

Table 1: SRA reads used in the study				
Sr. No.	Species	Sample Accession	SRA Accession	Library Type
1	<i>Pavo muticus</i>	SAMN17255116	SRR13424288	Genomic
2	<i>Pavo muticus</i>	SAMN17255114	SRR13424290	Genomic
3	<i>Pavo muticus</i>	SAMN15488465	SRR12223809	Genomic
4	<i>Pavo muticus</i>	SAMN15488464	SRR12223810	Genomic
5	<i>Pavo muticus</i>	SAMN15488463	SRR12223811	Genomic
6	<i>Pavo muticus</i>	SAMN15488455	SRR12223821	Genomic
7	<i>Pavo cristatus</i>	SAMN05660020	SRR4068854	Genomic
8	<i>Pavo cristatus</i>	SAMN03322586	SRR1797848	Transcriptomic
9	<i>Pavo cristatus</i>	SAMN03322585	SRR1797865	Transcriptomic
10	<i>Pavo cristatus</i>	SAMN03322587	SRR1797860	Transcriptomic
11	<i>Pavo cristatus</i>	SAMN03322588	SRR1797873	Transcriptomic

<b>Table2: Summary statistics of acoustic measurements.</b>			
<b>Pavo cristatus (N=23)</b>	<b>Mean</b>	<b>SD</b>	<b>Range (Min-Max)</b>
<b>Call Period (sec)</b>	0.653	0.072	0.520-0.769
<b>Fundamental Frequency (Hz)</b>	756.394	66.393	602.93-843.75
<b>Dominant Frequency (Hz)</b>	1488.663	122.945	1205.859-1687.5
<b>Pavo muticus (N=20)</b>			
<b>Call Period (sec)</b>	0.908	0.195	0.512-1.251
<b>Fundamental Frequency (Hz)</b>	551.25	70.696	516.797-689.062
<b>Dominant Frequency (Hz)</b>	1111.114	111.431	947.461-1378.125

Table 3: Acoustic measurements used in the study.						
Sr. No.	ID	Call period	Fundamental frequency	Dominant Frequency	Species	Location
1	PCMH	0.7690	843.75	1593.75	<i>P. cristatus</i>	Maharashtra
2	PCMH	0.6941	843.75	1593.75	<i>P. cristatus</i>	Maharashtra
3	PCMH	0.7000	843.75	1593.75	<i>P. cristatus</i>	Maharashtra
4	PCMH	0.7560	843.75	1687.5	<i>P. cristatus</i>	Maharashtra
5	PCMH	0.7552	843.75	1500	<i>P. cristatus</i>	Maharashtra
6	PCMY	0.6281	775.195	1550.391	<i>P. cristatus</i>	Mysore
7	PCMY	0.5319	775.195	1550.391	<i>P. cristatus</i>	Mysore
8	PCMY	0.5458	775.195	1636.523	<i>P. cristatus</i>	Mysore
9	PCMY	0.5926	775.195	1636.523	<i>P. cristatus</i>	Mysore
10	PCMY	0.6547	775.195	1636.523	<i>P. cristatus</i>	Mysore
11	PCRJ	0.6546	775.195	1464.258	<i>P. cristatus</i>	Rajasthan
12	PCRJ	0.6369	775.195	1550.391	<i>P. cristatus</i>	Rajasthan
13	PCRJ	0.6748	775.195	1464.258	<i>P. cristatus</i>	Rajasthan
14	PCRJ	0.7012	775.195	1464.258	<i>P. cristatus</i>	Rajasthan
15	PCTN	0.5614	689.062	1378.125	<i>P. cristatus</i>	Tamilnadu
16	PCTN	0.6615	689.062	1378.125	<i>P. cristatus</i>	Tamilnadu
17	PCTN	0.6655	689.062	1378.125	<i>P. cristatus</i>	Tamilnadu
18	PCTN	0.7076	689.062	1378.125	<i>P. cristatus</i>	Tamilnadu
19	PCTN	0.6628	689.062	1464.258	<i>P. cristatus</i>	Tamilnadu
20	PCUK	0.5633	775.195	1464.258	<i>P. cristatus</i>	Uttarakhand
21	PCUK	0.6575	689.062	1291.992	<i>P. cristatus</i>	Uttarakhand
22	PCUK	0.7207	602.93	1205.859	<i>P. cristatus</i>	Uttarakhand
23	PCUK	0.5197	689.062	1378.125	<i>P. cristatus</i>	Uttarakhand
24	PMCB1	0.5956	516.797	1205.859	<i>P. muticus</i>	Combodia
25	PMCB1	0.5121	516.797	1119.727	<i>P. muticus</i>	Combodia
26	PMCB1	0.6964	516.797	1033.594	<i>P. muticus</i>	Combodia
27	PMCB1	0.8908	516.797	1119.727	<i>P. muticus</i>	Combodia
28	PMCB2	0.8722	516.797	1119.727	<i>P. muticus</i>	Combodia
29	PMCB2	0.8431	516.797	1033.594	<i>P. muticus</i>	Combodia
30	PMCB2	0.7921	516.797	947.461	<i>P. muticus</i>	Combodia
31	PMCB2	0.8552	516.797	1033.594	<i>P. muticus</i>	Combodia
32	PMIN	0.8600	516.797	1119.727	<i>P. muticus</i>	Indonesia
33	PMIN	0.9058	516.797	1033.594	<i>P. muticus</i>	Indonesia
34	PMIN	0.8009	516.797	1119.727	<i>P. muticus</i>	Indonesia
35	PMTH1	0.8276	516.797	1033.594	<i>P. muticus</i>	Thailand
36	PMTH1	0.9271	516.797	1033.594	<i>P. muticus</i>	Thailand
37	PMTH3	1.0518	516.797	1119.727	<i>P. muticus</i>	Thailand
38	PMTH3	1.0212	516.797	1033.594	<i>P. muticus</i>	Thailand

39	PMTH3	0.9230	516.797	1033.594	<i>P. muticus</i>	Thailand
40	PMVI	1.1252	689.062	1205.859	<i>P. muticus</i>	Vietnam
41	PMVI	1.2508	689.062	1119.727	<i>P. muticus</i>	Vietnam
42	PMVI	1.2275	689.062	1378.125	<i>P. muticus</i>	Vietnam
43	PMVI	1.1857	689.062	1378.125	<i>P. muticus</i>	Vietnam

Table 4: Amino acid changes across KEGG signalling pathways.				
<b>1. Hedgehog</b>				
Sr No	Gene	position	<i>P. muticus</i>	<i>P. cristatus</i>
1	EFCAB7	407	L	S
2	HHAT	205	R	Q
3	KIF7	695	L	S
	KIF7	1292	T	A
4	MGRN1	504	T	S
<b>2. Melanogenesis</b>				
1	CREB3	339	A	T
2	PLCB1	908	L	S
<b>3. TGF-beta</b>				
1	RBL1	211	F	L
	RBL1	507	L	S
2	THBS1	797	N	S
3	ZFYVE16	31	A	T
	ZFYVE16	282	C	Y
	ZFYVE16	335	S	F
	ZFYVE16	599	Q	E
<b>4. Wnt</b>				
1	APC	277	G	A
	APC	877	P	A
	APC	909	M	T
	APC	1216	P	Q
	APC	1309	D	H
2	GPC4	556	V	M
3	INVS	828	I	R
4	PLCB1	908	L	S
5	ROR2	149	H	Y
<b>5. Notch</b>				
1	DLL1	573	I	V
2	DLL4	385	I	V
<b>6. Extracellular matrix interaction</b>				
1	AGRN	786	G	S
2	COL4A2	362	V	L
3	GP1BB	142	A	T
	GP1BB	179	A	T
4	HSPG2	966	R	H

5	ITGB1	12	V	I
6	LAMA4	435	H	R
7	LAMA5	686	M	T
	LAMA5	1728	V	I
	LAMA5	1814	A	G
	LAMA5	3225	W	R
	LAMA5	3450	I	V
	LAMA5	3560	T	M
8	LAMC1	272	A	S
	LAMC1	1075	V	I
	LAMC1	1208	G	D
9	SDC1	180	P	L
10	THBS1	797	N	S
11	VWF	652	G	S
<b>7. Actin cytoskeleton</b>				
1	ACTN1	851	E	D
2	ACTN4	850	E	D
3	APC	277	G	A
	APC	877	P	A
	APC	909	M	T
	APC	1216	P	Q
	APC	1309	D	H
5	ITGB1	12	V	I
6	MYLK	920	G	V
7	NCKAP1L	579	I	V
8	SSH2	1218	C	G
9	SSH3	409	Q	R
10	VCL	534	M	L
<b>8. Focal adhesion</b>				
1	KDR	1336	V	A
2	MYLK	920	G	V
3	VEGFC	265	T	A
4	ZYX	289	V	A
5	ITGB1	12	V	I
6	VCL	534	M	L
7	ACTN1	851	E	D
8	ACTN4	850	E	D
9	VWF	652	G	S
10	THBS1	797	N	S

<b>11</b>	LAMA4	435	H	R
<b>12</b>	LAMA5	686	M	T
	LAMA5	1728	V	I
	LAMA5	1814	A	G
	LAMA5	3225	W	R
	LAMA5	3450	I	V
	LAMA5	3560	T	M
<b>13</b>	LAMC1	272	A	S
	LAMC1	1075	V	I
	LAMC1	1208	G	D
<b>14</b>	COL4A2	362	V	L

**Table 5: The genes showing amino acid differences between *Pavo cristatus* and *Pavo muticus*.**

Sr. No.	Gene	amino acid #	<i>P. muticus</i>	<i>P. cristatus</i>		
<b>1</b>	AASDH	26	N	S		
	AASDH	279	V	A		
	AASDH	661	S	N		
<b>2</b>	ABCC10	13	P	L		
	ABCC10	372	L	F		
	ABCC10	948	I	T		
	ABCC10	1004	P	L		
<b>3</b>	AKAP9	878	V	M		
	AKAP9	1156	E	A		
	AKAP9	1733	G	R		
	AKAP9	2711	I	V		
	AKAP9	3093	T	S		
<b>4</b>	ALMS1	214	R	G		
	ALMS1	1168	V	L		
	ALMS1	2290	I	R		
<b>5</b>	AMOTL1	831	T	I		
<b>6</b>	ANAPC1	1900	V	M		
<b>7</b>	ANK2	2422	Y	F		
	ANK2	2591	I	M		
	ANK2	2631	G	S		
<b>8</b>	APC	289	G	A		
	APC	954	M	T		
	APC	1261	P	Q		
	APC	1354	D	H		
<b>9</b>	ARID1B	798	T	A		
<b>10</b>	BBS12	81	T	I		
	BBS12	431	T	A		
	BBS12	464	K	R		
	BBS12	557	E	A		
	BBS12	656	D	G		
<b>11</b>	BICC1	665	A	T		
<b>12</b>	BMP2K	790	S	G		
	BMP2K	799	L	I		
	BMP2K	1043	I	M		
<b>13</b>	BOD1L1	1285	S	N		
	BOD1L1	1402	E	K		
	BOD1L1	1702	G	E		
	BOD1L1	2324	T	A		
<b>14</b>	BRAT1	574	M	V		



	BRAT1	585	I	V		
	BRAT1	645	T	A		
	BRAT1	746	G	D		
	BRAT1	748	H	Q		
<b>15</b>	BRCA1	317	Q	R		
	BRCA1	319	S	G		
	BRCA1	812	I	M		
	BRCA1	1571	I	V		
<b>16</b>	BRCA2	694	N	S		
	BRCA2	1081	S	N		
	BRCA2	1870	I	S		
	BRCA2	1974	H	Q		
	BRCA2	2834	V	I		
	BRCA2	3305	L	P		
<b>17</b>	C1orf21	75	S	P		
<b>18</b>	C1R	161	Q	R		
<b>19</b>	C8orf48	21	W	R		
	C8orf48	48	R	H		
	C8orf48	198	R	Q		
<b>20</b>	CCP110	608	R	Q		
	CCP110	984	S	R		
<b>21</b>	CDK5RAP2	338	A	V		
	CDK5RAP2	586	V	I		
	CDK5RAP2	2005	G	S		
	CDK5RAP2	2059	N	D		
<b>22</b>	CENPE	782	T	S		
	CENPE	1598	D	N		
	CENPE	1851	T	A		
	CENPE	1951	N	T		
	CENPE	2015	F	Y		
	CENPE	2084	M	I		
<b>23</b>	CENPF	1267	H	L		
<b>24</b>	CEP164	1550	D	E		
<b>25</b>	CGGBP1	79	I	V		
<b>26</b>	CKAP2L	383	M	T		
<b>27</b>	CMYA5	677	S	C		
	CMYA5	3014	E	Q		
<b>28</b>	COBLL1	361	Y	H		
	COBLL1	424	R	C		
<b>29</b>	COL15A1	282	I	T		
<b>30</b>	CPED1	376	V	I		

<b>31</b>	CRYBG3	405	Q	H		
	CRYBG3	597	H	D		
	CRYBG3	898	I	T		
	CRYBG3	907	M	K		
	CRYBG3	1427	K	E		
	CRYBG3	1505	S	N		
<b>32</b>	CSPG4B	2491	R	S		
<b>33</b>	CUL9	925	M	L		
	CUL9	1968	N	S		
	CUL9	1970	P	S		
	CUL9	2010	T	A		
<b>34</b>	DACH2	290	A	T		
<b>35</b>	DYNC2H1	1079	Q	R		
	DYNC2H1	3505	T	I		
<b>36</b>	EP400	1815	S	T		
<b>37</b>	FAM214B	14	H	R		
	FAM214B	390	S	A		
	FAM217B	483	T	A		
<b>38</b>	GCC1	128	G	A		
<b>39</b>	GCC2	291	M	V		
	GCC2	781	D	N		
	GCC2	1437	S	G		
	GCC2	1492	A	T		
	GCC2	1497	V	L		
	GCC2	1500	S	N		
<b>40</b>	GLTSCR1L	960	I	T		
<b>41</b>	GSAP	292	A	T		
<b>42</b>	HABP4	98	E	Q		
	HABP4	100	D	E		
	HABP4	155	R	H		
<b>43</b>	HELQ	577	K	E		
<b>44</b>	HMCN1	1851	V	I		
	HMCN1	2030	I	V		
	HMCN1	2244	S	L		
	HMCN1	2307	A	T		
	HMCN1	3456	G	S		
	HMCN1	4582	R	C		
	HMCN1	4948	N	S		
	HMCN1	5315	S	A		
<b>45</b>	IGF2R	753	V	I		
	IGF2R	920	R	Q		

	IGF2R	1878	L	F		
<b>46</b>	KAT6B	1348	E	Q		
<b>47</b>	KCTD20	57	N	S		
<b>48</b>	KDELC2	80	I	T		
<b>49</b>	KIF7	695	L	S		
	KIF7	1293	T	A		
<b>50</b>	KMT2A	2242	V	G		
	KMT2A	2722	A	V		
	KMT2A	3306	A	T		
<b>51</b>	LACTB2	276	C	R		
<b>52</b>	LOC101750635	797	V	A		
<b>53</b>	LTBP1	309	G	S		
<b>54</b>	LTK	436	T	I		
<b>55</b>	MBTPS1	124	M	T		
	MBTPS1	672	M	V		
<b>56</b>	METTL2B	133	M	T		
<b>57</b>	MKI67	190	A	E		
	MKI67	428	V	A		
	MKI67	847	N	S		
	MKI67	1045	G	D		
	MKI67	1542	G	E		
	MKI67	1868	N	S		
	MKI67	1934	I	M		
<b>58</b>	MXRA5	897	V	L		
	MXRA5	1435	P	R		
	MXRA5	1495	A	V		
	MXRA5	2560	Q	R		
<b>59</b>	NBAS	286	Y	S		
	NBAS	1135	V	I		
<b>60</b>	NBEAL1	1451	N	D		
	NBEAL1	2224	Y	H		
<b>61</b>	NBR1	327	I	V		
	NRP2	846	L	S		
<b>62</b>	PALB2	95	R	G		
<b>63</b>	PCNT	379	V	I		
	PCNT	460	N	D		
	PCNT	931	V	M		
	PCNT	1054	I	V		
	PCNT	1935	F	L		
	PCNT	2028	K	R		
	PCNT	2584	R	C		

<b>64</b>	PDZD2	1523	T	M		
	PDZD2	1662	T	A		
	PDZD2	1735	V	L		
<b>65</b>	PHYKPL	372	I	V		
<b>66</b>	RALB	51	R	S		
<b>67</b>	RNF213	1199	I	V		
	RNF213	3024	V	I		
	RNF213	4420	S	G		
<b>68</b>	RNF217	353	S	T		
<b>69</b>	RTEL1	921	T	A		
<b>70</b>	RUFY3	536	R	W		
	RUFY3	569	D	G		
<b>71</b>	SECISBP2	227	L	S		
	SECISBP2	271	S	L		
	SECISBP2	440	F	I		
	SECISBP2	455	R	W		
	SECISBP2	881	K	E		
<b>72</b>	SH3TC2	258	E	V		
<b>73</b>	SIK1	511	S	T		
<b>74</b>	SIK2	298	I	V		
	SIK2	528	V	M		
<b>75</b>	SIMC1	692	V	A		
<b>76</b>	SLC44A5	586	D	E		
<b>77</b>	SLF2	428	D	N		
	SLF2	434	E	K		
	SLF2	442	A	D		
	SLF2	452	S	N		
	SLF2	901	Q	R		
<b>78</b>	SMS	75	S	N		
	SMS	77	S	N		
<b>79</b>	SON	851	I	T		
	SON	1186	M	V		
	SON	1302	K	M		
	SON	1355	T	A		
	SON	1469	I	V		
<b>80</b>	SPICE1	304	A	T		
	SPICE1	376	C	S		
	SPICE1	752	V	A		
	SPICE1	788	R	T		
	SPICE1	859	T	I		
<b>81</b>	STON1	44	H	P		

	STON1	191	N	S		
	STON1	267	W	R		
<b>82</b>	TDRD3	561	Q	H		
	TDRD3	589	H	N		
<b>83</b>	TET2	149	C	R		
	TET2	234	A	T		
	TET2	605	H	Q		
	TET2	791	Q	H		
<b>84</b>	TGS1	178	V	I		
	TGS1	284	M	V		
	TGS1	298	L	P		
	TGS1	300	T	A		
	TGS1	310	P	L		
	TGS1	329	D	H		
	TGS1	335	V	I		
	TGS1	607	T	I		
<b>85</b>	TJP3	387	E	D		
	TJP3	547	L	M		
	TJP3	556	H	R		
<b>86</b>	TMEM14C	68	V	I		
<b>87</b>	TMEM38B	73	E	A		
<b>88</b>	TRAF6	45	L	P		
<b>89</b>	UACA	282	E	D		
	UACA	658	S	F		
<b>90</b>	UIMC1	667	V	D		
<b>91</b>	USP47	175	A	S		
<b>92</b>	USPL1	521	R	Q		
<b>93</b>	VCPIP1	760	T	A		
<b>94</b>	VPS13B	2051	F	I		
	VPS13B	2386	S	T		
<b>95</b>	YAE1D1	173	G	S		
	YAE1D1	178	D	G		
	YAE1D1	181	G	R		
<b>96</b>	ZBTB21	287	R	K		
	ZBTB21	429	T	S		
<b>97</b>	ZNF318	172	L	P		
	ZNF318	672	L	P		
	ZNF318	689	I	V		
	ZNF318	1863	S	P		
<b>98</b>	ZNF407	223	K	R		
	ZNF407	498	H	L		

	ZNF407	711	I	V		
	ZNF407	991	C	S		
	ZNF407	1103	T	A		
<b>99</b>	ZNF410	163	A	T		
<b>100</b>	ZNF462	410	T	A		
<b>101</b>	ZNF648	253	A	T		
<b>Melanogenesis related genes</b>						
<b>Sr. No.</b>	<b>Gene</b>	<b>amino acid #</b>	<b><i>P. muticus</i></b>	<b><i>P. cristatus</i></b>		
<b>1</b>	LOC416959	478	R	H		
	LOC416959	735	V	I		
<b>2</b>	MELTF	179	S	N		
<b>3</b>	KIF14	71	C	F		
	KIF14	1409	H	R		
<b>4</b>	KIF18A	524	R	H		
<b>5</b>	KIF4B	616	N	S		
	KIF4B	751	N	S		
<b>6</b>	KIF27	566	D	N		
<b>7</b>	KIF11	846	Q	R		
	KIF11	1188	E	D		
<b>8</b>	KIF9	393	V	L		
	KIF9	502	F	L		
<b>9</b>	KIF13A	1612	G	S		
	KIF21A	585	R	K		
	KIF21A	1608	M	V		
<b>10</b>	KIF7	695	L	S		
	KIF7	1293	T	A		
<b>11</b>	KIF26B	583	V	L		
<b>12</b>	DYNC2H1	1079	Q	R		
	DYNC2H1	3505	T	I		
<b>13</b>	DYNC1LI1	157	N	S		
<b>14</b>	DNAAF1	55	C	G		
<b>15</b>	DNAAF5	744	A	T		
	DNAAF5	827	Q	R		
<b>16</b>	DRC3	515	T	I		
<b>17</b>	DYNC2LI1	178	T	I		
<b>18</b>	HPGDS	37	V	A		
<b>19</b>	PLCB1	908	L	S		
<b>20</b>	CREB3L4	339	A	T		
<b>Chr Z genes</b>						

<b>1</b>	ADAMTS12	1257	V	L		
<b>2</b>	AGGF1	111	V	A		
<b>3</b>	ANKRD31	394	C	S		
	ANKRD31	1354	N	S		
	ANKRD31	1449	H	R		
<b>4</b>	AOPEP	370	L	P		
<b>5</b>	APC	289	G	A		
	APC	954	M	T		
	APC	1261	P	Q		
	APC	1354	D	H		
<b>6</b>	ARSB	450	M	T		
<b>7</b>	BDP1	871	S	A		
	BDP1	1389	S	P		
	BDP1	2029	D	E		
	BDP1	2098	T	I		
<b>8</b>	C6	192	R	C		
	C6	231	L	S		
	C6	711	H	R		
<b>9</b>	CCDC112	263	E	K		
<b>10</b>	CCDC125	116	T	I		
<b>11</b>	CCDC171	919	N	S		
	CCDC171	1157	S	R		
<b>12</b>	CEP120	450	A	V		
	CEP120	830	E	Q		
<b>13</b>	CEP78	373	L	V		
	CEP78	382	I	L		
<b>14</b>	CMYA5	677	S	C		
	CMYA5	3014	E	Q		
<b>15</b>	CNTLN	256	T	A		
	CNTLN	725	R	C		
	CNTLN	943	T	I		
<b>16</b>	CPLANE1	2982	M	V		
<b>17</b>	CR1	1793	L	P		
	CR1	2509	Y	H		
	CR1	2869	V	I		
	CR1	3223	V	I		
<b>18</b>	CREB3L4	339	A	T		
<b>19</b>	CSPG4B	2491	R	S		
<b>20</b>	DGKQ	679	I	V		
<b>21</b>	DIMT1	118	V	A		
<b>22</b>	DOCK8	1959	Q	R		

<b>23</b>	EPG5	2021	G	D		
<b>24</b>	ERCC6L2	192	R	C		
	ERCC6L2	231	L	S		
	ERCC6L2	711	H	R		
<b>25</b>	FAM214B	14	H	R		
	FAM214B	390	S	A		
<b>26</b>	FBN2	419	D	G		
<b>27</b>	FYB1	435	I	V		
	FYB1	739	P	S		
<b>28</b>	GAK	803	H	R		
	GAK	1051	G	D		
<b>29</b>	GFM2	160	T	A		
<b>30</b>	GRAMD3	405	T	I		
<b>31</b>	GRHPR	318	E	K		
<b>32</b>	HABP4	98	E	Q		
	HABP4	100	D	E		
	HABP4	155	R	H		
<b>33</b>	HAUS1	47	F	I		
<b>34</b>	HAUS6	98	E	K		
	HAUS6	258	H	R		
	HAUS6	361	E	K		
<b>35</b>	IDNK	129	I	V		
<b>36</b>	IKBKAP	648	S	N		
<b>37</b>	IL6ST	14	A	V		
	IL6ST	379	S	T		
<b>38</b>	KANK1	1052	P	A		
<b>39</b>	KIAA0368	209	S	T		
<b>40</b>	KIAA2026	1279	T	A		
	KIAA2026	1879	T	A		
	KIAA2026	1961	V	M		
<b>41</b>	KIF27	566	D	N		
<b>42</b>	LIFR	101	A	T		
<b>43</b>	LNPEP	567	M	T		
	LNPEP	1013	T	I		
<b>44</b>	LOC112530730	48	R	Q		
	LOC112530730	60	N	D		
<b>41</b>	LOC112530732	48	R	Q		
	LOC112530732	60	N	D		
<b>42</b>	LOC112530763	60	R	Q		
	LOC112530763	63	G	R		
<b>43</b>	LOC407092	158	N	S		



<b>44</b>	MAP1B	1038	Y	C		
<b>45</b>	MOCS2	66	I	M		
<b>46</b>	MPDZ	1043	R	P		
	MPDZ	1070	S	P		
	MPDZ	1937	A	G		
<b>47</b>	MTMR12	656	I	M		
	MTMR12	686	N	S		
<b>48</b>	NANS	141	P	L		
<b>49</b>	NOL6	308	N	S		
<b>50</b>	NUDT12	181	L	H		
	NUDT12	189	S	N		
<b>51</b>	PALM2AKAP2	591	N	D		
	PALM2AKAP2	724	S	N		
<b>52</b>	PDZD2	1523	T	M		
	PDZD2	1662	T	A		
	PDZD2	1735	V	L		
<b>53</b>	PIGG	463	S	C		
	PIGG	621	S	R		
<b>54</b>	PLAA	767	F	V		
<b>55</b>	POC5	240	H	R		
<b>56</b>	POLK	15	S	*		
<b>57</b>	PTAR1	362	R	H		
	PTAR1	434	D	G		
<b>58</b>	PUM3	137	M	V		
	PUM3	600	R	Q		
<b>59</b>	RIOK2	404	L	V		
<b>60</b>	RLN3	160	S	T		
<b>67</b>	RMI1	396	R	Q		
	RMI1	441	I	S		
<b>68</b>	ROR2	149	H	Y		
<b>69</b>	RUSC2	565	T	A		
	RUSC2	807	S	N		
<b>70</b>	SECISBP2	227	L	S		
	SECISBP2	271	S	L		
	SECISBP2	440	F	I		
	SECISBP2	455	R	W		
	SECISBP2	881	K	E		
<b>71</b>	SHLD3	226	I	L		
<b>72</b>	SLC24A2	23	G	D		
<b>73</b>	SLC25A51	93	G	R		
<b>74</b>	SLC44A1	264	Q	R		

<b>75</b>	SLF1	643	M	V		
<b>76</b>	SLF2	428	D	N		
	SLF2	434	E	K		
	SLF2	442	A	D		
	SLF2	452	S	N		
	SLF2	901	Q	R		
<b>77</b>	SNCAIP	849	M	L		
	SNCAIP	939	V	I		
<b>78</b>	SUSD1	233	V	I		
	SUSD1	278	Q	H		
<b>79</b>	SYK	10	S	N		
<b>80</b>	TAF1C	263	R	C		
<b>81</b>	TBC1D2	96	S	Y		
<b>82</b>	TMC1	17	A	P		
	TMC1	912	P	L		
<b>83</b>	TMEM38B	73	E	A		
<b>84</b>	TMEM8B	463	H	R		
<b>85</b>	TRIM36	559	S	T		
	TRIM36	662	S	A		
<b>86</b>	TTC33	197	E	Q		
<b>87</b>	UBQLN1	125	S	T		
<b>88</b>	VPS13A	2044	S	G		
	VPS13A	2404	E	G		
<b>89</b>	WDR36	733	T	A		
<b>90</b>	WDR41	419	A	V		
<b>91</b>	ZBTB5	175	I	M		
<b>92</b>	ZCCHC6	668	C	Y		
	ZCCHC6	673	T	K		
<b>93</b>	ZDHHC21	48	V	L		
<b>94</b>	ZFYVE16	31	A	T		
	ZFYVE16	282	C	Y		
	ZFYVE16	335	S	F		
	ZFYVE16	599	Q	E		
<b>95</b>	ZNF462	410	T	A		

: Previously published divergence time estimates between <i>Pavo cristatus</i> and <i>Pavo muticus</i> .					
Sr. No.	Title	Author	Journal	Year	Split time (MYA)
1	Resolution of the Phylogenetic Position of the Congo Peafowl, <i>Afropavo congensis</i> : A Biogeographic and Evolutionary Enigma	Kimball et al.	Proc R Soc B	1997	
	cytochrome b - 4.2 mya				4.2
	D-loop - 6.2 mya				6.2
2	The global diversity of birds in space and time	Jetz et al.	Nature	2012	
	nuclear + mitochondrial markers tree - 1.5 Mya				1.5
3	A molecular genetic time scale demonstrates Cretaceous origins and multiple diversification rate shifts within the order Galliformes (Aves)	Stein et al.	MPE	2015	2.27
	nuclear + mitochondrial markers tree				
4	Genetic Divergence between <i>Pavo muticus</i> and <i>Pavo cristatus</i>	Ouyang, Y. N., et al.	Journal of Yunnan	2009	2.96
	by Cyt b gene.		Agricultural University		
	Cyt b				
5	A Phylogenomic Supertree of Birds	Kimball et al.	Diversity	2019	3.17
	WGS+UCE supertree				
6	Ancestral range reconstruction of Galliformes: the effects of topology and taxon sampling	Wang et al.	Journal of Biogeography	2016	2.58
	nuclear + mitochondrial markers tree				
7	Divergence time estimation of Galliformes based on the best gene shopping scheme of ultraconserved elements	Chen et al.	BMC Ecology and Evolution	2021	3.12
	UCE				
8	this study (UCE)				2.02
9	this study (PSMC)				1.1