.683	0.054	2.297×10^{-12}	0.335
rs1379300[C]	chr5:110441439	TSLP	0.457	0.638	7.81×10^{-11}	0.064	0.444	0.741	1.41×10^{-3}	0.100	0.678	0.054	9.752×10^{-13}	0.440
rs2034896[A]	chr5:110441533	TSLP	0.457	0.638	7.79×10^{-11}	0.064	0.444	0.741	1.41×10^{-3}	0.100	0.678	0.054	9.755×10^{-13}	0.439
rs10043631[T]	chr5:110443228	TSLP	0.457	0.637	7.24×10^{-11}	0.064	0.445	0.745	1.77×10^{-3}	0.100	0.679	0.054	1.166×10^{-12}	0.406
rs10038058[G]	chr5:110443281	TSLP	0.456	0.639	8.63×10^{-11}	0.064	0.445	0.745	1.77×10^{-3}	0.100	0.680	0.054	1.372×10^{-12}	0.413

rs13178997[T]	chr5:110444249	TSLP	0.441	0.654	8.80×10^{-10}	0.064	0.435	0.710	2.96×10^{-4}	0.100	0.681	0.055	2.003×10^{-12}	0.815
rs13161853[A]	chr5:110446741	TSLP	0.441	0.654	8.96×10^{-10}	0.064	0.432	0.709	2.88×10^{-4}	0.100	0.681	0.055	1.987×10^{-12}	0.823
chr5:110449140:I[CT]	chr5:110449140	TSLP	0.439	0.654	6.46×10^{-10}	0.064	0.437	0.716	3.49×10^{-4}	0.101	0.679	0.055	1.745×10^{-12}	0.764
rs2112541[C]	chr5:110449346	TSLP	0.441	0.653	8.17×10^{-10}	0.064	0.437	0.726	6.11×10^{-4}	0.100	0.684	0.055	3.757×10^{-12}	0.692
rs10060003[G]	chr5:110449357	TSLP	0.441	0.653	8.17×10^{-10}	0.064	0.437	0.726	6.11×10^{-4}	0.100	0.684	0.055	3.757×10^{-12}	0.692
rs10055177[G]	chr5:110450584	TSLP	0.441	0.653	8.07×10^{-10}	0.064	0.437	0.724	5.91×10^{-4}	0.100	0.684	0.055	3.6×10^{-12}	0.694
rs6880351[G]	chr5:110451664	TSLP	0.441	0.653	8.00×10^{-10}	0.064	0.436	0.731	8.92×10^{-4}	0.100	0.686	0.055	5.367×10^{-12}	0.629
rs6881147[C]	chr5:110451936	TSLP	0.441	0.653	7.82×10^{-10}	0.064	0.436	0.728	6.60×10^{-4}	0.100	0.685	0.055	3.888×10^{-12}	0.676
rs6884870[G]	chr5:110452084	TSLP	0.350	1.501	1.88×10^{-10}	0.068	0.352	1.218	0.013	0.105	1.468	0.058	2.988×10^{-11}	0.176
rs10059658[C]	chr5:110452815	TSLP	0.438	0.649	3.92×10^{-10}	0.064	0.435	0.726	5.39×10^{-4}	0.100	0.679	0.055	1.663×10^{-12}	0.658
rs10051830[A]	chr5:110452845	TSLP	0.441	0.653	7.02×10^{-10}	0.064	0.435	0.722	4.54×10^{-4}	0.100	0.682	0.055	2.433×10^{-12}	0.727
rs77793850[A]	chr5:110452944	TSLP	0.350	1.502	1.88×10^{-10}	0.068	0.350	1.219	0.011	0.105	1.470	0.058	2.471×10^{-11}	0.191
rs17624321[G]	chr5:110453076	TSLP	0.350	1.502	1.85×10^{-10}	0.068	0.352	1.218	0.012	0.105	1.469	0.058	2.701×10^{-11}	0.184
rs7732974[C]	chr5:110455381	TSLP	0.441	0.653	7.21×10^{-10}	0.064	0.435	0.725	5.28×10^{-4}	0.100	0.683	0.055	2.888×10^{-12}	0.707
rs17624673[T]	chr5:110457158	TSLP	0.350	1.503	1.86×10^{-10}	0.068	0.352	1.218	0.012	0.105	1.469	0.058	2.715×10^{-11}	0.184
rs6594498[A]	chr5:110458351	TSLP	0.441	0.653	7.08×10^{-10}	0.064	0.432	0.716	3.32×10^{-4}	0.101	0.680	0.055	1.812×10^{-12}	0.783
rs6889889[A]	chr5:110458416	TSLP	0.352	1.490	5.67×10^{-10}	0.068	0.353	1.233	8.64×10^{-3}	0.105	1.461	0.058	4.798×10^{-11}	0.257
rs113295611[G]	chr5:110458605	TSLP	0.350	1.502	1.95×10^{-10}	0.068	0.352	1.217	0.013	0.105	1.467	0.058	3.134×10^{-11}	0.176
rs7702774[T]	chr5:110460851	TSLP	0.441	0.652	6.75×10^{-10}	0.064	0.434	0.715	3.33×10^{-4}	0.101	0.680	0.055	1.735×10^{-12}	0.781
rs1043828[C]	chr5:110464008	TSLP	0.360	1.540	2.49×10^{-11}	0.066	0.366	1.225	9.72×10^{-3}	0.102	1.478	0.056	3.461×10^{-12}	0.159
rs1438673[T]	chr5:110467499	TSLP	0.496	0.626	2.74×10^{-12}	0.063	0.490	0.793	3.84×10^{-3}	0.099	0.671	0.054	1.507×10^{-13}	0.193
rs1438672[A]	chr5:110467753	TSLP	0.457	0.638	6.08×10^{-11}	0.064	0.441	0.780	8.36×10^{-3}	0.100	0.687	0.055	6.019×10^{-12}	0.206
rs34962275[G]	chr5:110468977	TSLP	0.363	1.528	5.24×10^{-11}	0.066	0.368	1.241	8.52×10^{-3}	0.102	1.472	0.056	5.738×10^{-12}	0.185
rs6594499[A]	chr5:110470137	TSLP	0.493	0.633	4.89×10^{-12}	0.064	0.483	0.779	2.48×10^{-3}	0.100	0.669	0.055	1.47×10^{-13}	0.259
rs6594500[A]	chr5:110470994	TSLP	0.395	1.466	2.11×10^{-9}	0.066	0.410	1.164	0.092	0.102	1.392	0.056	3.399×10^{-9}	0.072
rs12186767[G]	chr5:110471218	TSLP	0.358	1.525	3.90×10^{-11}	0.067	0.358	1.211	0.015	0.105	1.475	0.057	8.541×10^{-12}	0.141
rs72784258[C]	chr5:110471615	TSLP	0.391	1.454	4.10×10^{-9}	0.066	0.404	1.197	0.048	0.104	1.402	0.057	2.203×10^{-9}	0.143
rs73786772[G]	chr5:110471791	TSLP	0.326	1.455	1.06×10^{-9}	0.070	0.343	1.257	5.11×10^{-3}	0.106	1.478	0.059	5.004×10^{-11}	0.306
rs55684690[T]	chr11:76057946	c11orf30	0.038	2.109	4.20×10^{-8}	0.169	0.040	2.132	6.81×10^{-5}	0.270	2.637	0.149	6.961×10^{-11}	0.652
chr11:76114003:D[T]	chr11:76114003	c11orf30	0.162	1.637	4.56×10^{-9}	0.086	0.177	1.352	9.26×10^{-3}	0.133	1.578	0.075	1.007×10^{-9}	0.344
rs12420744[G]	chr11:76114021	c11orf30	0.159	1.620	1.27×10^{-8}	0.087	0.171	1.372	5.14×10^{-3}	0.137	1.585	0.076	1.232×10^{-9}	0.509
rs1893870[T]	chr11:76117879	c11orf30	0.257	1.451	4.34×10^{-8}	0.073	0.272	1.171	0.131	0.115	1.397	0.064	1.699×10^{-7}	0.108
rs7927830[A]	chr11:76120315	c11orf30	0.241	1.493	2.47×10^{-8}	0.074	0.259	1.126	0.240	0.114	1.392	0.065	3.175×10^{-7}	0.046
rs2156708[C]	chr11:76122213	c11orf30	0.241	1.493	2.50×10^{-8}	0.075	0.260	1.127	0.236	0.114	1.392	0.065	3.117×10^{-7}	0.047

SNP	Position	Gene											
rs871911[G]	chr11:76123849	c11orf30	0.235	1.504	9.49×10^{-9}	0.076	0.261	1.125	0.242	0.114	1.408	0.065	1.73×10^{-7}	0.034
rs59382353[A]	chr11:76137243	c11orf30	0.156	1.637	1.18×10^{-8}	0.086	0.168	1.393	4.82×10^{-3}	0.136	1.586	0.076	1.085×10^{-9}	0.514
rs73004436[G]	chr11:76144139	c11orf30	0.155	1.636	1.19×10^{-8}	0.087	0.167	1.384	5.38×10^{-3}	0.136	1.585	0.076	1.225×10^{-9}	0.495
rs4426156[G]	chr11:76149594	c11orf30	0.156	1.634	1.35×10^{-8}	0.087	0.167	1.384	5.36×10^{-3}	0.136	1.583	0.076	1.361×10^{-9}	0.503
rs61894509[C]	chr11:76171935	c11orf30	0.157	1.622	3.05×10^{-8}	0.086	0.167	1.368	7.57×10^{-3}	0.136	1.560	0.076	3.938×10^{-9}	0.495
rs61696910[G]	chr11:76190383	c11orf30	0.155	1.622	3.27×10^{-8}	0.086	0.167	1.364	8.14×10^{-3}	0.136	1.558	0.076	4.531×10^{-9}	0.484
rs61894530[A]	chr11:76192036	c11orf30	0.155	1.622	3.27×10^{-8}	0.086	0.167	1.364	8.14×10^{-3}	0.136	1.558	0.076	4.531×10^{-9}	0.484
rs11532107[T]	chr11:76194993	c11orf30	0.155	1.622	3.27×10^{-8}	0.086	0.167	1.364	8.14×10^{-3}	0.136	1.558	0.076	4.531×10^{-9}	0.484
rs142931944[G]	chr11:76196566	c11orf30	0.155	1.622	3.27×10^{-8}	0.086	0.167	1.364	8.14×10^{-3}	0.136	1.558	0.076	4.528×10^{-9}	0.484
rs11236766[A]	chr11:76208451	c11orf30	0.155	1.618	4.07×10^{-8}	0.086	0.166	1.373	6.89×10^{-3}	0.137	1.558	0.076	4.564×10^{-9}	0.532
rs61894534[T]	chr11:76210929	c11orf30	0.155	1.618	4.06×10^{-8}	0.086	0.166	1.373	6.90×10^{-3}	0.137	1.558	0.076	4.554×10^{-9}	0.532
rs11236767[A]	chr11:76211421	c11orf30	0.155	1.618	4.06×10^{-8}	0.086	0.166	1.373	6.90×10^{-3}	0.137	1.558	0.076	4.557×10^{-9}	0.532
rs57790584[C]	chr11:76212164	c11orf30	0.155	1.618	4.06×10^{-8}	0.086	0.166	1.373	6.90×10^{-3}	0.137	1.558	0.076	4.557×10^{-9}	0.532
rs7940373[T]	chr11:76216873	c11orf30	0.155	1.618	4.07×10^{-8}	0.086	0.166	1.373	6.87×10^{-3}	0.137	1.558	0.076	4.542×10^{-9}	0.532
rs61894541[G]	chr11:76231227	c11orf30	0.156	1.616	4.35×10^{-8}	0.086	0.167	1.351	9.13×10^{-3}	0.136	1.550	0.076	6.522×10^{-9}	0.481
rs1939469[G]	chr11:76236220	c11orf30	0.156	1.617	3.98×10^{-8}	0.086	0.167	1.360	8.38×10^{-3}	0.136	1.553	0.075	5.512×10^{-9}	0.492
rs11236775[A]	chr11:76239148	c11orf30	0.156	1.615	4.93×10^{-8}	0.086	0.166	1.362	6.90×10^{-3}	0.137	1.556	0.076	5.354×10^{-9}	0.550
rs61894547[T]	chr11:76248630	c11orf30	0.043	2.210	2.01×10^{-9}	0.155	0.048	1.818	7.49×10^{-4}	0.238	2.439	0.135	3.643×10^{-11}	0.661
chr11:76251777:D[T]	chr11:76251777	c11orf30	0.156	1.617	3.41×10^{-8}	0.086	0.166	1.350	8.05×10^{-3}	0.137	1.560	0.076	4.585×10^{-9}	0.499
rs3758716[T]	chr11:76254529	c11orf30	0.156	1.617	3.33×10^{-8}	0.086	0.166	1.349	8.24×10^{-3}	0.137	1.560	0.076	4.604×10^{-9}	0.493
rs3758715[T]	chr11:76254539	c11orf30	0.156	1.617	3.33×10^{-8}	0.086	0.166	1.349	8.24×10^{-3}	0.137	1.560	0.076	4.608×10^{-9}	0.493
rs17134961[C]	chr11:76257759	c11orf30	0.156	1.611	3.49×10^{-8}	0.087	0.166	1.343	9.62×10^{-3}	0.136	1.556	0.076	5.746×10^{-9}	0.456
rs2155221[T]	chr11:76266267	c11orf30	0.156	1.604	4.44×10^{-8}	0.087	0.166	1.338	0.010	0.137	1.552	0.076	7.621×10^{-9}	0.461
rs55646091[A]	chr11:76299431	c11orf30	0.044	2.219	5.38×10^{-10}	0.157	0.050	1.584	4.33×10^{-3}	0.237	2.414	0.135	7.672×10^{-11}	0.315
rs167769[T]	chr12:57503775	STAT6	0.377	1.498	2.29×10^{-8}	0.066	0.367	1.123	0.209	0.105	1.351	0.058	2.199×10^{-7}	0.064
rs73120411[T]	chr12:57519826	STAT6	0.345	1.475	2.59×10^{-8}	0.069	0.341	1.080	0.245	0.111	1.368	0.061	3.089×10^{-7}	0.056
rs3815700[C]	chr19:33093252	ANKRD27	0.140	1.653	4.54×10^{-12}	0.092	0.144	1.098	0.413	0.144	1.618	0.081	2.366×10^{-9}	0.003
rs10410895[G]	chr19:33093655	ANKRD27	0.140	1.474	2.27×10^{-8}	0.096	0.148	1.066	0.522	0.144	1.485	0.083	1.847×10^{-6}	0.012
rs8008716[G]	chr14:27125765	NOVA1	0.087	1.455	2.07×10^{-6}	0.117	0.092	1.579	0.002	0.164	1.712	0.100	6.93×10^{-8}	0.793

Supplementary Table 2: Conditional analyses at the c11orf30 and STAT6 loci on EoE comorbidity status. *P* values were generated using a missing data likelihood score test as implemented in SNPTEST2 with and without conditioning on comorbidities.

Variant [Effect Allele]	chr:pos hg19	Gene	effect allele MAF	Not conditioning on comorbidities			Conditional analysis		
				OR	Pval	SE	OR	Pval	SE
rs55684690[T]	chr11:76057946	c11orf30	0.038	2.305	4.85×10^{-6}	0.250	2.128	1.88×10^{-4}	0.339
chr11:76114003:D[T]	chr11:76114003	c11orf30	0.162	1.709	2.98×10^{-7}	0.127	1.791	1.51×10^{-3}	0.162
rs12420744[G]	chr11:76114021	c11orf30	0.159	1.719	2.50×10^{-7}	0.128	1.781	1.39×10^{-3}	0.163
rs1893870[T]	chr11:76117879	c11orf30	0.258	1.532	1.52×10^{-5}	0.106	1.510	6.82×10^{-3}	0.137
rs7927830[A]	chr11:76120315	c11orf30	0.240	1.535	1.78×10^{-5}	0.109	1.596	4.47×10^{-3}	0.140
rs2156708[C]	chr11:76122213	c11orf30	0.241	1.534	1.83×10^{-5}	0.109	1.595	4.58×10^{-3}	0.140
rs871911[G]	chr11:76123849	c11orf30	0.235	1.520	2.27×10^{-5}	0.111	1.595	5.04×10^{-3}	0.142
rs59382353[A]	chr11:76137243	c11orf30	0.157	1.753	1.37×10^{-7}	0.128	1.854	1.80×10^{-4}	0.160
rs73004436[G]	chr11:76144139	c11orf30	0.157	1.747	1.44×10^{-7}	0.128	1.852	1.68×10^{-4}	0.160
rs4426156[G]	chr11:76149594	c11orf30	0.157	1.745	1.54×10^{-7}	0.128	1.850	1.70×10^{-4}	0.160
rs61894509[C]	chr11:76171935	c11orf30	0.158	1.733	2.12×10^{-7}	0.128	1.823	3.58×10^{-4}	0.160
rs61696910[G]	chr11:76190383	c11orf30	0.157	1.725	2.96×10^{-7}	0.128	1.815	2.98×10^{-4}	0.160
rs61894530[A]	chr11:76192036	c11orf30	0.157	1.725	2.96×10^{-7}	0.128	1.815	2.98×10^{-4}	0.160
rs11532107[T]	chr11:76194993	c11orf30	0.157	1.725	2.96×10^{-7}	0.128	1.815	2.98×10^{-4}	0.160
rs142931944[G]	chr11:76196566	c11orf30	0.157	1.725	2.96×10^{-7}	0.128	1.815	2.98×10^{-4}	0.160
rs11236766[A]	chr11:76208451	c11orf30	0.157	1.721	2.90×10^{-7}	0.128	1.813	2.99×10^{-4}	0.160
rs61894534[T]	chr11:76210929	c11orf30	0.157	1.721	2.89×10^{-7}	0.128	1.813	2.98×10^{-4}	0.160
rs11236767[A]	chr11:76211421	c11orf30	0.157	1.721	2.89×10^{-7}	0.128	1.813	2.98×10^{-4}	0.160
rs57790584[C]	chr11:76212164	c11orf30	0.157	1.721	2.89×10^{-7}	0.128	1.813	2.98×10^{-4}	0.160
rs7940373[T]	chr11:76216873	c11orf30	0.157	1.721	2.89×10^{-7}	0.128	1.813	2.98×10^{-4}	0.160
rs61894541[G]	chr11:76231227	c11orf30	0.157	1.728	2.14×10^{-7}	0.128	1.808	3.23×10^{-4}	0.160
rs1939469[G]	chr11:76236220	c11orf30	0.157	1.727	2.23×10^{-7}	0.128	1.807	3.26×10^{-4}	0.160
rs11236775[A]	chr11:76239148	c11orf30	0.157	1.717	3.11×10^{-7}	0.128	1.810	3.08×10^{-4}	0.160
rs61894547[T]	chr11:76248630	c11orf30	0.043	2.202	3.20×10^{-6}	0.237	2.288	3.27×10^{-3}	0.301
chr11:76251777:D[T]	chr11:76251777	c11orf30	0.157	1.718	2.95×10^{-7}	0.128	1.809	2.84×10^{-4}	0.160
rs3758716[T]	chr11:76254529	c11orf30	0.158	1.717	3.05×10^{-7}	0.128	1.809	2.83×10^{-4}	0.160
rs3758715[T]	chr11:76254539	c11orf30	0.158	1.717	3.05×10^{-7}	0.128	1.809	2.83×10^{-4}	0.160

rs17134961[C]	chr11:76257759	c11orf30	0.157	1.729	1.97×10^{-7}	0.128	1.779	5.56×10^{-4}	0.161
rs2155221[T]	chr11:76266267	c11orf30	0.158	1.721	2.37×10^{-7}	0.128	1.777	5.46×10^{-4}	0.161
rs55646091[A]	chr11:76299431	c11orf30	0.044	2.138	9.32×10^{-7}	0.240	2.344	1.97×10^{-3}	0.299
rs167769[T]	chr12:57503775	STAT6	0.377	1.455	7.72×10^{-5}	0.096	1.680	0.01	0.154
rs73120411[T]	chr12:57519826	STAT6	0.346	1.469	4.02×10^{-5}	0.101	1.669	5.37×10^{-3}	0.163

Supplementary Table 3: P-values following conditional analysis on rs55646091 and rs11236791 in the discovery cohort. Variants that show significant increase in P-value following the conditional analyses are highlighted in bold and shaded. *P* values were generated using a missing data likelihood score test as implemented in SNPTEST2.

c11orf30			Discovery	Conditional analyses	
chromosome	pos	all_maf	Pval	Pval-cond-rs55646091	Pval-cond-rs11236791
rs55684690[T]	76057946	0.028	4.23X10-8	**0.0402196**	3.56E-10
rs61894547[T]	76248630	0.032	2.01X10-9	**0.425467**	1.81X10-9
rs2212434[T]	76281593	0.413	9.14X10-7	2.31X10-8	**0.636761**
rs61893460[A]	76291154	0.418	1.26X10-6	3.36X10-8	**0.186305**
rs7126418[T]	76292573	0.419	1.27X10-6	5.43X10-8	**0.0682383**
rs7110818[T]	76292575	0.419	1.27X10-6	5.43X10-8	**0.0682379**
rs7114362[T]	76293070	0.455	3.73X10-5	1.37X10-7	**0.769806**
rs7936070[T]	76293527	0.409	4.07X10-6	5.93X10-6	**0.873197**
rs7936312[T]	76293726	0.461	7.15X10-6	9.65X10-7	**0.218637**
rs7936323[A]	76293758	0.449	3.68X10-6	2.25X10-7	**0.373308**
rs4494327[T]	76294836	0.480	2.79X10-6	**0.00945432**	6.83X10-4
rs11236791[A]	76295598	0.406	1.60X10-6	1.90X10-9	**0.999358**
rs10160518[G]	76296671	0.466	2.21X10-6	**0.0403663**	3.79X10-5
chr11:76298625:I[GT]	76298625	0.405	1.56X10-6	1.22X10-9	**0.395477**
rs2155219[T]	76299194	0.467	1.30X10-6	**0.0242987**	1.28X10-4
rs55646091[A]	76299431	0.033	5.38X10-10	**0.999701**	2.19X10-9
rs11236797[A]	76299649	0.407	1.58X10-6	2.51X10-9	**0.81221**
chr11:76299844:D[C]	76299844	0.469	1.52X10-6	**0.0277185**	1.33X10-4
rs7930763[A]	76302073	0.466	1.65X10-6	**0.0294863**	1.28X10-4

Supplementary Table 4: Transcriptome sequencing of genes under the GWAS peaks from eosphageal epithelium of EoE cases and controls. **FPKM,** Fragments Per Kilobase of transcript per Million mapped reads. *P* values calculated from a negative binomial model estimated from data to obtain variance estimates. **Log2 fold change,** change in the expression level between cases and controls.

Gene	Chr	FPKM case	FPKM control	Log2 (fold change)	Pval
CAPN14	2	9.828	0.631	3.962	**5.00×10^{-5}**
GALNT14	2	14.391	13.102	0.135	0.604
TSLP	5	2.232	1.755	0.347	0.525
WDR36	5	7.398	8.403	-0.184	0.439
c110rf30	11	1.790	1.926	-0.106	0.860
LRRC32	11	0.125	0.040	1.6391	1
STAT6	12	48.3	45.6	0.08	0.737
ANKRD27	19	12.38	12.23	0.018	0.939
NOVA1	14	0.58	0.94	-0.698	0.610

Supplementary Table 5: Pathway analysis of differentially expressed genes from the transcriptome sequencing of EoE and control esophageal epithelial cells. Direction: indicates whether the term was enriched in genes whose expression was increased in cases vs controls (☐) or decreased in cases vs controls (☐). Category: GOTERM is a GO Biological process terms and SP_PIR refers to Protein Information Resource (PIR) Keywords. Gene count: number of genes in the differentially expressed list that mapped to the term. Benjamini: FDR corrected P-value. *P* values derived from a Fisher-exact test of the target gene list compared to the genome background

Direction	Category	Term	Gene count	P-value	Benjamini
↑	GOTERM_BP_FAT	epidermis development	23	9.80×10^{-12}	1.50×10^{-8}
↑	GOTERM_BP_FAT	ectoderm development	23	4.70×10^{-11}	3.60×10^{-8}
↑	SP_PIR_KEYWORDS	glycoprotein	126	3.10×10^{-10}	1.20×10^{-7}
↑	SP_PIR_KEYWORDS	signal	103	4.10×10^{-10}	7.60×10^{-8}
↑	GOTERM_BP_FAT	epithelial cell differentiation	16	7.10×10^{-8}	3.60×10^{-5}
↑	SP_PIR_KEYWORDS	protease inhibitor	13	3.50×10^{-7}	4.30×10^{-5}
↑	GOTERM_BP_FAT	epidermal cell differentiation	11	1.20×10^{-6}	4.80×10^{-4}
↑	SP_PIR_KEYWORDS	Serine protease inhibitor	11	1.20×10^{-6}	1.10×10^{-4}
↑	GOTERM_MF_FAT	serine-type endopeptidase inhibitor activity	12	1.30×10^{-6}	6.00×10^{-4}
↑	GOTERM_BP_FAT	epithelium development	18	2.30×10^{-6}	6.90×10^{-4}
↑	GOTERM_CC_FAT	cornified envelope	7	2.70×10^{-6}	7.00×10^{-4}
↑	GOTERM_MF_FAT	endopeptidase inhibitor activity	14	3.70×10^{-6}	8.90×10^{-4}
↑	GOTERM_BP_FAT	keratinocyte differentiation	10	5.00×10^{-6}	1.30×10^{-3}
↑	GOTERM_MF_FAT	peptidase inhibitor activity	14	6.70×10^{-6}	1.10×10^{-3}
↑	GOTERM_BP_FAT	peptide cross-linking	7	8.70×10^{-6}	1.90×10^{-3}
↑	SP_PIR_KEYWORDS	Secreted	54	1.70×10^{-5}	1.30×10^{-3}
↑	SP_PIR_KEYWORDS	polymorphism	238	1.80×10^{-5}	1.10×10^{-3}

↑	GOTERM_CC_FAT	apical plasma membrane	12	4.90×10^{-5}	6.50×10^{-3}
↑	GOTERM_MF_FAT	enzyme inhibitor activity	17	5.70×10^{-5}	6.90×10^{-3}
↑	SP_PIR_KEYWORDS	disulfide bond	78	8.80×10^{-5}	4.60×10^{-3}
↑	SP_PIR_KEYWORDS	Ichthyosis	6	1.50×10^{-4}	7.00×10^{-3}
↑	GOTERM_CC_FAT	apical part of cell	13	1.70×10^{-4}	1.50×10^{-2}
↑	GOTERM_CC_FAT	extracellular region	61	2.20×10^{-4}	1.40×10^{-2}
↑	GOTERM_MF_FAT	protein binding, bridging	9	4.10×10^{-4}	3.80×10^{-2}
↑	GOTERM_MF_FAT	structural molecule activity	26	4.30×10^{-4}	3.40×10^{-2}
↑	GOTERM_CC_FAT	plasma membrane part	64	4.80×10^{-4}	2.50×10^{-2}
↑	SP_PIR_KEYWORDS	keratinization	6	6.10×10^{-4}	2.50×10^{-2}
↑	GOTERM_MF_FAT	serine-type endopeptidase activity	11	7.00×10^{-4}	4.70×10^{-2}
↑	SP_PIR_KEYWORDS	ectodermal dysplasia	5	7.20×10^{-4}	2.60×10^{-2}
↑	SP_PIR_KEYWORDS	membrane	137	9.20×10^{-4}	3.00×10^{-2}
↑	GOTERM_CC_FAT	plasma membrane	96	1.10×10^{-3}	4.80×10^{-2}
↑	SP_PIR_KEYWORDS	cell adhesion	18	1.20×10^{-3}	3.60×10^{-2}
↑	SP_PIR_KEYWORDS	disease mutation	45	1.40×10^{-3}	4.00×10^{-2}
↑	SP_PIR_KEYWORDS	calcium	27	1.80×10^{-3}	4.60×10^{-2}
↓	GOTERM_BP_FAT	M phase	34	2.30×10^{-26}	2.80×10^{-23}
↓	GOTERM_BP_FAT	cell cycle phase	36	1.90×10^{-25}	1.10×10^{-22}
↓	GOTERM_BP_FAT	nuclear division	29	3.10×10^{-25}	1.20×10^{-22}
↓	GOTERM_BP_FAT	mitosis	29	3.10×10^{-25}	1.20×10^{-22}
↓	GOTERM_BP_FAT	M phase of mitotic cell cycle	29	5.10×10^{-25}	1.50×10^{-22}
↓	GOTERM_BP_FAT	organelle fission	29	9.60×10^{-25}	2.30×10^{-22}
↓	GOTERM_BP_FAT	mitotic cell cycle	34	1.00×10^{-24}	2.10×10^{-22}
↓	SP_PIR_KEYWORDS	mitosis	25	1.10×10^{-23}	2.40×10^{-21}
↓	GOTERM_BP_FAT	cell cycle process	37	5.40×10^{-22}	9.20×10^{-20}

↓	SP_PIR_KEYWORDS	cell cycle	32	1.30×10^{-21}	1.50×10^{-19}
↓	SP_PIR_KEYWORDS	cell division	26	4.20×10^{-21}	3.10×10^{-19}
↓	GOTERM_BP_FAT	cell cycle	40	3.30×10^{-20}	4.90×10^{-18}
↓	GOTERM_CC_FAT	spindle	21	6.30×10^{-19}	1.10×10^{-16}
↓	GOTERM_BP_FAT	cell division	24	5.40×10^{-16}	7.40×10^{-14}
↓	GOTERM_CC_FAT	microtubule cytoskeleton	29	8.50×10^{-15}	7.50×10^{-13}
↓	GOTERM_CC_FAT	chromosome, centromeric region	16	1.30×10^{-13}	7.50×10^{-12}
↓	GOTERM_CC_FAT	cytoskeletal part	34	1.30×10^{-12}	5.60×10^{-11}
↓	GOTERM_CC_FAT	condensed chromosome, centromeric region	12	7.50×10^{-12}	2.70×10^{-10}
↓	GOTERM_BP_FAT	microtubule-based process	18	5.50×10^{-11}	6.60×10^{-9}
↓	GOTERM_CC_FAT	condensed chromosome	14	6.30×10^{-11}	1.90×10^{-9}
↓	GOTERM_BP_FAT	chromosome segregation	12	9.20×10^{-11}	1.00×10^{-8}
↓	SP_PIR_KEYWORDS	cytoskeleton	24	1.50×10^{-10}	8.70×10^{-9}
↓	SP_PIR_KEYWORDS	centromere	9	2.30×10^{-10}	1.10×10^{-8}
↓	SP_PIR_KEYWORDS	kinetochore	10	6.60×10^{-10}	2.50×10^{-8}
↓	GOTERM_CC_FAT	condensed chromosome kinetochore	10	1.30×10^{-9}	3.30×10^{-8}
↓	GOTERM_CC_FAT	cytoskeleton	36	1.40×10^{-9}	3.20×10^{-8}
↓	GOTERM_CC_FAT	kinetochore	10	1.70×10^{-8}	3.40×10^{-7}
↓	GOTERM_BP_FAT	regulation of cell cycle	17	2.50×10^{-8}	2.50×10^{-6}
↓	SP_PIR_KEYWORDS	phosphoprotein	85	2.90×10^{-8}	9.40×10^{-7}
↓	GOTERM_BP_FAT	spindle organization	8	1.00×10^{-7}	9.60×10^{-6}
↓	GOTERM_CC_FAT	chromosomal part	17	1.60×10^{-7}	2.90×10^{-6}
↓	GOTERM_CC_FAT	chromosome	18	3.30×10^{-7}	5.30×10^{-6}

↓	GOTERM_BP_FAT	microtubule cytoskeleton organization	11	5.60×10^{-7}	4.80×10^{-5}
↓	GOTERM_BP_FAT	regulation of mitotic cell cycle	11	7.60×10^{-7}	6.10×10^{-5}
↓	GOTERM_BP_FAT	cytoskeleton organization	17	1.00×10^{-6}	7.80×10^{-5}
↓	GOTERM_CC_FAT	non-membrane-bounded organelle	45	1.20×10^{-6}	1.80×10^{-5}
↓	GOTERM_CC_FAT	intracellular non-membrane-bounded organelle	45	1.20×10^{-6}	1.80×10^{-5}
↓	GOTERM_BP_FAT	organelle localization	9	1.30×10^{-6}	8.80×10^{-5}
↓	SP_PIR_KEYWORDS	cytoplasm	48	1.50×10^{-6}	4.10×10^{-5}
↓	GOTERM_BP_FAT	mitotic cell cycle checkpoint	7	1.70×10^{-6}	1.20×10^{-4}
↓	GOTERM_MF_FAT	microtubule motor activity	8	2.30×10^{-6}	6.10×10^{-4}
↓	GOTERM_BP_FAT	spindle checkpoint	5	2.50×10^{-6}	1.60×10^{-4}
↓	GOTERM_CC_FAT	microtubule	13	3.70×10^{-6}	5.00×10^{-5}
↓	GOTERM_CC_FAT	spindle microtubule	6	4.10×10^{-6}	5.30×10^{-5}
↓	GOTERM_BP_FAT	microtubule-based movement	9	5.90×10^{-6}	3.50×10^{-4}
↓	GOTERM_BP_FAT	regulation of cell cycle process	9	6.30×10^{-6}	3.60×10^{-4}
↓	SP_PIR_KEYWORDS	microtubule	11	6.60×10^{-6}	1.70×10^{-4}
↓	GOTERM_BP_FAT	establishment of chromosome localization	5	6.70×10^{-6}	3.70×10^{-4}
↓	GOTERM_BP_FAT	chromosome localization	5	6.70×10^{-6}	3.70×10^{-4}
↓	GOTERM_CC_FAT	spindle pole	6	9.40×10^{-6}	1.10×10^{-4}
↓	GOTERM_BP_FAT	cell cycle checkpoint	8	1.30×10^{-5}	7.00×10^{-4}

↓	GOTERM_CC_FAT	midbody	5	1.40×10^{-5}	1.60×10^{-4}
↓	GOTERM_BP_FAT	mitotic sister chromatid segregation	6	1.40×10^{-5}	6.80×10^{-4}
↓	GOTERM_BP_FAT	sister chromatid segregation	6	1.60×10^{-5}	7.40×10^{-4}
↓	GOTERM_BP_FAT	establishment of organelle localization	7	2.80×10^{-5}	1.30×10^{-3}
↓	GOTERM_BP_FAT	regulation of mitotic metaphase/anaphase transition	5	3.40×10^{-5}	1.50×10^{-3}
↓	SP_PIR_KEYWORDS	motor protein	8	4.70×10^{-5}	1.10×10^{-3}
↓	GOTERM_CC_FAT	outer kinetochore of condensed chromosome	4	4.90×10^{-5}	5.10×10^{-4}
↓	GOTERM_CC_FAT	microtubule organizing center	11	5.90×10^{-5}	5.80×10^{-4}
↓	SP_PIR_KEYWORDS	Chromosome partition	5	6.90×10^{-5}	1.40×10^{-3}
↓	SP_PIR_KEYWORDS	chromosomal protein	8	8.50×10^{-5}	1.60×10^{-3}
↓	SP_PIR_KEYWORDS	ubl conjugation	15	8.70×10^{-5}	1.50×10^{-3}
↓	GOTERM_BP_FAT	negative regulation of mitotic metaphase/anaphase transition	4	9.90×10^{-5}	4.20×10^{-3}
↓	GOTERM_BP_FAT	mitotic cell cycle spindle assembly checkpoint	4	9.90×10^{-5}	4.20×10^{-3}
↓	GOTERM_BP_FAT	cell proliferation	14	1.00×10^{-4}	4.10×10^{-3}
↓	GOTERM_CC_FAT	centrosome	10	1.20×10^{-4}	1.20×10^{-3}
↓	GOTERM_BP_FAT	negative regulation of mitosis	4	1.30×10^{-4}	5.20×10^{-3}

↓	GOTERM_BP_FAT	negative regulation of nuclear division	4	1.30×10^{-4}	5.20×10^{-3}
↓	GOTERM_MF_FAT	motor activity	8	1.30×10^{-4}	1.70×10^{-2}
↓	GOTERM_CC_FAT	chromosome passenger complex	3	2.10×10^{-4}	1.90×10^{-3}
↓	GOTERM_CC_FAT	microtubule associated complex	7	2.30×10^{-4}	2.00×10^{-3}
↓	GOTERM_BP_FAT	mitotic spindle organization	4	2.70×10^{-4}	1.00×10^{-2}
↓	SP_PIR_KEYWORDS	extracellular matrix	9	3.50×10^{-4}	5.70×10^{-3}
↓	SP_PIR_KEYWORDS	polymorphism	103	4.30×10^{-4}	6.50×10^{-3}
↓	GOTERM_BP_FAT	negative regulation of organelle organization	6	7.10×10^{-4}	2.60×10^{-2}
↓	SP_PIR_KEYWORDS	metalloprotease	7	7.80×10^{-4}	1.10×10^{-2}
↓	GOTERM_BP_FAT	phosphoinositide-mediated signaling	6	9.80×10^{-4}	3.50×10^{-2}
↓	GOTERM_BP_FAT	centromere complex assembly	3	1.10×10^{-3}	3.80×10^{-2}
↓	SP_PIR_KEYWORDS	heparin-binding	5	1.20×10^{-3}	1.60×10^{-2}
↓	GOTERM_BP_FAT	negative regulation of cell cycle process	4	1.30×10^{-3}	4.20×10^{-2}
↓	GOTERM_BP_FAT	regulation of mitosis	5	1.40×10^{-3}	4.50×10^{-2}
↓	GOTERM_BP_FAT	regulation of nuclear division	5	1.40×10^{-3}	4.50×10^{-2}
↓	GOTERM_BP_FAT	G2 phase of mitotic cell cycle	3	1.50×10^{-3}	4.80×10^{-2}
↓	GOTERM_BP_FAT	G2 phase	3	1.50×10^{-3}	4.80×10^{-2}