

Appendix A Significant enriched biological processes by gene ontology analysis based on the Fst

Term	Input number	Background number	<i>P</i> -value	Corrected <i>P</i> -value
Neuroactive ligand-receptor interaction	20	267	1.19E-06	1.95E-05
Focal adhesion	13	187	0.000175	0.001498
Adrenergic signaling in cardiomyocytes	10	123	0.000305	0.002375
TGF-beta signaling pathway	8	79	0.000314	0.002436
Calcium signaling pathway	11	161	0.00062	0.004435
Melanogenesis	8	90	0.000701	0.004939
Oocyte meiosis	8	92	0.000801	0.00557
FoxO signaling pathway	9	127	0.001496	0.009168
GnRH signaling pathway	7	81	0.00174	0.010337
Ribosome biogenesis in eukaryotes	6	66	0.002907	0.016165
Cell cycle	8	115	0.003003	0.016575
Endocytosis	12	238	0.004102	0.021415
Ubiquitin mediated proteolysis	8	125	0.004827	0.024367
ECM-receptor interaction	6	74	0.004905	0.024596
Purine metabolism	9	154	0.005041	0.025067
Regulation of actin cytoskeleton	10	185	0.005369	0.026414
VEGF signaling pathway	5	57	0.007381	0.034244
Cytokine-cytokine receptor interaction	9	171	0.009427	0.041179
Cardiac muscle contraction	5	62	0.010176	0.042479
AGE-RAGE signaling pathway in diabetic complications	6	89	0.011115	0.045511
Insulin signaling pathway	7	121	0.013343	0.050782
Porphyrin and chlorophyll metabolism	3	24	0.015502	0.056127
Adherens junction	5	70	0.016027	0.057362

Homologous recombination	3	26	0.018816	0.0635
Progesterone-mediated oocyte maturation	5	77	0.022695	0.07239
Influenza A	7	138	0.024648	0.077077
Gap junction	5	81	0.027206	0.081796
Base excision repair	3	31	0.028684	0.085539
Non-homologous end-joining	2	12	0.029939	0.087641
Tight junction	6	122	0.040793	0.109294
Ribosome	6	123	0.042106	0.112477
RNA degradation	4	67	0.050983	0.129758
Salmonella infection	4	68	0.053181	0.131516
Metabolic pathways	30	1092	0.054954	0.135291
Vascular smooth muscle contraction	5	103	0.061844	0.14824
Mismatch repair	2	21	0.074199	0.169115
Sphingolipid metabolism	3	47	0.074905	0.170197
ErbB signaling pathway	4	80	0.083437	0.184327
Protein processing in endoplasmic reticulum	6	149	0.08564	0.186717
Dorso-ventral axis formation	2	23	0.085785	0.186717
Herpes simplex infection	6	150	0.087677	0.190252
Oxidative phosphorylation	5	117	0.092739	0.198766
Toll-like receptor signaling pathway	4	87	0.104237	0.215204

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Appendix B Sample and sequencing data quality control

Tissue	Sample	Raw data		Valid data		Q20%	Q30%	GC content (%)	Mapped reads(Mb)	Mapping ratio (%)
		Read (Mb)	Base (Gb)	Read (Mb)	Base (Gb)					
Splen	P010303	48.40	7.26	46.66	6.25	98.08%	94.29%	49.01%	43.38	92.97%
Splen	P020113	45.39	6.81	43.34	5.77	98.00%	94.12%	49.34%	39.95	92.17%
Splen	P020211	51.49	7.72	48.63	6.49	97.85%	93.79%	50.07%	44.50	91.50%
Splen	P060308	45.09	6.76	42.78	5.69	98.04%	94.19%	49.49%	39.47	92.26%
Splen	P090219	46.03	6.90	44.24	5.88	98.10%	94.31%	49.36%	41.13	92.95%
Splen	P100314	50.66	7.60	48.85	6.55	98.17%	94.49%	48.68%	45.57	93.30%
Splen	P120316	50.61	7.59	49.18	6.58	97.96%	93.97%	50.31%	44.77	91.03%
Splen	P120320	51.24	7.69	48.97	6.56	97.94%	93.96%	48.93%	45.33	92.57%
Splen	P120323	49.37	7.41	47.29	6.31	98.08%	94.29%	48.78%	43.83	92.68%
Splen	P220110	53.23	7.98	50.56	6.71	98.09%	94.39%	49.35%	46.56	92.10%
Splen	P220113	46.94	7.04	44.01	5.87	97.81%	93.75%	49.59%	40.38	91.75%
Splen	P230115	33.93	5.09	29.46	3.94	97.15%	92.44%	50.52%	26.58	90.23%
Splen	P230119	47.45	7.12	44.07	5.88	97.91%	94.00%	49.48%	40.13	91.06%
Splen	P230211	47.25	7.09	44.29	5.89	97.97%	94.08%	49.54%	40.71	91.91%
Splen	P230212	54.26	8.14	51.70	6.89	97.93%	93.93%	48.88%	47.75	92.36%
Splen	P230314	45.60	6.84	42.69	5.72	97.86%	93.86%	50.81%	38.22	89.52%
Splen	P230320	56.66	8.50	53.81	7.19	98.03%	94.25%	49.30%	49.35	91.70%